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(*S*)-5-Benzylimidazolidine-2,4-dione monohydrate

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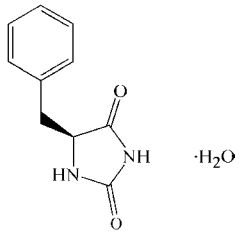
The crystal structure of the title compound, $C_{10}H_{10}N_2O_2\cdot H_2O$, also known as L-5-benzylhydantoin monohydrate, is described in terms of two-dimensional supramolecular arrays built up from infinite chains assembled *via* N—H···O and O—H···O hydrogen bonds among the organic molecules and solvent water molecules, with graph-set $R_3^3(10)C(5)C_2^2(6)$. The hydrogen-bond network is reinforced by stacking of the layers through C—H···π interactions.

Comment

Imidazolidine-2,4-dione, or hydantoin, is a five-membered heterocyclic ring containing a reactive cyclic urea nucleus. This heterocycle represents a significant molecular template in combinatorial chemistry libraries (Boeijen *et al.*, 1998; Park *et al.*, 2001), principally because of the four possible substitution points. Solid-phase syntheses including hydantoin as a starting building block have been reported recently (Ganesan, 2003; Vázquez *et al.*, 2004; Alsina *et al.*, 2005). Hydantoin derivatives have attracted much interest in drug innovation because of their wide range of therapeutic properties (Mutschler & Derendorf, 1995). In particular, the hydantoins substituted at the 5-position have been found to be valuable precursors of a great variety of heterocyclic systems that are associated with a wide range of biological activities, including antiarrhythmic (Knabe *et al.*, 1997), anticonvulsant (Singh *et al.*, 2005) and antitumoral agents (Carmi *et al.*, 2006). The best known hydantoin is 5,5-diphenylhydantoin, or phenytoin, which has been the most widely used anti-epileptic drug since the experimental determination of its anticonvulsant properties (Putnam & Merrit, 1937). In addition, they are known for their uses as herbicides (Shiozaki, 2002) and fungicides (Marton *et al.*, 1993). On the other hand, the biocatalytic conversion of 5-subtituted hydantoins and the related *N*-carbamoyl compounds to amino acids has recently received considerable attention for their potential applications in the industrial production of optically pure amino acids, through an enantioselective enzymatic reaction (Wilms *et al.*, 2001; Chen *et al.*, 2003; Burton & Dorrington, 2004).

Continuing our studies on *N*-carbamoyl amino acids and hydantoin compounds (Seijas *et al.*, 2006, 2007), in this work we report the crystal structure of the title compound, (I), a new 5-subtituted hydantoin derivative.



(I)

The asymmetric unit of (I) consists of one L-5-benzylhydantoin molecule and a solvent water molecule. The dihedral angle between the hydantoin and benzene rings is 55.6 (3)°. The organic molecule adopts a *gauche* conformation (Fig. 1). The hydantoin ring is essentially planar, with maximum deviations of 0.024 (4) Å for C4 and −0.023 (4) Å for C5. The N1—C2—O2 angle is greater than the N3—C2—O2 angle (Table 1). This difference is also observed in the hydantoin molecule (Yu *et al.*, 2004) and 50 other hydantoin derivatives reported in the Cambridge Structural Database (Version 5.28; Allen, 2002) with both NH groups unsubstituted and sp^3-hybridization at C5.

The structure of (I) is built up from the self-assembly of the hydantoin molecules with solvent water molecules *via* hydrogen-bonding interactions. The water molecule is involved as a donor and an acceptor of hydrogen bonds. Molecules of (I) form four conventional hydrogen bonds. The

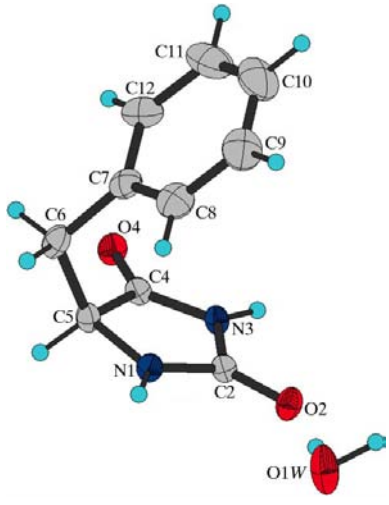


Figure 1
A view of (I), showing the atomic numbering scheme. Displacement ellipsoids are drawn at the 20% probability level and H atoms are shown as spheres of arbitrary radii.

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N3—H3···O1W(x + 1, y, z) and O1W—H1W···O4(x − 1, y − 1, z) interactions form infinite chains, which run along the b axis. These chains may be described in graph-set notation as $C_2^2(6)$ (Bernstein *et al.*, 1995) (Fig. 2). Adjacent chains are linked laterally by O1W—H2W···O2(x, y, z) and N1—H1···O4(x − 1, y − 1, z) hydrogen bonds, forming infinite chains parallel to the a axis, with graph-set motifs $C_2^2(6)$ and $C(5)$, respectively (Fig. 2). Together, these hydrogen-bond patterns produce a two-dimensional array parallel to the ab plane with graph set $R_3^3(10)$ and the formation of a 15-atom macrocycle (Fig. 2). This graph set is also observed in the hydantoin compounds ROKSOZ (Gauthier *et al.* 1997) and SINZEU (Galdecki & Karolak-Wojciechowska, 1986). Details of the hydrogen-bonding geometry are given in Table 2. Layers join pairwise by C—H···π interactions (Fig. 3). The C10—H10 group of the benzene ring is oriented towards the face of the aromatic ring of a neighboring molecule [C10—H10···Cg($-x$ + 1, y − $\frac{1}{2}$, $-z$ + 1) = 3.13 (3) Å; Cg is the centroid of the C7–C12 ring]. This interaction generates a herring-bone-like array in the bc plane (Fig. 3).

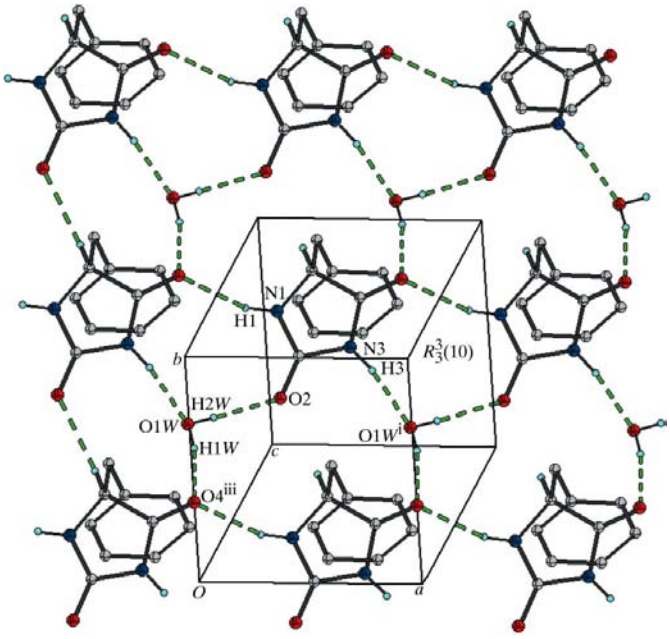

Figure 2
A partial packing view of (I). Hydrogen bonds are shown as dashed lines. H atoms not involved in hydrogen bonding have been omitted for clarity. [Symmetry codes: (i) x + 1, y, z; (ii) x − 1, y, z; (iii) x − 1, y − 1, z.]

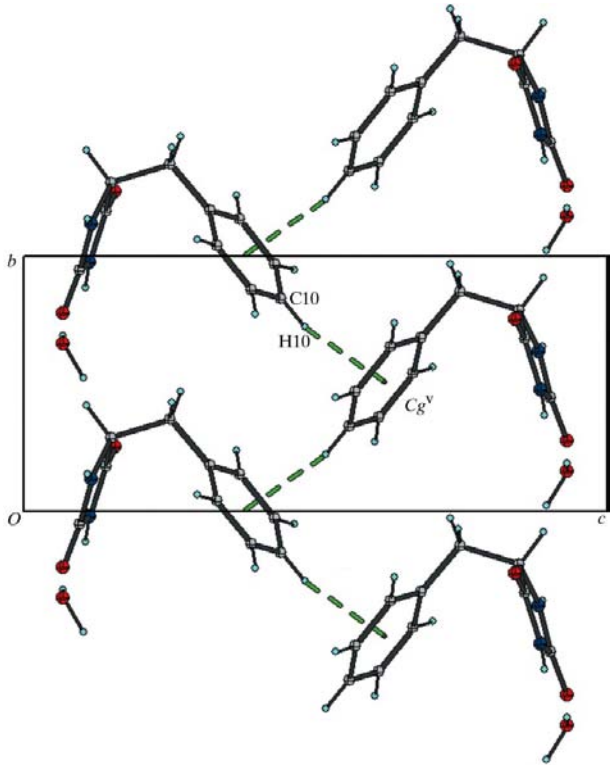

Figure 3
A packing view of (I) in the bc plane, showing the herring-bone-like array. [Symmetry code: (v) $-x$ + 1, y − $\frac{1}{2}$, $-z$ + 1.]

Experimental

L-Phenylalanine (500 mg, 3.0 mmol) was dissolved in water (20 ml) and the solution was acidified with concentrated HCl (37% v/v) to pH 5.5. KOCN (1458 mg, 18.0 mmol) was then added to this solution. The mixture was warmed, with agitation, to 333 K over a period of 4 h. The resulting solution was cooled at room temperature and acidified with concentrated HCl (37% v/v) to pH 1, at which point a white solid precipitated. The solid was filtered off and washed with cool water (m.p. 467–469 K). Crystals of (I) suitable for X-ray diffraction analysis were obtained by slow evaporation of a 1:1 water–ethanol solution.

Crystal data

$C_{10}H_{10}N_2O_2\cdot H_2O$
M_r = 208.22
Monoclinic, $P2_1$
a = 6.229 (2) Å
b = 6.244 (3) Å
c = 14.475 (3) Å
β = 99.05 (3)°
V = 556.0 (3) Å^3
Z = 2
Mo $K\alpha$ radiation
μ = 0.09 mm^{-1}
T = 293 (2) K
0.40 × 0.36 × 0.20 mm

Data collection

Rigaku AFC-7S diffractometer
1192 measured reflections
1088 independent reflections
976 reflections with $I > 2\sigma(I)$
R_{int} = 0.006
3 standard reflections
every 150 reflections
intensity decay: none

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.047
$wR(F^2)$ = 0.141
S = 1.06
1088 reflections
138 parameters
1 restraint
H-atom parameters constrained
$\Delta\rho_{max}$ = 0.56 e Å^{-3}
$\Delta\rho_{min}$ = −0.27 e Å^{-3}

Table 1
Selected geometric parameters (Å, °).

N1—C2	1.325 (5)	N3—C4	1.339 (5)
N1—C5	1.447 (5)	C4—O4	1.240 (4)
C2—O2	1.226 (5)	C4—C5	1.512 (5)
C2—N3	1.394 (4)		
C2—N1—C5	112.6 (3)	O4—C4—N3	125.9 (3)
O2—C2—N1	129.2 (3)	O4—C4—C5	126.6 (4)
O2—C2—N3	123.3 (3)		

Table 2
Hydrogen-bond geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
N3—H3···O1W^{i}	0.86	1.90	2.750 (4)	169
O1W—H2W···O2	0.87	1.85	2.712 (4)	175
N1—H1···O4^{ii}	0.86	2.24	3.040 (4)	154
O1W—H1W···O4^{iii}	0.99	1.88	2.864 (5)	172
C5—H5···O2^{iv}	0.98	2.44	3.336 (5)	152

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

All H atoms attached to C atoms were positioned geometrically and assigned U_{iso}(H) values equal to $1.2U_{eq}$(C). The H atoms of the water molecule were located in the final difference Fourier map and the U_{iso}(H) values were set at $1.5U_{eq}$(O). The absolute structure was assigned from the known configuration of L-phenylalanine.

Data collection: *MSC/AFC Diffractometer Control Software* (Molecular Structure Corporation, 1993); cell refinement: *MSC/AFC Diffractometer Control Software*; data reduction: *TEXSAN* (Molecular Structure Corporation, 1995); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *DIAMOND* (Brandenburg, 2001); software used to prepare material for publication: *PLATON* (Spek, 2003) and *publCIF* (Westrip, 2007).

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: SK3128). Services for accessing these data are described at the back of the journal.

References

Allen, F. H. (2002). *Acta Cryst.* B**58**, 380–388.

Alsina, J., Scott, W. L. & O'Donnell, M. J. (2005). *Tetrahedron Lett.* **46**, 3131–3135.

Bernstein, J., Davis, R. E., Shimoni, L. & Chang, N.-L. (1995). *Angew. Chem. Int. Ed. Engl.* **34**, 1555–1573.

Boeijen, A., Kruijtzer, J. A. & Liskamp, R. M. (1998). *Bioorg. Med. Chem. Lett.* **8**, 2375–2380.

Brandenburg, K. (2001). *DIAMOND*. Version 2.1e. Crystal Impact GbR, Bonn, Germany.

Burton, S. G. & Dorrington, R. A. (2004). *Tetrahedron Asymmetry*, **15**, 2737–2741.

Carmi, C., Cavazzoni, A., Zuliani, V., Lodola, A., Bordi, F., Plazzi, P. V., Alfieri, R. R., Petronini, P. G. & Mor, M. (2006). *Bioorg. Med. Chem. Lett.* **16**, 4021–4025.

Chen, H., Ho, C., Liu, J., Lin, K., Wang, Y., Lu, Ch. & Liu, H. (2003). *Biotechnol. Prog.* **19**, 864–873.

Galdecki, Z. & Karolak-Wojciechowska, J. (1986). *J. Crystallogr. Spectrosc. Res.* **16**, 467–474.

Ganesan, A. (2003). *Methods Enzymol.* **369**, 415–434.

Gauthier, T. J., Yokum, T. S., Morales, G. A., McLaughlin, M. L., Liu, Y.-H. & Fronczek, F. R. (1997). *Acta Cryst.* C**53**, 1659–1661.

Knabe, J., Baldauf, J. & Ahlhem, A. (1997). *Pharmazie*, **52**, 912–919.

Marton, J., Enisz, J., Hosztafi, S. & Timar, T. (1993). *J. Agric. Food Chem.* **41**, 148–152.

Molecular Structure Corporation (1993). *MSC/AFC Diffractometer Control Software*. Version 5.1.0. MSC, The Woodlands, Texas, USA.

Molecular Structure Corporation (1995). *TEXSAN*. MSC, The Woodlands, Texas, USA.

Mutschler, E. & Derendorf, H. (1995). *Drug Actions, Basic Principles and Therapeutic Aspects.* Stuttgart: Medpharm Scientific Publishers.

Park, K. H., Ehrler, J., Spoerri, H. & Kurth, M. J. (2001). *J. Comb. Chem.* **3**, 171–176.

Putnam, T. J. & Merrit, H. H. (1937). *Science*, **85**, 525–526.

Seijas, L. E., Delgado, G. E., Mora, A. J., Bahsas, A. & Briceño, A. (2007). *Acta Cryst.* C**63**, o303–o305.

Seijas, L. E., Delgado, G. E., Mora, A. J., Bahsas, A. & Uzcátegui, J. (2006). *Av. Quim.* **1**, 3–7.

Sheldrick, G. M. (1997). *SHELXS97* and *SHELXL97*. University of Göttingen, Germany.

Shiozaki, M. (2002). *Carbohydr. Res.* **337**, 2077–2088.

Singh, G., Driever, P. H. & Sander, J. W. (2005). *Brain*, **128**, 7–17.

Spek, A. L. (2003). *J. Appl. Cryst.* **36**, 7–13.

Vázquez, J., Royo, M. & Albericio, F. (2004). *Lett. Org. Chem.* **1**, 224–226.

Westrip, S. P. (2007). *publCIF*. In preparation.

Wilms, B., Wiese, A., Syldatk, C., Mattes, R. & Altenbuchner, J. (2001). *J. Biotechnol.* **86**, 19–30.

Yu, F.-L., Schwalbe, C. H. & Watkin, D. J. (2004). *Acta Cryst.* C**60**, o714–o717.