

Pyrazolidine-3,5-dione angiotensin-II receptor antagonists

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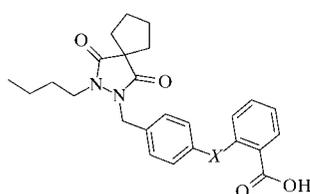
Received 29 June 2001

Accepted 13 August 2001

The crystal structures of three angiotensin-II receptor antagonists involving different spacer groups (CO, CONH and NHCO) between the aryl rings are presented, namely 2-{4-[(3-butyl-1,4-dioxo-2,3-diazaspiro[4.4]non-2-yl)methyl]benzoyl}benzoic acid, C₂₆H₂₈N₂O₅, (I), 2-{4-[(3-butyl-1,4-dioxo-2,3-diazaspiro[4.4]non-2-yl)methyl]benzamido}benzoic acid, C₂₆H₂₉N₃O₅, (II), and 2-{4-[(3-butyl-1,4-dioxo-2,3-diazaspiro[4.4]non-2-yl)methyl]anilino}benzoic acid monohydrate, C₂₆H₂₉N₃O₅·H₂O, (III). The aryl rings of (II) are almost coplanar, in contrast with compounds (I) and (III). The conformation of (II) is induced by an intramolecular N—H···O hydrogen bond between the amide and carboxylic acid groups.

Comment

The renin-angiotensin system (RAS) plays an important role in the regulation of blood pressure and electrolyte balance. Non-peptide AT1-selective angiotensin-II receptor antagonists which block the RAS are of great interest in the treatment of hypertension and other cardiovascular diseases (Wexler *et al.*, 1996). Recently, we reported new pyrazolidine-3,5-dione derivatives displaying AT1-binding affinity (Le Bourdonnec *et al.*, 2000). In this paper, we compare the X-ray structures of three compounds from this series, (I), (II) and (III), involving different spacer groups between the two aryl rings.



- (I) X = CO
(II) X = CONH
(III) X = NHCO, H₂O

The atom-numbering schemes and molecular conformations adopted by compounds (I), (II) and (III) are depicted in

Figs. 1, 2 and 3, respectively. For each compound, the pyrazolidine-3,5-dione heterocycle is almost planar; the displacement of the atoms from their mean plane does not exceed 0.096 Å. The C24 and C6 substituents deviate from this plane by distances ranging from 0.35 to 0.78 Å. In (III), the terminal part of the butyl chain and the spiropentyl groups are disordered. Two orientations were found for these moieties, with occupancy factors of 0.57 and 0.43 for C26—C27 and C26'—C27', and 0.63 and 0.37 for C29—C30 and C29'—C30'.

The three compounds present some differences in the conformation of the Ph—X—PhCO₂H_{ortho} moiety. Indeed, the orientation of the central aryl ring (C7—C12) is quite different for (I) when compared with the other two. The N1—C6—C7—C8 torsion angles are −2.6 (3), −78.4 (3) and −98.4 (2)° for (I), (II) and (III), respectively. Furthermore, the angle between the planes of the two aryl rings varies depending on the nature of the linkage (carbonyl, amide or retroamide). In compound (I), the two rings form a dihedral angle of 82.8 (1)°, with the carbonyl function almost in the same plane as the central aryl ring [C11—C10—C34—O35 −10.5 (3)°]. In (II), the two phenyl rings are twisted slightly from coplanarity [dihedral angle between the planes 32.3 (1)°], whereas in (III), they are distorted by 88.0 (1)°. In fact, for these two latter derivatives, the amide function is in the same plane as the central aryl ring [the dihedral angle between the planes is 11.5 (5)° for (II) and 10.5 (2)° for (III)]. However, there is a difference in the orientation of the terminal phenyl ring (C13—C18) with respect to the amide function. In (II), the aryl and amide moieties are almost coplanar [dihedral angle 21.1 (4)°]. This conformation is stabilized by an intramolecular hydrogen bond between the amide and carboxylic acid moieties (N36—H36···O21; Table 2). In (III), this intramolecular hydrogen bond is not present and the terminal aryl ring is perpendicular to the retroamide group [dihedral angle 81.7 (1)°]. For all three derivatives, the carboxylic acid function is almost coplanar with the corresponding phenyl ring, with C13—C14—C19—O21 torsion angles of 3.7 (3), −12.1 (5) and

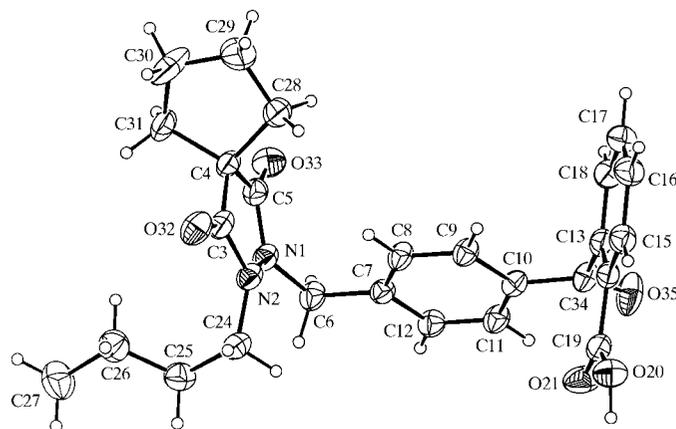


Figure 1

A view of the molecule of compound (I), with displacement ellipsoids drawn at the 30% probability level and H atoms shown as small spheres of arbitrary radii.

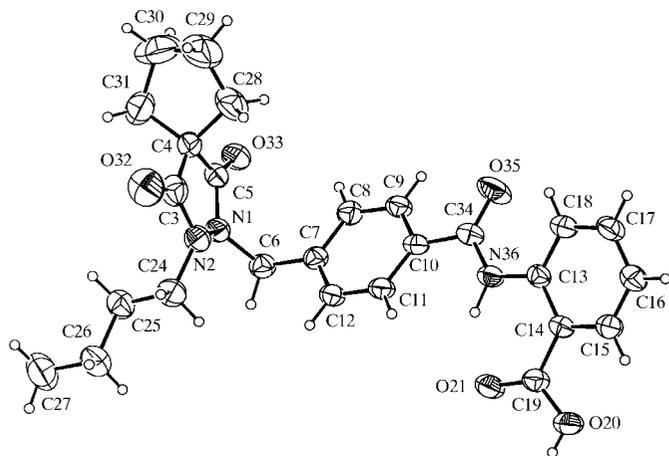


Figure 2

A view of the molecule of compound (II), with displacement ellipsoids drawn at the 30% probability level and H atoms shown as small spheres of arbitrary radii.

4.9 (3)° for (I), (II) and (III), respectively. The C14–C19 distances, ranging from 1.480 to 1.489 Å, are shorter than common single bonds, indicative of a delocalization between the two groups.

In addition to the intramolecular hydrogen bond observed in (II), some intermolecular donor–acceptor interactions are also found for the three derivatives; details of these are given in Tables 1, 2 and 3. For (I) and (II), the carboxylic acid group is involved in a hydrogen bond with the O33 acceptor atom (O20–H20···O33; Tables 1 and 2). For compound (III), the cocrystallized water molecule is involved in the hydrogen-bonding pattern. It interacts as a double H-atom donor with the pyrazolidine-3,5-dione heterocycle (O37–H37A···O33 and O37–H37B···O32; Table 3) and as an H-atom acceptor with the carboxylic acid moiety (O20–H20···O37; Table 3). Furthermore, an intermolecular hydrogen bond exists between the amide functions (N36–H36···O35; Table 3).

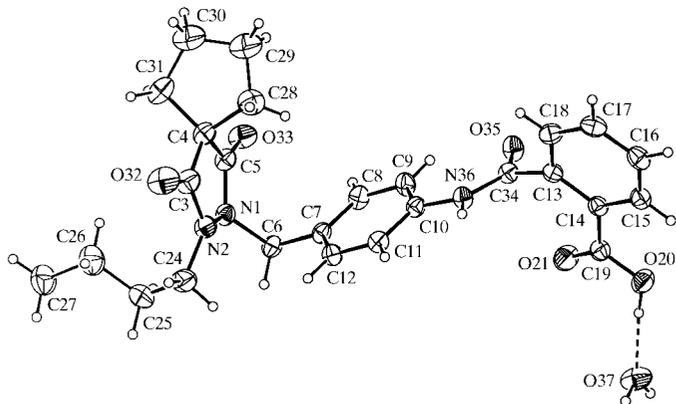


Figure 3

A view of the molecule of compound (III), with displacement ellipsoids drawn at the 30% probability level and H atoms shown as small spheres of arbitrary radii. Only one conformation of the terminal part of the alkyl chain (C26–27) and the spiropentyl group (C29–C30) is shown.

Experimental

The syntheses of compounds (I), (II) and (III) have been reported previously by Le Bourdonnec *et al.* (2000). Crystals were obtained by slow evaporation of an isooctane–ethyl acetate solution for (I), a toluene–ethyl acetate solution for (II) and an ethyl acetate solution for (III), all at room temperature.

Compound (I)

Crystal data

C₂₆H₂₈N₂O₅
M_r = 448.50
 Triclinic, *P* $\bar{1}$
a = 10.530 (1) Å
b = 11.469 (1) Å
c = 11.491 (1) Å
 α = 109.589 (8)°
 β = 112.690 (8)°
 γ = 97.640 (9)°
V = 1150.02 (18) Å³

Z = 2
D_x = 1.295 Mg m⁻³
 Cu *K*α radiation
 Cell parameters from 25 reflections
 θ = 40–50°
 μ = 0.73 mm⁻¹
T = 293 (2) K
 Block, colourless
 0.31 × 0.29 × 0.23 mm

Data collection

Enraf–Nonius CAD-4 diffractometer
 $\theta/2\theta$ scans
 Absorption correction: ψ scan (North *et al.*, 1968)
T_{min} = 0.804, *T_{max}* = 0.849
 4750 measured reflections
 4511 independent reflections
 3537 reflections with *I* > 2σ(*I*)

R_{int} = 0.043
 θ_{max} = 71.9°
h = -12 → 12
k = 0 → 14
l = -14 → 13
 3 standard reflections every 200 reflections
 frequency: 60 min
 intensity decay: 2%

Refinement

Refinement on *F*²
R [*F*² > 2σ(*F*²)] = 0.050
wR (*F*²) = 0.152
S = 1.04
 4511 reflections
 302 parameters
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0781P)^2 + 0.3037P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} = 0.002$
 $\Delta\rho_{\text{max}} = 0.28 \text{ e \AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.28 \text{ e \AA}^{-3}$

Table 1

Hydrogen-bonding geometry (Å, °) for (I).

<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>
O20–H20···O33 ⁱ	0.90 (3)	1.79 (3)	2.687 (3)	174 (3)

Symmetry code: (i) *x*, *y* – 1, *z*.

Compound (II)

Crystal data

C₂₆H₂₉N₃O₅
M_r = 463.52
 Monoclinic, *P*₂₁/*c*
a = 16.122 (1) Å
b = 12.682 (1) Å
c = 11.920 (1) Å
 β = 97.139 (7)°
V = 2418.3 (3) Å³
Z = 4

D_x = 1.273 Mg m⁻³
 Cu *K*α radiation
 Cell parameters from 25 reflections
 θ = 40–50°
 μ = 0.73 mm⁻¹
T = 293 (2) K
 Platelet, colourless
 0.29 × 0.10 × 0.03 mm

Data collection

Enraf–Nonius CAD-4 diffractometer
 $\theta/2\theta$ scans
 Absorption correction: ψ scan (North *et al.*, 1968)
 $T_{\min} = 0.817$, $T_{\max} = 0.979$
 6842 measured reflections
 4757 independent reflections
 1972 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.026$
 $\theta_{\text{max}} = 71.9^\circ$
 $h = -19 \rightarrow 14$
 $k = -15 \rightarrow 0$
 $l = -14 \rightarrow 14$
 3 standard reflections every 200 reflections
 frequency: 60 min
 intensity decay: 5%

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.053$
 $wR(F^2) = 0.164$
 $S = 0.96$
 4757 reflections
 315 parameters

H atoms treated by a mixture of independent and constrained refinement
 $w = 1/[\sigma^2(F_o^2) + (0.0743P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} = 0.001$
 $\Delta\rho_{\text{max}} = 0.16 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.19 \text{ e } \text{\AA}^{-3}$

Table 2

Hydrogen-bonding geometry (\AA , $^\circ$) for (II).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$N36-H36 \cdots O21$	0.95 (4)	1.86 (4)	2.686 (3)	144 (3)
$O20-H20 \cdots O33^{\text{ii}}$	0.83 (4)	1.79 (4)	2.611 (3)	169 (4)

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

Compound (III)

Crystal data

$C_{26}H_{29}N_3O_5 \cdot H_2O$
 $M_r = 481.54$
 Monoclinic, $P2_1/c$
 $a = 18.681 (1) \text{ \AA}$
 $b = 9.565 (1) \text{ \AA}$
 $c = 14.837 (1) \text{ \AA}$
 $\beta = 111.904 (7)^\circ$
 $V = 2459.7 (3) \text{ \AA}^3$
 $Z = 4$

$D_x = 1.300 \text{ Mg m}^{-3}$
 Cu $K\alpha$ radiation
 Cell parameters from 25 reflections
 $\theta = 40-50^\circ$
 $\mu = 0.76 \text{ mm}^{-1}$
 $T = 293 (2) \text{ K}$
 Platelet, colourless
 $0.26 \times 0.11 \times 0.07 \text{ mm}$

Table 3

Hydrogen-bonding geometry (\AA , $^\circ$) for (III).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$O20-H20 \cdots O37$	0.95 (4)	1.70 (4)	2.623 (3)	163 (4)
$O37-H37A \cdots O33^{\text{iii}}$	0.84 (4)	1.93 (4)	2.759 (3)	171 (4)
$O37-H37B \cdots O32^{\text{iv}}$	0.89 (4)	1.91 (4)	2.793 (3)	174 (3)
$N36-H36 \cdots O35^{\text{v}}$	0.93 (3)	2.08 (3)	3.002 (2)	171 (2)

Symmetry codes: (iii) $1 - x, 2 - y, -z$; (iv) $1 - x, 1 - y, -z$; (v) $1 - x, y - \frac{1}{2}, \frac{1}{2} - z$.

Data collection

Enraf–Nonius CAD-4 diffractometer
 $\theta/2\theta$ scans
 Absorption correction: ψ scan (North *et al.*, 1968)
 $T_{\min} = 0.826$, $T_{\max} = 0.948$
 6162 measured reflections
 4835 independent reflections
 3166 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.013$
 $\theta_{\text{max}} = 71.9^\circ$
 $h = -23 \rightarrow 21$
 $k = -7 \rightarrow 11$
 $l = 0 \rightarrow 18$
 3 standard reflections every 200 reflections
 frequency: 60 min
 intensity decay: 4%

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.049$
 $wR(F^2) = 0.151$
 $S = 1.02$
 4835 reflections
 333 parameters
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0704P)^2 + 0.7853P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} = 0.008$
 $\Delta\rho_{\text{max}} = 0.36 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.28 \text{ e } \text{\AA}^{-3}$
 Extinction correction: *SHELXL97* (Sheldrick, 1997)
 Extinction coefficient: 0.0016 (2)

H atoms attached to C atoms were treated as riding using *SHELXL97* (Sheldrick, 1997) defaults, whereas the H atoms of the N–H and O–H groups were refined on position and with isotropic displacement parameters.

For all compounds, data collection: *CAD-4 EXPRESS* (Enraf–Nonius, 1992); cell refinement: *CAD-4 EXPRESS*; data reduction: *PLATON* (Spek, 2000); program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1999); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON*; software used to prepare material for publication: *SHELXL97*.

CC thanks UCB S.A., Pharma Sector, for financial support. The authors thank the Facultés Universitaires Notre-Dame de la Paix for the use of the Scientific Computing Facility.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: GG1071). Services for accessing these data are described at the back of the journal.

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