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Key indicators

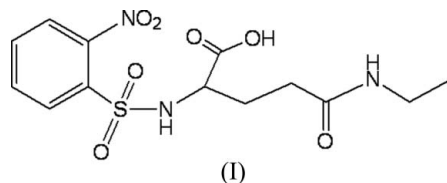
Single-crystal X-ray study
 $T = 294$ K
Mean $\sigma(\text{C}-\text{C}) = 0.003$ Å
 R factor = 0.026
 wR factor = 0.070
Data-to-parameter ratio = 10.9For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.**(S)-N⁵-Ethyl-N²-(2-nitrophenylsulfonyl)glutamine**

The title compound, $\text{C}_{13}\text{H}_{17}\text{N}_3\text{O}_7\text{S}$, is a potential AHAS (acetohydroxyacid synthase) inhibitor. In the crystal structure, the nitro group is twisted away from the plane of the aromatic ring and the glutamine residue adopts a folded conformation. The crystal packing is stabilized by intermolecular $\text{N}-\text{H}\cdots\text{O}$ and $\text{O}-\text{H}\cdots\text{O}$ hydrogen bonds.

Received 21 March 2007
Accepted 16 April 2007

Comment

Based on the AHAS (acetohydroxyacid synthase, EC 2.2.1.6) crystal structure (McCourt *et al.*, 2006), we have succeeded in identifying a few novel AHAS inhibitors (Wang, *et al.*, 2007). Among the 296 possible inhibitors from that virtual screening, we have also synthesized some new compounds with altered structure and validated their *in vivo* and *in vitro* biological activity (Wang *et al.*, 2006). These results indicated that it was possible to design new lead herbicidal AHAS inhibitors from a computer-aided design strategy. We previously reported the crystal structure of N^2 -(2-nitrophenylsulfonyl)- N^5 -*n*-propylglutamine, (II) (Xiao *et al.*, 2005). In order to further investigate the structure–activity relationship of this series of compounds, we have obtained and determined the crystal structure of another compound, (I), in this series (Fig. 1).



The X-ray crystallographic analysis reveals that all the bond lengths and angles in (I) show normal values (Allen *et al.*,

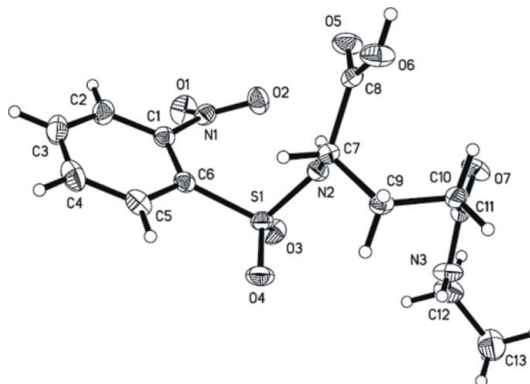


Figure 1
The molecular structure of (I), with displacement ellipsoids drawn at the 30% probability level (arbitrary spheres for the H atoms).

1987). The chiral atom C7 has an *S* configuration. The C9—C10—C11—O7 and C9—C10—C11—N3 torsion angles of 115.8 (2) and $-65.7(2)^\circ$, respectively, are significantly different from the corresponding values of 127.2 (2) and $-54.1(2)^\circ$ in (II).

The crystal structure of (I) is stabilized by N—H \cdots O and O—H \cdots O hydrogen bonds (Table 1 and Fig. 2).

Experimental

The title compound was synthesized according to the method of Srikanth *et al.* (2002). Colourless single crystals of (I) were obtained by recrystallization from ethanol and water (19:1 *v/v*).

Crystal data

$C_{13}H_{17}N_3O_7S$	$V = 796.6(2) \text{ \AA}^3$
$M_r = 359.36$	$Z = 2$
Monoclinic, $P2_1$	Mo $K\alpha$ radiation
$a = 6.7756(10) \text{ \AA}$	$\mu = 0.25 \text{ mm}^{-1}$
$b = 7.4223(11) \text{ \AA}$	$T = 294(2) \text{ K}$
$c = 15.848(2) \text{ \AA}$	$0.22 \times 0.16 \times 0.14 \text{ mm}$
$\beta = 91.901(2)^\circ$	

Data collection

Bruker SMART CCD diffractometer	4510 measured reflections
Absorption correction: multi-scan (SADABS; Bruker, 1999)	2469 independent reflections
$T_{\min} = 0.928$, $T_{\max} = 0.966$	2350 reflections with $I > 2\sigma(I)$
	$R_{\text{int}} = 0.023$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.026$	H atoms treated by a mixture of independent and constrained refinement
$wR(F^2) = 0.070$	$\Delta\rho_{\text{max}} = 0.15 \text{ e \AA}^{-3}$
$S = 1.06$	$\Delta\rho_{\text{min}} = -0.21 \text{ e \AA}^{-3}$
2469 reflections	Absolute structure: Flack (1983), 722 Friedel Pairs
227 parameters	Flack parameter: $-0.08(6)$
1 restraint	

Table 1

Hydrogen-bond geometry (\AA , $^\circ$).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
N2—H2 \cdots O5	0.81 (2)	2.25 (2)	2.641 (2)	110.7 (19)
N2—H2 \cdots O2	0.81 (2)	2.29 (2)	2.918 (2)	135 (2)
N3—H3 \cdots O5 ⁱ	0.73 (3)	2.35 (3)	3.053 (3)	164 (3)
O6—H6 \cdots O7 ⁱⁱ	0.79 (3)	1.77 (3)	2.546 (2)	173 (3)

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

The N- and O-bound H atoms were located in difference maps and their positions were freely refined with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{carrier})$. The C-bound H atoms were positioned geometrically (C—H = 0.93–0.98 \AA) and refined as riding with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ or $1.5U_{\text{eq}}(\text{methyl C})$.

Data collection: SMART (Bruker, 1999); cell refinement: SAINT (Bruker, 1999); data reduction: SAINT; program(s) used to solve

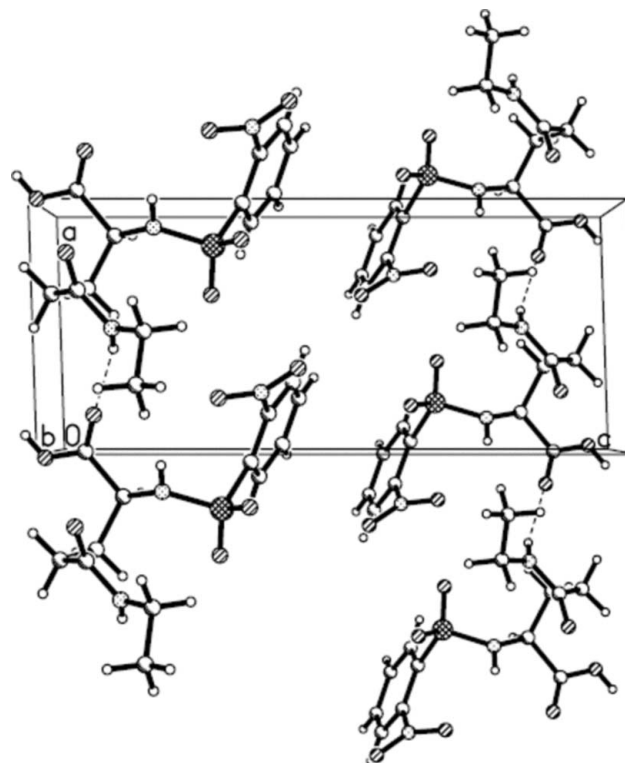


Figure 2

The packing in (I), with hydrogen bonds shown as dashed lines.

structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Bruker, 1999); software used to prepare material for publication: SHELXTL.

This project was supported by the National Natural Science Foundation of China (No. 20602021) and the Basic Research Development Program of China (973 Program) (grant No. 2003CB114406).

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