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6-Hydrazinylnicotinic acid: a powder study

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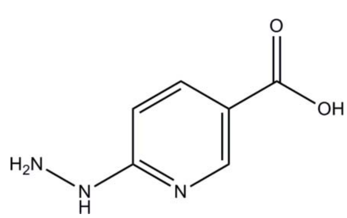
Key indicators: powder X-ray study; T = 298 K; mean σ(C–C) = 0.013 Å; R factor = 0.000; wR factor = 0.000; data-to-parameter ratio = 0.0.

The structure of the title compound, $C_6H_7N_3O_2$, is of interest with respect to radiopharmacueticals. The crystal packing is characterized by N—H···O and O—H···N hydrogen bonds, which form a three-dimensional network. The molecule is planar except for one of the amine H atoms.

Related literature

For background on radiopharmacueticals, see: Callahan *et al.* (1996); Rennen *et al.* (2000). For general background, see: Abrams *et al.* (1990). For details of the synthesis, see: Schwartz *et al.* (1995). For geometric data, see: Allen *et al.* (1987). For descriptions of the powder diffraction profile, see: Thompson *et al.* (1987); Finger *et al.* (1994); Stephens (1999); Von Dreele (1997). For refinement by the LeBail method, see: Le Bail *et al.* (1988).



Experimental

Crystal data

$C_6H_7N_3O_2$
M_r = 153.15
Monoclinic, $P2_1/c$
a = 6.69930 (14) Å
b = 13.8834 (2) Å
c = 7.10677 (9) Å
β = 91.7805 (11)°
V = 660.67 (2) Å^3
Z = 4
Cu $K\alpha_1$ radiation
λ = 1.5406 Å
μ = 1.01 mm^{-1}
T = 298 K
Flat sheet, 8 × 8 mm

Data collection

Stoe STADI P diffractometer
Specimen mounting: powder loaded between two Mylar foils
Data collection mode: transmission
Scan method: step
Absorption correction: for a cylinder mounted on the φ axis [flat-plate transmission absorption correction (*GSAS* absorption/surface roughness correction function number 4 with a non-refined term of μd = 0.1482)]
T_{min} = 0.732, T_{max} = 0.795
$2\theta_{min}$ = 9.969°, $2\theta_{max}$ = 84.949°, $2\theta_{step}$ = 0.02°

Refinement

R_p = 0.023
R_{wp} = 0.030
R_{exp} = 0.021
$R(F^2)$ = 0.01796
χ^2 = 2.016
4250 data points
146 parameters
26 restraints
Only H-atom coordinates refined

Table 1
Hydrogen-bond geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
N2—H1N2···O1^{i}	0.89 (3)	1.94 (2)	2.792 (8)	158 (4)
N3—H1N3···O2^{ii}	0.87 (3)	2.39 (4)	2.967 (10)	124 (6)
N3—H2N3···O1^{iii}	0.87 (3)	2.23 (6)	2.950 (11)	141 (5)
O2—H1O2···N1^{iv}	0.822 (15)	1.818 (16)	2.622 (10)	165.2 (18)

Symmetry codes: (i) $-x, y+\frac{1}{2}, -z+\frac{3}{2}$; (ii) $-x+1, y+\frac{1}{2}, -z+\frac{3}{2}$; (iii) $x+1, -y+\frac{1}{2}, z+\frac{1}{2}$; (iv) $-x, y-\frac{1}{2}, -z+\frac{3}{2}$.

Data collection: *WinXPOW* (Stoe & Cie, 1999); cell refinement: *FULLPROF* (Rodriguez-Carvajal, 2001) and *GSAS* (Larson & Von Dreele, 2004); data reduction: *WinXPOW*, *DICVOL04* (Boultif & Louër, 2004), and *CheckGroup* interfaced by *WinPLOTR* (Roisnel & Rodriguez-Carvajal, 2001); program(s) used to solve structure: *EXPO2009* (Altomare *et al.*, 2009); program(s) used to refine structure: *GSAS* interfaced by *EXPGUI* (Toby, 2001); molecular graphics: *ORTEP-3* (Farrugia, 1997); software used to prepare material for publication: *publCIF* (Westrip, 2010).

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: FY2040).

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supplementary materials

Acta Cryst. (2012). E**68**, o783–o784 [doi:10.1107/S160053681200637X]

6-Hydrazinylnicotinic acid: a powder study

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Comment

6-Hydrazinylnicotinic acid (I) introduced by Abrams *et al.*, (1990), functions as a bifunctional chelating agent, forming a bridge between biomolecules and technetium (Callahan *et al.*, 1996; Rennen *et al.*, 2000). The (I) conjugated molecules react as monodentate ligands. Compound (I) is often used to synthesize bioconjugates for radiolabelling with ^{99m}Tc and it is capable of efficient capture of technetium at extremely low concentrations. Compound (I) has a tendency to crystallize in the form of very fine pale yellow powder. Since no single-crystal of sufficient thickness and quality could be obtained, a structure determination by powder X-ray diffraction data was attempted. An *ORTEP* (Farrugia, 1997) view of compound (I) with atomic labeling is shown in Fig. 1. Bond lengths and angles in compound (I) are in their normal ranges (Allen *et al.*, 1987). The crystal packing is characterized by intermolecular hydrogen bonds involving the hydroxyl H atom and the amine H atom (Table 1).The hydrogen bonds form a three dimensional network (Fig. 2).

Experimental

The synthesis of 6-hydrazinylnicotinic acid (I) was achieved according to the reported method (Schwartz *et al.*, 1995). 6-Chloronicotinic acid (8.0 g) was added to 35 ml of 85% hydrazine hydrate. The reaction mixture was heated at 373 K for 4 h. The homogeneous reaction mixture was concentrated to dryness to give a white solid. This solid was dissolved in water and on acidification to pH 5.5 with concentrated hydrochloric acid a precipitate formed. The precipitate was filtered and the solid was washed with 95% ethanol and ether to give 4.52 g of a pale brown solid (I); yield 58%.

^{1}H and ^{13}C{1H} NMR spectra were recorded in DMSO-D6 on a Bruker Biospin 400 spectrometer. IR spectrum was recorded on a Jasco FT–IR 300E instrument.

Spectroscopic data for (I): ^{1}H NMR (DMSO-D6): δ 6.71 (*d*, 1H, py, J = 8.8 Hz),7.86 (*dd*, 1H, py, J = 2.4, 8.8 Hz), 8.52 (*d*, 1H, py, J = 2 Hz); ^{13}C NMR (DMSO-D6) δ: 105.2 (py), 114.9 (py), 138.1 (py), 151.1 (py), 164 (py), 167.2 (CO); IR (KBr, v, cm^{-1}): 3309, 3231 (NH_2).

Refinement

For pattern indexing, the extraction of the peak positions was carried out with the program *WinPLOTR* (Roisnel & Rodriguez-Carvajal, 2001). Pattern indexing was performed with the program *DicVol4.0* (Boultif & Louër, 2004). The first 20 lines of powder pattern were completely indexed on the basis of monoclinic system. The absolute error on each observed line was fixed at 0.02° (2θ). The figures of merit are sufficiently high to support the obtained indexing results [$M(20)$ = 40.2, F(20) = 62.6(0.0045, 71)]. The whole powder diffraction pattern from 10 to 95° (2θ) was subsequently refined with cell and resolution constraints (Le Bail *et al.*, 1988) with a space group without systematic extinctions in monoclinic system, $P2/m$, using the `profile matching' option of the program *FullProf* (Rodriguez-Carvajal, 2001). The best estimated space group in the monoclinic system was $P2_1/c$ which determined with the help of the program *Check Group* interfaced by *WinPLOTR* (Roisnel & Rodriguez-Carvajal, 2001). The number of molecules per unit cell was estimated to be equal to $Z = 4$, it can be concluded that the number of molecules in the asymmetric unit is $Z' = 1$ for the space group $P2_1/c$.

The structure was solved *ab initio* by direct methods using the program *EXPO2009* (Altomare *et al.*, 2009). The model found by this program was introduced in the program *GSAS* (Larson & Von Dreele, 2004) implemented in *EXPGUI* (Toby, 2001) for Rietveld refinements. During the Rietveld refinements, the effect of the asymmetry of low-order peaks was corrected using a pseudo-Voigt description of the peak shape (Thompson *et al.*, 1987) which allows for angle-dependent asymmetry with axial divergence (Finger *et al.*, 1994). The two asymmetry parameters of this function *S/L* and *D/L* were both fixed at 0.0225 during the Rietveld refinement. An excluded region from 85 to 95° (2θ) was used, which leads to better molecular geometry.

Non-H atoms were not restrained, but several restraints on bonds lengths and angles were applied to H atoms (see below). A planar group restraints to the aromatic ring and the carboxyl group, including their H atoms were also applied.

The H atoms of the NH, NH_2, OH groups were located in a difference map. The aromatic H atoms were positioned in their idealized geometries using a riding model with C—H = 0.99 Å. The coordinates of these H atoms restrained to the distances N—H = 0.89 (1) Å, N—H_2 = 0.87 (1) Å, O—H = 0.82 (1) Å and C—H = 0.99 (1) Å. All H atoms were refined with isotropic displacement parameters (set to 1.2 times of the U_{eq} of the parent atom for aromatic H atoms and to 1.5 times of the U_{eq} of the parent atom for NH, NH_2, OH groups).

Intensities were corrected from absorption effects with a $\mu.d$ value of 0.148. A spherical harmonics correction (Von Dreele, 1997) of intensities for preferred orientation was applied in the final refinement with 12 coefficients. The use of the preferred orientation correction leads to better molecular geometry with better agreement factors. The final Rietveld agreement factors are $R_p = 0.023$, $R_{wp} = 0.030$ $R_{exp} = 0.022$, $\chi^2 = 1.904$, and $R_F^2 = 0.02438$. The final Rietveld plot of the X-ray diffraction pattern is given in Fig. 3.

Computing details

Data collection: WinXPOW (Stoe & Cie, 1999); cell refinement: FULLPROF (Rodriguez-Carvajal, 2001) and *GSAS* (Larson & Von Dreele, 2004); data reduction: WinXPOW (Stoe & Cie, 1999), DICVOL04 (Boultif & Louër, 2004), and CheckGroup interfaced by WinPLOTR (Roisnel & Rodriguez-Carvajal, 2001); program(s) used to solve structure: EXPO2009 (Altomare *et al.*, 2009); program(s) used to refine structure: *GSAS* (Larson & Von Dreele, 2004) interfaced by EXPGUI (Toby, 2001); molecular graphics: *ORTEP-3* (Farrugia, 1997); software used to prepare material for publication: *publCIF* (Westrip, 2010).

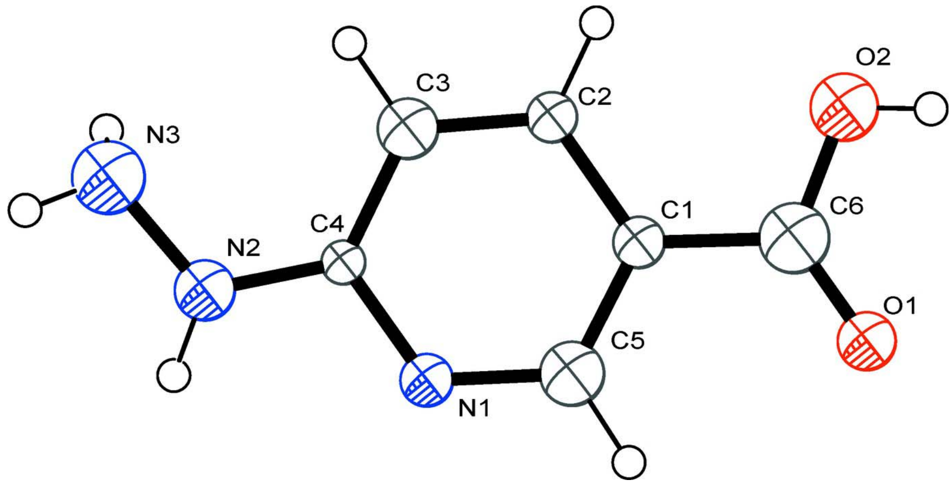

Figure 1

The molecule structure of (I), showing the atom numbering. Displacement ellipsoids are drown at the 50% probability level and H atoms are shown as small spheres of arbitrary radii.

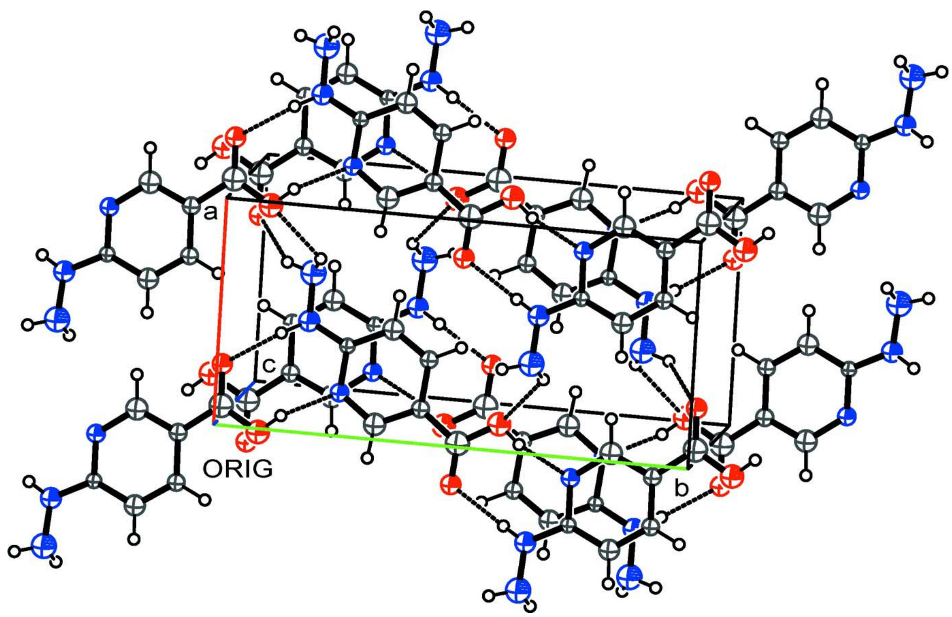

Figure 2

View of crystal packing of compound (I). Hydrogen bonds are shown as dashed lines.

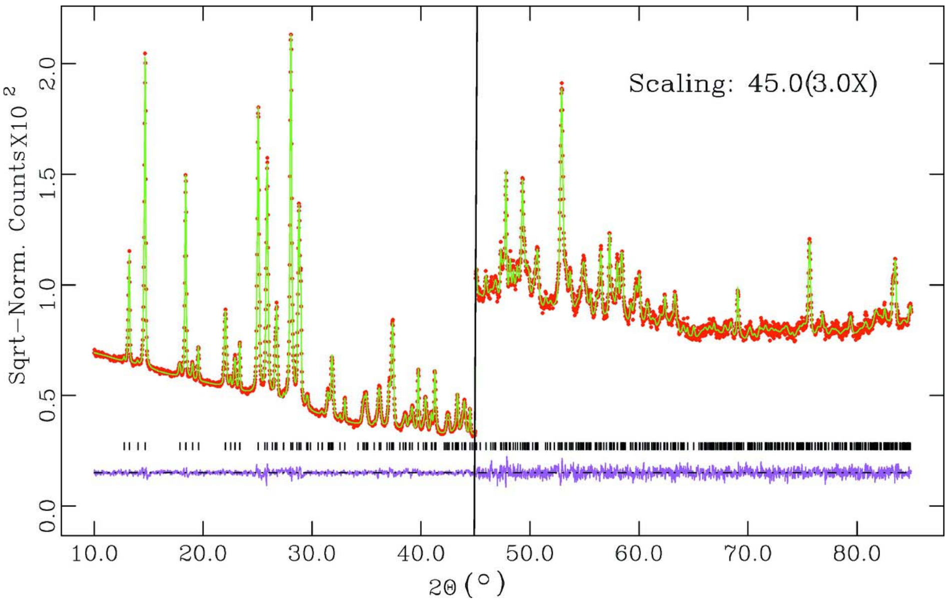

Figure 3

Final Rietveld plot of compound (I). Observed data points are indicated by dots, the best-fit profile (upper trace) and the difference pattern (lower trace) are solid lines. The vertical bars indicate the positions of Bragg peaks.

6-Hydrazinylpyridine-3-carboxylic acid

Crystal data

$C_6H_7N_3O_2$
M_r = 153.15
Monoclinic, $P2_1/c$
Hall symbol: -P 2ybc
a = 6.69930 (14) Å
b = 13.8834 (2) Å
c = 7.10677 (9) Å
β = 91.7805 (11)°
V = 660.67 (2) Å^3
Z = 4
$F(000)$ = 320
D_x = 1.54 Mg m^{-3}
Cu $K\alpha_1$ radiation, λ = 1.5406 Å
μ = 1.01 mm^{-1}
T = 298 K
Particle morphology: Fine powder
pale brown
flat sheet, 8 × 8 mm
Specimen preparation: Prepared at 298 K and 101.3 kPa

Data collection

Stoe STADI P diffractometer
Radiation source: sealed X-ray tube
Curved Ge(111) monochromator
Specimen mounting: powder loaded between two Mylar foils
Data collection mode: transmission
Scan method: step
Absorption correction: for a cylinder mounted on the φ axis [Flat-plate transmission absorption correction (*GSAS* absorption/surface roughness correction function number 4 with a non-refined term of μd = 0.1482)]
T_{min} = 0.732, T_{max} = 0.795
$2\theta_{min}$ = 9.969°, $2\theta_{max}$ = 84.949°, $2\theta_{step}$ = 0.02°

Refinement

Least-squares matrix: full
R_p = 0.023
R_{wp} = 0.030
R_{exp} = 0.021
$R(F^2)$ = 0.01796
χ^2 = 2.016
4250 data points
Excluded region(s): The use of the excluded region from 85 to 95° (2θ) leads to better molecular geometry.

Profile function: GSAS CW profile function number 4 with 21 terms, i.e., pseudovoigt profile coefficients as parameterized in (Thompson *et al.*, 1987), asymmetry correction of Finger *et al.* (1994) and microstrain broadening by Stephens (1999). #1(GU) = 0.000 #2(GV) = 0.000 #3(GW) = 8.378 #4(GP) = 0.000 #5(LX) = 1.698 #6(ptec) = 0.00 #7(trns) = 0.00 #8(shft) = 0.0000 #9(sfec) = 0.00 #10(S/L) = 0.0225 #11(H/L) = 0.0228 #12(eta) = 0.6000 #13(S400) = 2.2E-01 #14(S040) = 3.7E-03 #15(S004) = 4.3E-01 #16(S220) = 3.8E-02 #17(S202) = 2.3E-01 #18(S022) = 5.1E-01 #19(S301) = -2.6E-01 #20(S103) = 1.6E-01 #21(S121) = -1.9E-01. Peak tails are ignored where the intensity is below 0.0010 times the peak. Aniso. broadening axis 0.0 0.0 1.0

146 parameters

26 restraints

Primary atom site location: structure-invariant direct methods

Secondary atom site location: difference Fourier map

Hydrogen site location: difference Fourier map

Only H-atom coordinates refined

$(\Delta/\sigma)_{max} = 0.03$

Background function: Shifted Chebyshev function of 1st kind (GSAS Background function number 1) with 15 terms 1: 1800.66 2: -1847.80 3: 941.880 4: -249.680 5: 12.6164 6: 58.5368 7: -22.4573 8: -39.9081 9: 32.2315 10: 0.665645 11: -20.8095 12: 16.0647 13: -6.68008 14: -5.95330 15: 5.95798

Preferred orientation correction: spherical hamonics function

Special details

Experimental. The sample was ground lightly in a mortar, loaded between two Mylar foils and fixed in the sample holder with a mask of 8.0 mm internal diameter.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å²)

	x	*y*	*z*	U_{iso}*/U_{eq}
C1	0.0949 (15)	0.0911 (6)	0.7824 (15)	0.025 (3)*
C2	0.3019 (11)	0.0838 (5)	0.8434 (12)	0.024 (3)*
C3	0.4127 (11)	0.1653 (6)	0.8763 (12)	0.035 (4)*
C4	0.3286 (12)	0.2568 (6)	0.8428 (14)	0.018 (3)*
C5	0.0146 (12)	0.1829 (7)	0.7521 (12)	0.039 (5)*
C6	−0.035 (2)	0.0069 (9)	0.7503 (17)	0.047 (4)*
N1	0.1331 (11)	0.2628 (5)	0.7828 (11)	0.026 (3)*
N2	0.4164 (12)	0.3424 (4)	0.8716 (12)	0.034 (3)*
N3	0.6139 (10)	0.3455 (6)	0.9453 (13)	0.050 (3)*
O1	−0.2097 (8)	0.0126 (4)	0.7110 (10)	0.032 (3)*
O2	0.0600 (8)	−0.0758 (5)	0.7824 (11)	0.043 (3)*
H2	0.362 (2)	0.0198 (11)	0.869 (3)	0.029 (4)*
H3	0.554 (3)	0.1597 (10)	0.917 (3)	0.042 (4)*
H5	−0.127 (3)	0.1905 (12)	0.707 (3)	0.047 (5)*
H1N2	0.364 (4)	0.3948 (12)	0.816 (6)	0.052 (4)*
H1N3	0.696 (2)	0.325 (5)	0.861 (5)	0.075 (5)*
H2N3	0.644 (4)	0.4040 (17)	0.977 (10)	0.075 (5)*
H1O2	−0.018 (3)	−0.1211 (10)	0.768 (4)	0.065 (4)*

Geometric parameters (Å, º)

C1—C2	1.444 (10)	C6—C1	1.471 (15)
C2—C3	1.369 (9)	C6—O1	1.198 (12)
C2—H2	0.990 (14)	C6—O2	1.328 (11)
C3—C4	1.407 (10)	N2—C4	1.339 (7)
C3—H3	0.981 (14)	N2—N3	1.409 (7)

C4—N1	1.367 (9)	N2—H1N2	0.89 (3)
N1—C5	1.378 (9)	N3—H1N3	0.87 (3)
C5—C1	1.397 (12)	N3—H2N3	0.87 (3)
C5—H5	0.997 (14)	O2—H1O2	0.824 (14)
C2—C1—C5	118.2 (7)	C1—C5—H5	120.3 (13)
C2—C1—C6	123.3 (9)	N1—C5—H5	120.2 (13)
C5—C1—C6	118.6 (9)	C1—C6—O1	123.5 (12)
C1—C2—C3	120.3 (6)	C1—C6—O2	112.5 (10)
C1—C2—H2	119.9 (6)	O1—C6—O2	123.8 (13)
C3—C2—H2	119.7 (6)	C4—N1—C5	122.8 (8)
C2—C3—C4	120.3 (7)	C4—N2—N3	119.2 (7)
C2—C3—H3	119.8 (6)	C4—N2—H1N2	119 (2)
C4—C3—H3	119.8 (6)	N3—N2—H1N2	119.4 (18)
C3—C4—N1	118.9 (7)	N2—N3—H1N3	110 (2)
C3—C4—N2	127.1 (8)	N2—N3—H2N3	110 (2)
N1—C4—N2	113.9 (8)	H1N3—N3—H2N3	110 (5)
C1—C5—N1	119.5 (6)	C6—O2—H1O2	109.9 (15)
C4—N1—C5—C1	−0.1 (13)	C5—C1—C2—C3	2.2 (14)
C5—N1—C4—N2	−177.5 (8)	C2—C1—C6—O2	−0.5 (15)
C5—N1—C4—C3	−0.5 (13)	C5—C1—C6—O1	−4.9 (17)
N3—N2—C4—N1	175.9 (8)	C2—C1—C6—O1	175.2 (10)
N3—N2—C4—C3	−0.8 (15)	C5—C1—C6—O2	179.4 (9)
C2—C1—C5—N1	−0.7 (13)	C1—C2—C3—C4	−2.9 (13)
C6—C1—C5—N1	179.5 (9)	C2—C3—C4—N2	178.6 (9)
C6—C1—C2—C3	−178.0 (10)	C2—C3—C4—N1	2.1 (13)

Hydrogen-bond geometry (Å, º)

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N2—H1*N*2···O1^{i}	0.89 (3)	1.94 (2)	2.792 (8)	158 (4)
N3—H1*N*3···O2^{ii}	0.87 (3)	2.39 (4)	2.967 (10)	124 (6)
N3—H2*N*3···O1^{iii}	0.87 (3)	2.23 (6)	2.950 (11)	141 (5)
O2—H1*O*2···N1^{iv}	0.822 (15)	1.818 (16)	2.622 (10)	165.2 (18)

Symmetry codes: (i) −*x*, *y*+1/2, −*z*+3/2; (ii) −*x*+1, *y*+1/2, −*z*+3/2; (iii) *x*+1, −*y*+1/2, *z*+1/2; (iv) −*x*, *y*−1/2, −*z*+3/2.