Heterocyclic Tautomerism. V [1]. 2-Guanidinobenzimidazole

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A single-crystal X-ray structure analysis of 2-guanidinobenzimidazole shows the molecule exists in the solid state as tautomer **1**, with an intramolecular hydrogen bond between the benzimidazole-N3 and a guanidino-NH_2. The guanidino group is inclined at an angle of 13.8° to the benzimidazole plane. Other nitrogen atoms and their attached hydrogens are involved in additional intermolecular hydrogen bonds that connect the molecules in a complex three-dimensional network.

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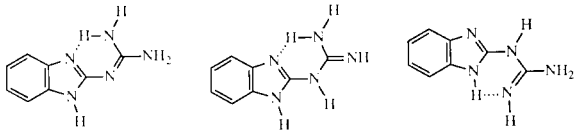
Although 2-guanidinobenzimidazole has been much studied because of its biological activity and has found use as a chelating and binucleating ligand in coordination chemistry, there is nevertheless some doubt about the actual structure of this molecule in solution and in the solid state. It could exist as a number of different tautomeric structures stabilised by intra- and inter-molecular hydrogen bonds. Theoretical calculations [2] predicted that in the gas phase 2-guanidinobenzimidazole would exist as tautomer **1** rather than either of the two conformers of an alternative tautomer **2**, all of which possess intramolecular hydrogen bonds. However, nmr studies [2,3] of solutions of 2-guanidinobenzimidazole were unable to definitively assign a structure to the major species in solution. In the solid state two X-ray crystal structures have been reported [4,5] in which 2-guanidinobenzimidazole was a guest to crown ether hosts. However, in both cases there was extensive hydrogen bonding between the host and guest, a factor that might influence the relative stability of the possible tautomeric structures. In the present report the X-ray structure of free 2-guanidinobenzimidazole is described.



1 **2a** **2b**

Figure 1 shows a perspective view and atom labelling of the structure. Tables 1 and 2 list atom coordinates and bonding geometry respectively. A comparison of the C–N bond lengths combined with the location and successful refinement of the N–H hydrogen atoms clearly identify the structure as tautomer **1**, with an intramolecular hydrogen bond in which H41 interacts with N3 (N4···N3 = 2.751 Å, H41···N3 = 2.05 Å, N4–H41···N3 = 129°). The bonding geometry is in good agreement with the geometry of the two previously reported [4,5] X-ray structures in which 2-guanidinobenzimidazole was a guest to crown ether hosts. The agreement is not so good with the INDO calculated [2] geometry.

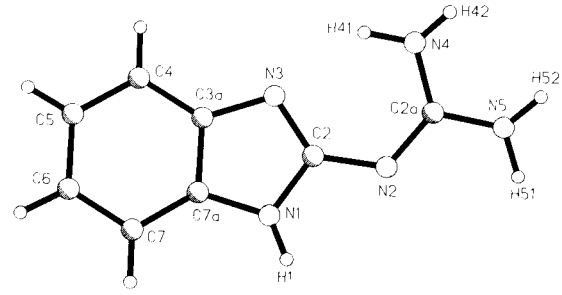


Figure 1. X-Ray structure and labelling of **1**.

In addition to the intramolecular hydrogen bond there is a complex system of intermolecular hydrogen bonding that interconnects the molecules in a three-dimensional network. For example, the molecules are connected in

Table 1.

Atomic coordinates (x10^4) and equivalent isotropic displacement coefficients (Å^{2}x10^3) for 2-guanidinobenzimidazole.

atom	x	y	z	U_{eq}*
N(1)	3285(5)	9641(2)	1045(1)	24(1)
N(2)	289(4)	9113(2)	512(1)	24(1)
N(3)	1520(4)	7624(2)	1105(1)	22(1)
N(4)	-2674(5)	7357(2)	581(1)	27(1)
N(5)	-2782(5)	8805(3)	2(1)	30(1)
C(2)	1581(5)	8751(2)	878(1)	20(1)
C(2A)	-1713(5)	8433(3)	382(1)	23(1)
C(3A)	3252(5)	7827(2)	1444(1)	21(1)
C(4)	3920(5)	7014(3)	1789(1)	26(1)
C(5)	5717(6)	7479(3)	2079(1)	29(1)
C(6)	6848(6)	8719(3)	2036(1)	32(1)
C(7)	6182(5)	9545(3)	1696(1)	30(1)
C(7A)	4374(5)	9080(3)	1409(1)	23(1)

* Equivalent isotropic U defined as one third of the trace of the orthogonalized U_{ij} tensor

Table 2.

Bond lengths (Å) and angles (°) for 2-guanidinobenzimidazole.

N(1)-C(2)	1.371 (3)	N(1)-C(7A)	1.388 (3)	N(2)-C(2)	1.373 (3)
N(2)-C(2A)	1.321 (4)	N(3)-C(2)	1.339 (3)	N(3)-C(3A)	1.405 (3)
N(4)-C(2A)	1.350 (4)	N(5)-C(2A)	1.357 (4)	C(3A)-C(4)	1.396 (4)
C(3A)-C(7A)	1.401 (4)	C(4)-C(5)	1.385 (4)	C(5)-C(6)	1.394 (4)
C(6)-C(7)	1.389 (4)	C(7)-C(7A)	1.384 (4)		

C(2)-N(1)-C(7A)	107.9(2)	C(2)-N(2)-C(2A)	120.5(2)
C(2)-N(3)-C(3A)	104.6(2)	N(1)-C(2)-N(2)	117.3(2)
N(1)-C(2)-N(3)	112.2(2)	N(2)-C(2)-N(3)	130.5(2)
N(2)-C(2A)-N(4)	125.4(2)	N(2)-C(2A)-N(5)	116.7(2)
N(4)-C(2A)-N(5)	117.7(3)	N(3)-C(3A)-C(4)	130.6(2)
N(3)-C(3A)-C(7A)	110.4(2)	C(4)-C(3A)-C(7A)	119.0(2)
C(3A)-C(4)-C(5)	118.0(2)	C(4)-C(5)-C(6)	122.3(3)
C(5)-C(6)-C(7)	120.4(3)	C(6)-C(7)-C(7A)	117.1(3)
N(1)-C(7A)-C(3A)	104.9(2)	N(1)-C(7A)-C(7)	131.8(2)
C(3A)-C(7A)-C(7)	123.2(2)		

chains along the *b* axis with H1 interacting with N3 of an adjacent molecule (N1···N3 = 3.024Å, H1···N3 = 2.21Å, N1-H1···N3 = 152°). Similarly adjacent molecules are mutually hydrogen bonded about a center of inversion with H51 interacting with N2 of an inversion related molecule (N5···N2 = 2.948Å, H51···N2 = 1.98Å, N5-H51···N2 = 167°). This intermolecular hydrogen bonding is undoubtedly responsible for the fact that the whole molecule is not quite planar (mean deviation from the meanplane: 0.151Å); the benzimidazole skeleton itself is planar (mean deviation: 0.009Å) but is inclined at an angle of 13.8° to the plane of the guanidino group.

EXPERIMENTAL

2-Guanidinobenzimidazole (Aldrich) was recrystallized from ethanol. Intensity data were collected at -100° on a yellow crystalline plate of dimensions 0.44 x 0.25 x 0.05 mm with a Nicolet R3m four-circle diffractometer by using monochromatized Mo Kα (λ = 0.71073Å) radiation. Cell parameters were determined by least squares refinement, the setting angles of 22 accurately centered reflections ($2\theta > 17°$) being used. Throughout data collection the intensities of three standard reflections (0020, 060, 200) were monitored at regular intervals and this indicated no significant crystal decomposition. The space group followed from systematic absences. The intensities were corrected for Lorentz and polarization effects but not for absorption. Reflections with $I > 3\sigma(I)$ were used for structure solution and refinement.

The structure was solved by direct methods, and refined by full-matrix least-squares procedures. All non-hydrogen atoms were refined with anisotropic thermal parameters. The N-H hydrogens were located from a difference Fourier synthesis and their positions refined, whereas the C-H hydrogen atoms were included in calculated positions. All hydrogens were assigned isotropic thermal parameters equal to the isotropic equivalent of their carrier atoms. The function minimized was $\Sigma w(|F_o| - |F_c|)^2$, with $w = [\sigma^2(F_o) + 0.0005F_o^2]^{-1}$. A final difference map showed no features greater or less than 0.21e⁻/Å³. Final non-hydrogen atom coordinates, bond lengths and bond angles are listed in Tables 1 and 2. Tabulations of hydrogen atom coordinates, anisotropic thermal parameters, structure factors and equations of meanplanes are available as supplementary material from the author.

Crystal data at -100°: $C_8H_9N_5$, Mr = 175.2, orthorhombic, space group Pbca, a = 5.258(4), b = 10.113(5), c = 30.997(16)Å, U = 1648(2)Å³, F(000) = 736, Z = 8, D_c = 1.412 g cm⁻³, μ(Mo-Kα) = 0.89 cm⁻¹, ω scans, $2\theta_{max}$ = 55°, N = 1886, N_o = 950, 133 parameters, S = 1.17, R = 0.043, R_w = 0.047.

REFERENCES AND NOTES

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