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Key indicators

Single-crystal X-ray study
 $T = 293$ K
Mean $\sigma(\text{C}-\text{C}) = 0.003$ Å
 R factor = 0.050
 wR factor = 0.135
Data-to-parameter ratio = 11.9

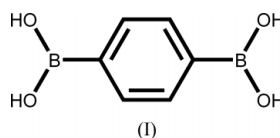
For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

1,4-Phenylenediboronic acid

In the crystal structure of the title compound, $\text{C}_6\text{H}_8\text{B}_2\text{O}_4$, centrosymmetric 1,4-phenylenediboronic acid molecules are linked by characteristic hydrogen bonding of $\text{B}(\text{OH})_2$ groups. Primary association involves the formation of centrosymmetric cyclic dimers which leads to the formation of linear chains; these, in turn, associate by secondary hydrogen bonding, *via* unit-cell translations in the a axis direction, to form sheets.

Comment

Boronic acids possess a $\text{B}(\text{OH})_2$ group as functional moiety and have applications in organic synthesis (Miyaura *et al.*, 1981; Corey & Helal, 1998), the molecular recognition of biochemically active molecules (Nozaki *et al.*, 1995; Shinkai *et al.*, 2001; Reetz *et al.*, 1991), as well as in medicine as antibiotics (Dunitz *et al.*, 1971; Nakamura *et al.*, 1977), inhibitors (Shenvi, 1986) and for the treatment of tumors (Soloway *et al.*, 1998). As a continuation of our recent interest in the structural elucidation of boronic acid derivatives (Fournier *et al.*, 2003; Rodríguez-Cuamatzi *et al.*, 2004), we present here the crystal structure of 1,4-phenylenediboronic acid, (I), which reveals interesting features, demonstrating the intriguing hydrogen-bonding patterns of boronic acid structures.



The crystal structure of (I) (Fig. 1) contains a two-dimensional arrangement of 1,4-phenylenediboronic acid molecules in the form of a layer, as shown in Fig. 2. Within these layers, two hydrogen-bonding motifs, *A* and *B*, can be distinguished, which are both centrosymmetric. Each $\text{B}(\text{OH})_2$ group has a *syn-anti* conformation (with respect to the H atoms) and participates in a total of four $\text{O}-\text{H}\cdots\text{O}$ hydrogen bonds. The

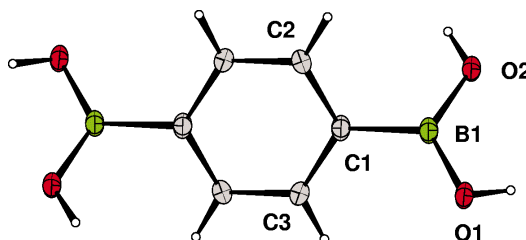


Figure 1

View of the title compound. Displacement ellipsoids are drawn at the 30% probability level. Unlabeled atoms are related by the symmetry code $(1-x, -y, 2-z)$.

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hydrogen-bonding pattern in motif A (Fig. 2 and first line of Table 1) is comparable to the one found generally in the dimeric units formed between carboxylic acids and has apparently similar stability, since it is found in most of the phenylboronic acid derivatives characterized so far by X-ray crystallography (Rettig & Trotter, 1977; Soundararajan *et al.*, 1993; Scouten *et al.*, 1994; Pilkington *et al.*, 1995; Gainsford *et al.*, 1995; Bradley *et al.*, 1996; Akita & Kobayashi, 1997; Schilling *et al.*, 1997; Norrild & Sotoftte, 2001; Fournier *et al.*, 2003; Braga *et al.*, 2003; Bresner *et al.*, 2004; Rodríguez-Cuamatzi *et al.*, 2004). Through these interactions one-dimensional linear chains are formed, which are aligned parallel to each other and interconnected through additional O—H...O bonds (motif B, second line of Table 1). The cyclic hydrogen-bonded motifs B are (OH)₄ units, which are frequently observed in the crystal structures of diols (Hawkins *et al.*, 1990).

Interestingly, the B(OH)₂ groups are twisted out of the mean plane of the phenylene group by approximately 35°, apparently as a result of these hydrogen-bonding requirements. In 1,4-phenylenediboronic acid tetrahydrate, in which linear chains of hydrogen-bonded boronic acid molecules were located between two-dimensional layers of water molecules (Rodríguez-Cuamatzi *et al.*, 2004), the twists of the B(OH)₂ groups had values of only 2 and 7°. The resulting overall conformation of the two-dimensional layer is shown in Fig. 3.

Experimental

1,4-Phenylenediboronic acid, (I), was synthesized by reaction of the Grignard reagent prepared from 1,4-dibromobenzene with tri-*n*-methyl borate, followed by hydrolysis (Coutts *et al.*, 1970). Crystals were grown from water.

Crystal data

C ₆ H ₈ B ₂ O ₄	<i>Z</i> = 1
<i>M_r</i> = 165.74	<i>D_x</i> = 1.479 Mg m ⁻³
Triclinic, <i>P</i> 1̄	Mo <i>K</i> α radiation
<i>a</i> = 4.989 (3) Å	Cell parameters from 1056 reflections
<i>b</i> = 5.305 (3) Å	<i>θ</i> = 4.0–27.3°
<i>c</i> = 7.368 (4) Å	<i>μ</i> = 0.12 mm ⁻¹
<i>α</i> = 104.429 (10)°	<i>T</i> = 293 (2) K
<i>β</i> = 97.886 (9)°	Block, colorless
<i>γ</i> = 93.797 (10)°	0.45 × 0.39 × 0.21 mm
<i>V</i> = 186.05 (19) Å ³	

Data collection

Bruker SMART CCD diffractometer	678 reflections with <i>I</i> > 2σ(<i>I</i>)
φ and ω scans	<i>R</i> _{int} = 0.036
Absorption correction: none	<i>θ</i> _{max} = 26.0°
1948 measured reflections	<i>h</i> = -6 → 6
728 independent reflections	<i>k</i> = -6 → 6
	<i>l</i> = -9 → 9

Refinement

Refinement on <i>F</i> ²	$w = 1/[\sigma^2(F_o^2) + (0.0588P)^2 + 0.0474P]$
$R[F^2 > 2\sigma(F^2)] = 0.050$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.135$	(Δ/σ) _{max} = 0.015
<i>S</i> = 1.21	Δρ _{max} = 0.20 e Å ⁻³
728 reflections	Δρ _{min} = -0.23 e Å ⁻³
61 parameters	
H atoms treated by a mixture of independent and constrained refinement	

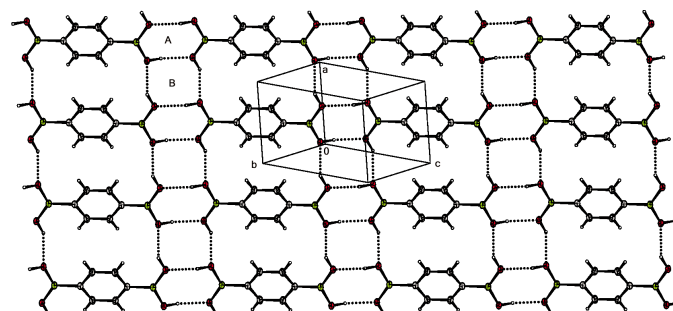


Figure 2
The packing arrangement of the two-dimensional layers in the unit cell, showing the hydrogen-bonding interactions as dashed lines.

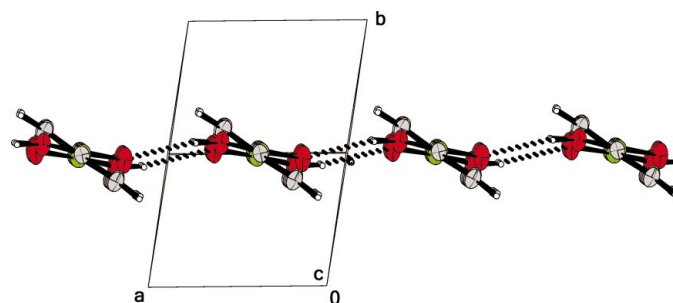


Figure 3
View of the unit cell along the *c* axis. Hydrogen bonds are shown as dashed lines.

Table 1

Hydrogen-bonding 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>
O1—H10...O2 ⁱ	0.84 (2)	1.93 (2)	2.761 (2)	172 (3)
O2—H20...O1 ⁱⁱ	0.841 (17)	2.036 (14)	2.781 (2)	148 (2)

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

H atoms of the benzene ring were placed in idealized positions and treated as riding, with C—H = 0.93 Å, while the H atoms bonded to O atoms were located in a difference Fourier map and refined with restraints on distances [0.84 (1) Å]. Isotropic displacement parameters of the H atoms were set at *U*_{iso} = 1.2*U*_{eq}(C) or 1.5*U*_{eq}(O).

Data collection: *SMART* (Bruker, 2000); cell refinement: *SAINTE* (Bruker, 2001); data reduction: *SAINTE*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *CAMERON* (Watkin *et al.*, 1996); software used to prepare material for publication: *SHELXTL* (Bruker, 2000).

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