

2-[4-(2-Hydroxyethyl)piperazin-1-yl]ethane-sulfonic acid

Fei Gao,^a Caixia Yin,^a Pin Yang^{a*}
and Gang Xue^b^aKey Laboratory of Chemical Biology and Molecular Engineering of the Education Ministry, Institute of Molecular Science, Shanxi University, Taiyuan, Shanxi 030006, People's Republic of China, and ^bState Key Laboratory of Crystal Materials, Shandong University, Jinan 250100, People's Republic of China

Correspondence e-mail: yangpin@sxu.edu.cn

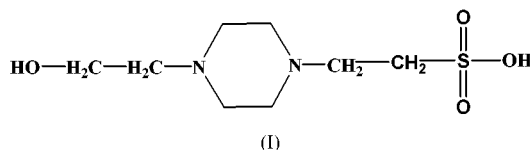
Key indicators

Single-crystal X-ray study
T = 298 K
Mean $\sigma(\text{C}-\text{C}) = 0.003 \text{ \AA}$
R factor = 0.041
wR factor = 0.115
Data-to-parameter ratio = 13.6For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

The title compound, $\text{C}_8\text{H}_{18}\text{N}_2\text{O}_4\text{S}$, is a useful buffer in the physiological pH range. In the crystal structure, the piperazine ring adopts a chair conformation. One weak intramolecular $\text{C}-\text{H}\cdots\text{O}$ hydrogen bond, together with one weak intermolecular $\text{C}-\text{H}\cdots\text{O}$ and two strong intermolecular $\text{O}-\text{H}\cdots\text{N}$ hydrogen bonds are present, the latter linking the molecules into a reticulation framework.

Comment

The title compound, (I), also known as HEPES, is one of the useful buffers extensively used in biochemical experiments in the physiological pH range (Han & Kim, 2002). Shipman (1969) found that HEPES, at a concentration of 0.01 M, produced adequate buffering in all cell systems tested and exhibited no metal binding, and was soluble to an extent of 2.25 M at 273 K. Furthermore, HEPES had minimal effect on the redox potential of well poised media. Ever since, HEPES has been widely used as a buffer. Its crystal structure, however, has not been reported hitherto.



Selected geometric parameters of (I) are listed in Table 1, and the molecular conformation and crystal packing are illustrated in Figs. 1 and 2, respectively. All bond lengths and angles are within normal ranges. The piperazine ring adopts a chair conformation. The two ethyl groups, at N1 and N2, adopt an *anti* conformation. The dihedral angle between the planes C2/C3/N2 and C1/C2/C3/C4 is $53.12(1)^\circ$, while the dihedral angle between the planes C1/C4/N1 and C1/C2/C3/C4 is $51.85(1)^\circ$.

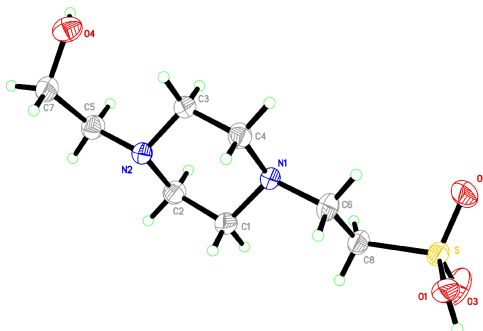


Figure 1

A view of the molecular structure of (I), with the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.

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There is an intramolecular C3—H3B···O4 hydrogen bond (Table 2). According to the study by Steiner (1997), C—H···O hydrogen bonds may form within a bond-angle range of 110–180°, since the C—H···O hydrogen bond can be easily bent. There are also intermolecular C—H···O and O—H···N hydrogen bonds, which link the molecules into a network.

Experimental

The title compound, HEPES, which is a product of Sigma (100 mg), was dissolved in water (10 ml). The aqueous solution was allowed to evaporate slowly at room temperature over several months. Green crystals suitable for an X-ray study were formed.

Crystal data

C ₈ H ₁₈ N ₂ O ₄ S	Mo K α radiation
$M_r = 238.30$	Cell parameters from 12566 reflections
Orthorhombic, <i>Pbca</i>	$\theta = 2.4\text{--}27.0^\circ$
$a = 8.3813$ (13) Å	$\mu = 0.29$ mm ⁻¹
$b = 9.6623$ (16) Å	$T = 298$ (2) K
$c = 27.056$ (4) Å	Plate, green
$V = 2191.1$ (6) Å ³	$0.58 \times 0.58 \times 0.06$ mm
$Z = 8$	
$D_x = 1.445$ Mg m ⁻³	

Data collection

Bruker SMART 1K CCD area-detector diffractometer	1919 independent reflections
φ and ω scans	1724 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Sheldrick, 2000)	$R_{\text{int}} = 0.027$
$T_{\text{min}} = 0.848$, $T_{\text{max}} = 0.983$	$\theta_{\text{max}} = 25.0^\circ$
9743 measured reflections	$h = -9 \rightarrow 7$
	$k = -11 \rightarrow 11$
	$l = -32 \rightarrow 25$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0636P)^2 + 1.4035P]$
$R[F^2 > 2\sigma(F^2)] = 0.041$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.115$	$(\Delta/\sigma)_{\text{max}} = 0.001$
$S = 1.06$	$\Delta\rho_{\text{max}} = 0.63$ e Å ⁻³
1919 reflections	$\Delta\rho_{\text{min}} = -0.32$ e Å ⁻³
141 parameters	Extinction correction: <i>SHELXL97</i>
H atoms treated by a mixture of independent and constrained refinement	Extinction coefficient: 0.0033 (6)

Table 1

Selected geometric parameters (Å, °).

S—O2	1.4424 (17)	N2—C3	1.469 (2)
S—O3	1.4424 (18)	N2—C2	1.471 (3)
S—O1	1.4617 (16)	N2—C5	1.472 (3)
S—C8	1.782 (2)	C1—C2	1.507 (3)
O4—C7	1.415 (3)	C3—C4	1.511 (3)
N1—C4	1.495 (3)	C5—C7	1.516 (3)
N1—C1	1.498 (3)	C6—C8	1.512 (3)
N1—C6	1.503 (3)		
C4—N1—C1—C2	56.4 (2)	C2—N2—C3—C4	-59.4 (2)
C3—N2—C2—C1	59.3 (2)	C1—N1—C4—C3	-57.1 (2)
N1—C1—C2—N2	-58.8 (2)	N2—C3—C4—N1	59.8 (2)

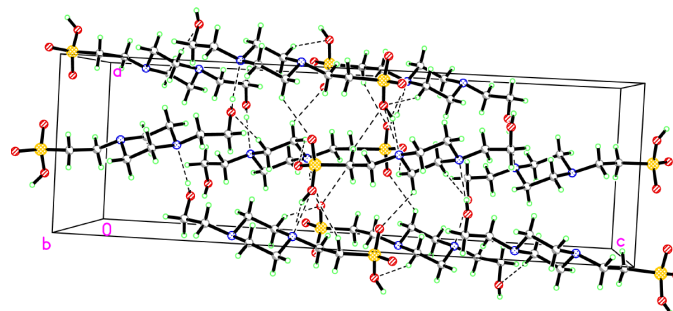


Figure 2

A packing diagram of (I). Dashed lines indicate hydrogen bonds.

Table 2

Hydrogen-bonding geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
O1—H1···N1 ⁱ	0.86	1.94	2.755 (2)	158
O4—H4···N2 ⁱⁱ	0.73 (3)	2.14 (3)	2.864 (2)	175 (3)
C1—H1A···O2 ⁱ	0.97	2.49	3.109 (3)	121
C3—H3B···O4	0.97	2.42	3.054 (2)	122

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

H atoms attached to C atoms were placed in geometrically idealized positions, with C—H = 0.97 Å, and constrained to ride on their parent atoms, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$. Hydroxyl H atoms were located in difference Fourier maps; H1 was constrained to ride on O, with O—H = 0.85 Å and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{O1})$; H4 was refined with the restraint O4—H4 = 0.73 (3) Å.

Data collection: *SMART* (Bruker, 2000); cell refinement: *SAINTE* (Bruker, 2000); data reduction: *SAINTE*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2000); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2000); molecular graphics: *SHELXTL/PC* (Sheldrick, 1999); software used to prepare material for publication: *SHELXTL/PC*.

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