

Lars Kr. Hansen,<sup>a\*</sup> German L. Perlovich<sup>b,c</sup> and Annette Bauer-Brandl<sup>b</sup><sup>a</sup>Department of Chemistry, University of Tromsø, 9037 Tromsø, Norway, <sup>b</sup>Department of Pharmaceutics and Biopharmaceutics, University of Tromsø, 9037 Tromsø, Norway, and <sup>c</sup>Institute of Solution Chemistry, Russian Academy of Sciences, 153045 Ivanovo, Russian Federation

Correspondence e-mail: larsk@chem.uit.no

## Key indicators

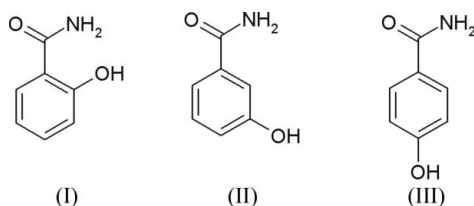
Single-crystal X-ray study  
 $T = 293\text{ K}$   
Mean  $\sigma(\text{C}-\text{C}) = 0.003\text{ \AA}$   
 $R$  factor = 0.046  
 $wR$  factor = 0.033  
Data-to-parameter ratio = 9.3For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

## Redetermination of 3-hydroxybenzamide

The crystal structure of the title compound,  $\text{C}_7\text{H}_7\text{NO}_2$ , has been redetermined [Katsube, Y. (1966). *Bull. Chem. Soc. Jpn.*, **39**, 2576–2588] to higher precision and with the hydrogen-bonding scheme established.Received 27 March 2007  
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## Comment

Hydroxybenzamides (I), (II) and (III) are often used as pro-drug compounds to model various physico-chemical processes of the drug molecules. Their different hydrogen-bonding patterns help to establish their structures and determine their solubilities.



The crystal structure of 2-hydroxybenzamide (salicylamide), (I), has been described in detail in the literature (Sasada *et al.*, 1964; Pertlik, 1990), whereas the structure of 4-hydroxybenzamide, (III), has not been reported at all. The structure of 3-hydroxybenzamide, (II), was studied some time ago by Katsube (1966) to moderate precision. Here we present a high-precision redetermination of (II) (Fig. 1) and describe its hydrogen-bonding scheme (Table 1).

The bond lengths and angles for (II) are within their normal ranges (Allen *et al.*, 1987). The data obtained by us for the non-H atoms are consistent with Katsube's, but improved by about a factor of twenty in precision. For example,  $\text{C7}-\text{O1} = 1.245(2)\text{ \AA}$ , compared with  $1.24(7)\text{ \AA}$  in Katsube's study. The dihedral angle between the mean plane of the aromatic ring and the plane of  $\text{C7}/\text{N1}/\text{O1}$  is  $22.9(2)^\circ$ .

The packing of (II) is shown in Fig. 2. The molecules form (101) layers held together by  $\text{N}-\text{H}\cdots\text{O}$  and  $\text{O}-\text{H}\cdots\text{O}$  hydrogen bonds. The layers interact with each other by van der Waals forces. The hydrogen-bond network can be described by the graph set assignments introduced by Etter (1990) as  $C(4)$ ,  $C(8)$ , and  $R_2^2(14)$ .

## Experimental

A commercial sample of 3-hydroxybenzamide (Sigma–Aldrich Co. Ltd, St Louis, USA) was used. Crystals of (II) were grown by slow evaporation of a methanol solution.

Crystal data

C<sub>7</sub>H<sub>7</sub>NO<sub>2</sub>  
*M<sub>r</sub>* = 137.14  
 Monoclinic, *P*2<sub>1</sub>/*n*  
*a* = 10.873 (5) Å  
*b* = 5.064 (2) Å  
*c* = 11.641 (5) Å  
 β = 92.414 (11)°

*V* = 640.4 (5) Å<sup>3</sup>  
*Z* = 4  
 Mo *K*α radiation  
 μ = 0.11 mm<sup>-1</sup>  
*T* = 293.1 K  
 0.50 × 0.20 × 0.10 mm

Data collection

Rigaku Saturn diffractometer  
 Absorption correction: multi-scan  
 (Jacobson, 1998)  
*T*<sub>min</sub> = 0.938, *T*<sub>max</sub> = 0.989

5804 measured reflections  
 1707 independent reflections  
 1103 reflections with *F*<sup>2</sup> > 2σ(*F*<sup>2</sup>)  
*R*<sub>int</sub> = 0.023

Refinement

*R*[*F*<sup>2</sup> > 2σ(*F*<sup>2</sup>)] = 0.046  
*wR*(*F*<sup>2</sup>) = 0.033  
*S* = 1.80  
 1103 reflections  
 119 parameters

All H-atom parameters refined  
 Δρ<sub>max</sub> = 0.23 e Å<sup>-3</sup>  
 Δρ<sub>min</sub> = -0.18 e Å<sup>-3</sup>

Table 1

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>
N1—H8...O2 <sup>i</sup>	0.93 (2)	2.07 (2)	2.990 (2)	168 (2)
N1—H7...O1 <sup>ii</sup>	0.90 (2)	2.15 (2)	2.988 (2)	153 (2)
O2—H6...O1 <sup>iii</sup>	0.97 (2)	1.86 (2)	2.798 (2)	164 (2)

Symmetry codes: (i) *x* + ½, -*y* + ¾, *z* - ½; (ii) *x*, *y* + 1, *z*; (iii) -*x* + 2, -*y* + 1, -*z* + 1.

The crystals were of poor quality and weakly diffracting, which accounts for the low fraction of measured reflections. The H atoms were located in difference maps and their positions and *U*<sub>iso</sub> values were freely refined [C—H = 0.963 (18)–1.007 (18) Å].

Data collection: *CrystalClear* (Rigaku/MSK, 2005); cell refinement: *CrystalClear*; data reduction: *CrystalStructure* (Rigaku/MSK, 2005); program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1994); program(s) used to refine structure: *CRYSTALS* (Betteridge *et al.*, 2003); molecular graphics: *ORTEX* (McArdle, 1993) and *ORTEPIII* (Burnett & Johnson, (1996)); software used to prepare material for publication: *CrystalStructure*.

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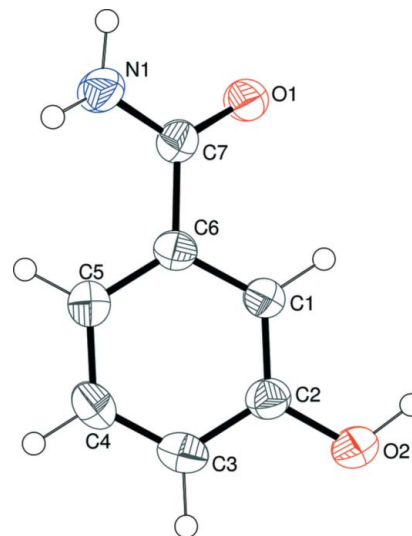


Figure 1

The molecular structure of (I), showing displacement ellipsoids drawn at the 40% probability level (arbitrary spheres for the H atoms).

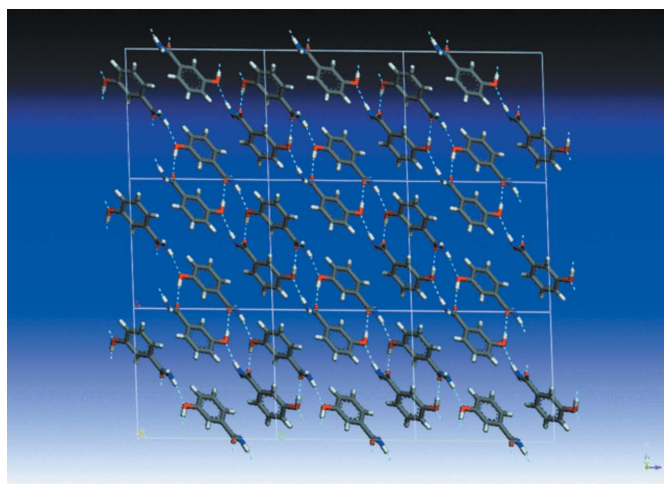


Figure 2

The packing of (I) with hydrogen bonds indicated by dashed lines.

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