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## Key indicators

Single-crystal X-ray study  
 $T = 173$  K  
Mean  $\sigma(C-C) = 0.004$  Å  
 $R$  factor = 0.048  
 $wR$  factor = 0.105  
Data-to-parameter ratio = 13.6For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.***trans*-(4-Methylcyclohexylcarbamoyl)phosphonic acid: a representative matrix metalloproteinase (MMP) inhibitor**

The title compound,  $C_8H_{16}NO_4P$ , is the first carbamoylphosphonic acid for which the crystal structure has been solved. The  $-PO_3H_2$  group has three distinct P—O bond distances of 1.483 (1), 1.506 (1) and 1.545 (2) Å. Hydrogen bonds of types P—O—H...O=C and N—H...O=P [2.416 (2) and 2.954 (2) Å, respectively] connect the molecules to form a chain of condensed ten-membered hydrogen-bonded rings. The second P—O—H group of each phosphonic acid is hydrogen-bonded to an O=P group of the next chain, so serving to link adjacent chains together.

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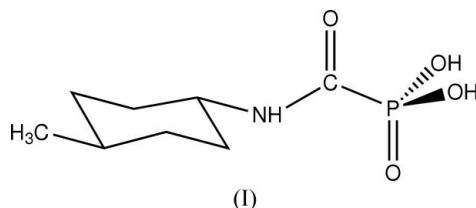
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Carbamoylphosphonate MMP inhibitors. V.

## Comment

Matrix metalloproteinases (MMPs) are enzymes that, if overexpressed, are involved in a wide range of harmful biological activities. Therefore, over the last two decades or so, there has been a worldwide research effort directed at the development of clinically useful inhibitors of these enzymes [for recent reviews, see Matter & Schudok (2004), Skiles *et al.* (2004) and Breuer *et al.* (2005)].



We have recently reported that some classes of carbamoylphosphonates act as potent non-toxic MMP inhibitors which are active *in vivo* (Breuer, Salomon *et al.*, 2004; Reich *et al.*, 2005). In the course of structure–activity relationship studies of our novel inhibitors for various medically important MMP subtypes, we required stereochemically defined *cis*- and *trans*-4-methylcyclohexylcarbamoylphosphonic acids (Breuer, Katz *et al.*, 2004). The title

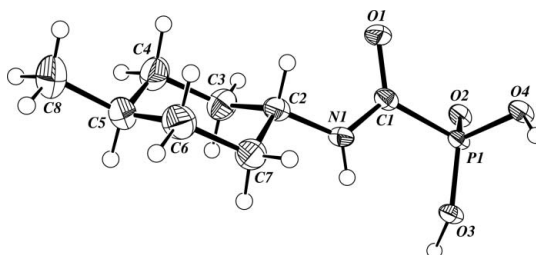


Figure 1

The molecular structure of (I), with the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level and H atoms are shown as small spheres of arbitrary radii.



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

<i>D</i> —H··· <i>A</i>	<i>D</i> —H	H··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> —H··· <i>A</i>
O4—H4···O2 <sup>i</sup>	0.80 (3)	1.72 (3)	2.5184 (19)	173 (3)
O3—H3···O1 <sup>ii</sup>	1.13 (3)	1.29 (3)	2.4156 (18)	173 (3)
N1—H1···O3	0.80 (2)	2.46 (2)	2.916 (2)	117 (2)
N1—H1···O2 <sup>ii</sup>	0.80 (2)	2.25 (2)	2.954 (2)	146 (2)
N1—H1···O3 <sup>iii</sup>	0.80 (2)	2.57 (2)	3.118 (2)	127 (2)

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

All H atoms were located in difference Fourier maps and were refined isotropically.

Data collection: *SMART* (Bruker, 2003); cell refinement: *SAINT-Plus* (Bruker, 2003); data reduction: *SAINT-Plus*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1990); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2000); software used to prepare material for publication: *SHELXTL*.

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