Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

## 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 = 298 K Mean  $\sigma$ (C–C) = 0.005 Å R factor = 0.038 wR factor = 0.104 Data-to-parameter ratio = 7.0

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

# **Redetermination and H-atom refinement of** (*S*)-(+)-ibuprofen. Corrigendum.

In the paper by Hansen, Perlovich & Bauer-Brandl [*Acta Cryst.* (2003), E**59**, o1357–o1358], the coordinates of the *R* enantiomer of the title compound,  $C_{13}H_{18}O_2$ , were incorrectly given instead of those of the *S* enantiomer. The correct coordinates of the *S* enantiomer are given here.

Received 8 May 2006 Accepted 31 May 2006

#### Comment

In the paper by Hansen *et al.* (2003), the coordinates of the R enantiomer were incorrectly given instead of those of the S enantiomer, (I). The correct coordinates of the S enantiomer are given in the deposited replacement CIF. Molecular geometry parameters are not affected, except for the signs of torsion angles; the correct values are given in Table 1 below for the torsion angles in Table 2 of the previous report (where there was also an error in the atom numbering). Fig. 1 shows the correct structure of the two independent molecules, which form a hydrogen-bonded dimer without crystallographic symmetry.



## **Experimental**

# Table 1Selected torsion angles (°).

-			
C5B-C4B-C2B-C3B	29.1 (4)	O1A - C1A - C2A - C4A	-81.7(4)
C7B-C10B-C11B-C12B	-68.0(5)	C3A-C2A-C4A-C5A	-144.4(4)
C4B-C2B-C1B-O1B	83.5 (3)	C7A-C10A-C11A-C13A	67.9 (5)

All H atoms were refined freely [C-H = 0.85 (3)-114 (5) Å].

Data collection: *CAD-4-PC* Software (Enraf–Nonius, 1992); cell refinement: *CELDIM* in *CAD-4-PC* Software; data reduction: *XCAD* (McArdle & Higgins, 1995); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1990); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEX* (McArdle, 1995); software used to prepare material for publication: *OSCAIL* (McArdle, 1993).

#### References

© 2006 International Union of Crystallography All rights reserved Enraf-Nonius (1992). CAD-4-PC Software. Enraf-Nonius, Delft, The Netherlands.

# addenda and errata



### Figure 1

The structure of the two independent molecules of (I). Displacement ellipsoids are shown at the 30% probability level. Hydrogen bonds are shown as dashed lines.

Hansen, L. K., Perlovich, G. L. & Bauer-Brandl, A. (2003). Acta Cryst. E59, 01357–01358.McArdle, P. (1993). J. Appl. Cryst. 26, 752.

McArdle, P. (1995). J. Appl. Cryst. 28, 65.

McArdle, P. & Higgins, T. (1995). *XCAD*. NUI Galway, Ireland. Sheldrick, G. M. (1990). *Acta Cryst.* A**46**, 467–473. Sheldrick, G. M. (1997). *SHELXL97*. University of Göttingen, Germany.