hydrogen bond [C(12)···O(15) 2·839 (4), H(12)··· O(15) 2·60 (4) Å, C(12)–H(12A)···O(15) 97 (2)°] which is compatible with the description of Taylor & Kennard (1982): a nearest-neighbour contact of 0·41 Å, and the immediate adjacency of a positively charged N to the proton donor. This provides a reasonable explanation as to why the C(12)–C(13)–C(14)–O(15) torsion angle is (−)-synclinal instead of antiperiplanar.

The packing of the crystal (Fig. 3) is essentially due to the presence of the water molecule. This molecule serves twice as a proton donor [O(17)···Br^i 3·322 (4), H(17B)···Br^i 2·38 (5) Å, O(17)–H(17B)···Br^i 174 (4)°; O(17)···O(2′)^{ii} 2·846 (5), H(17A)···O(2′)^{ii} 2·20 (6) Å, O(17)–H(17A)···O(2′)^{ii} 172 (6)°; (i) x, $y-1$, $z-1$; (ii) $-x+2$, $y-\frac{1}{2}$, $-z$] and once as acceptor [O(2′)···O(17) 2·653 (5), H(2′)···O(17) 1·92 (5) Å, O(2′)–H(2′)···O(17) 171 (6)°]. A hydrogen bond between piperidinium and bromide is also present [N(2)···Br 3·359 (3), H(2)···Br 2·45 (5) Å, N(2)–H(2)···Br 169 (3)°].

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(−)-(1R,5R,9R,2″R)-2′-Hydroxy-5,9-dimethyl-2-[2-(tetrahydro-2-furyl)ethyl]-6,7-benzomorphan Hydrobromide*†

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Abstract. $C_{20}H_{30}NO_2^+.Br^-$, $M_r = 396·37$, orthorhombic, $P2_12_12_1$, $a = 12·210$ (7), $b = 17·219$ (12), $c = 9·417$ (5) Å, $V = 1980$ (2) Å^3, $Z = 4$, $D_m = 1·33$ (2), $D_x = 1·330$ Mg m^{-3}, $\lambda(Mo\ K\alpha) = 0·71069$ Å, $\mu(Mo\ K\alpha) = 2·21$ mm^{-1}, $F(000) = 832$, 291 K, final $R = 0·061$ for 1598 observed reflections. The N-side-chain torsion angles starting from C(1) towards O(15) are approximately at the global energy minimum in the three-dimensional torsional space: (−)-synclinal, anti-periplanar and (−)-synclinal respectively.

Introduction. Both the title compound and its 3″S diastereoisomer have been classified as morphine-like opioid analgesics on the basis of *in vivo* pharmacological tests in mice, and they are about equipotent (Merz & Stockhaus, 1979). In contrast, their counterparts with a methylene instead of an ethylene bridge between N and tetrahydrofuryl (Peeters, De Ranter & Blaton, 1982) display a marked stereoselectivity, with the 2″S form being roughly 300 times more potent than the 2″R form. The present structure determination together with that of its diastereoisomer should provide some insight into the observed abolition of stereoselectivity.

Experimental. Crystals obtained at room temperature from an equimolar ethyl acetate–methanol solution. Density measured by flotation in n-heptane/CCl_4, $\sim0\cdot5 \times 0\cdot2 \times 0\cdot2$ mm, Syntex $P2_1$ computer-controlled four-circle diffractometer, graphite-monochromated Mo $K\alpha$ radiation, ω-scan technique ($2\theta_{max} = 50°$, $0 \leq h \leq 13$, $-18 \leq k \leq 18$, $-11 \leq l \leq 11$), cell dimensions by least-squares refinement of the setting angles of 15 reflections with $20 < 2\theta < 27°$, space group $P2_12_12_1$ from systematic absences $h00$ for h odd, $0k0$ for k odd, $00l$ for l odd respectively. Three standard reflections ($\overline{2}1\overline{1}$, $03\overline{1}$, 012) monitored after each 50 reflections fluctuated between 97·6 and 100·9% of their initial intensity. Merging equivalent reflections yielded 2771 independent reflections (R_{int} = 0·065) (Friedel's law not obeyed), 1598 observed reflections [$I > 2\sigma(I)$], Lorentz–polarization corrections, absorption corrections were omitted, scattering factors from Cromer & Mann (1968) and Stewart, Davidson & Simpson (1965) (for H), anomalous-dispersion correction for Br (*International Tables for X-ray Crystallography*, 1974).

The position of the Br obtained from a Patterson synthesis served as input for *DIRDIF* (Beurskens *et al.*, 1981). The resulting E map showed all non-hydrogen atoms present in the asymmetric unit. Refinement with *XRAY76* (Stewart, Machin, Dickinson, Ammon, Heck & Flack, 1976) by block-diagonal least squares on F, first with isotropic temperature factors and then anisotropically; full-matrix least squares finally executed. H positions from ΔF synthesis included in refinement with fixed positions and overall temperature factors; final $R = 0\cdot061$, $wR = 0\cdot037$ and $S = 1\cdot50$, $w = 1/[\sigma(|F_o|)^2]$, $(\Delta/\sigma)_{ave} = 0\cdot10$, $(\Delta/\sigma)_{max} = 0\cdot57$, $-1\cdot26 \leq$ final $\Delta\rho$ excursions $\leq 0\cdot93$ e $Å^{-3}$ (minimum and maximum are near the Br).

Discussion. The atomic numbering scheme is given in Fig. 1 and parameters are listed in Table 1.* Bond lengths and angles are given in Table 2. An *ORTEP* view (Johnson, 1965) is shown in Fig. 2. A few rather short bond distances are observed within the benzomorphan nucleus: C(2')—C(3'), C(7)—C(8), C(1)—C(9), C(3)—C(4) are all some 0·03 Å below expectations. Since absorption corrections have been omitted, such deviations from normal geometry should not be considered as significant. On the other hand, bond angles are fairly normal. The normal 6,7-benzomorphan features are clearly present: a planar aro-

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* Lists of structure factors, anisotropic thermal parameters and H-atom parameters have been deposited with the British Library Document Supply Centre as Supplementary Publication No. SUP 51007 (23 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

Table 1. *Atomic coordinates and equivalent isotropic thermal parameters with e.s.d.'s of the refined parameters in parentheses*

$$B_{eq} = \tfrac{4}{3}\Sigma_i\Sigma_j\beta_{ij}\mathbf{a}_r\cdot\mathbf{a}_r$$

	x	y	z	$B_{eq}(Å^2)$
Br	0·14610 (9)	0·06760 (8)	0·1157 (1)	5·3 (3)
C(1')	0·7166 (7)	0·1379 (5)	0·1218 (13)	3·5 (3)
C(2')	0·8215 (8)	0·1087 (6)	0·1078 (12)	3·4 (3)
O(2')	0·9074 (4)	0·1511 (3)	0·1639 (7)	4·5 (2)
C(3')	0·8370 (8)	0·0400 (6)	0·0392 (10)	3·9 (3)
C(4')	0·7485 (9)	0·0000 (6)	−0·0123 (10)	4·6 (3)
C(1)	0·4328 (8)	0·0130 (7)	−0·0193 (11)	3·3 (4)
N(2)	0·3870 (5)	−0·0126 (4)	0·1233 (10)	3·4 (2)
C(3)	0·4568 (8)	0·0180 (8)	0·2442 (11)	4·3 (4)
C(4)	0·4674 (9)	0·1039 (8)	0·2362 (13)	4·4 (4)
C(5)	0·5114 (7)	0·1327 (6)	0·0955 (13)	3·2 (3)
C(6)	0·6268 (7)	0·0971 (5)	0·0713 (9)	2·2 (3)
C(7)	0·6409 (9)	0·0261 (5)	0·0049 (9)	3·1 (3)
C(8)	0·5480 (8)	−0·0191 (6)	−0·0516 (10)	3·9 (3)
C(9)	0·4330 (9)	0·0992 (7)	−0·0207 (12)	3·4 (4)
C(10)	0·4589 (8)	0·1334 (6)	−0·1664 (10)	4·8 (4)
C(11)	0·5085 (6)	0·2204 (6)	0·1017 (12)	4·7 (3)
C(12)	0·3664 (9)	−0·0971 (6)	0·1381 (12)	4·5 (3)
C(13)	0·2873 (8)	−0·1332 (7)	0·0299 (10)	4·5 (3)
C(14)	0·2642 (9)	−0·2181 (7)	0·0648 (11)	5·0 (4)
O(15)	0·3632 (6)	−0·2594 (4)	0·0618 (7)	6·0 (2)
C(16)	0·3790 (11)	−0·2899 (8)	−0·0752 (15)	7·6 (5)
C(17)	0·2703 (13)	−0·2848 (7)	−0·1544 (14)	7·8 (6)
C(18)	0·1895 (9)	−0·2581 (8)	−0·0429 (17)	7·1 (5)

Table 2. *Bond lengths (Å) and bond angles (°)*

C(1')—C(2')	1·38 (1)	C(5)—C(6)	1·55 (1)
C(1')—C(6)	1·39 (1)	C(5)—C(9)	1·56 (2)
C(2')—O(2')	1·38 (1)	C(5)—C(11)	1·51 (1)
C(2')—C(3')	1·36 (1)	C(6)—C(7)	1·38 (1)
C(3')—C(4')	1·37 (1)	C(7)—C(8)	1·48 (1)
C(4')—C(7)	1·40 (1)	C(9)—C(10)	1·53 (1)
C(1)—N(2)	1·52 (1)	C(12)—C(13)	1·53 (1)
C(1)—C(8)	1·54 (1)	C(13)—C(14)	1·52 (2)
C(1)—C(9)	1·48 (2)	C(14)—O(15)	1·40 (1)
N(2)—C(3)	1·52 (1)	C(14)—C(18)	1·53 (2)
N(2)—C(12)	1·48 (1)	O(15)—C(16)	1·41 (2)
C(3)—C(4)	1·49 (2)	C(16)—C(17)	1·52 (2)
C(4)—C(5)	1·51 (2)	C(17)—C(18)	1·51 (2)

C(2')—C(1')—C(6)	121·0 (9)	C(1')—C(6)—C(5)	117·9 (8)
C(1')—C(2')—O(2')	118·3 (9)	C(1')—C(6)—C(7)	120·3 (9)
C(1')—C(2')—C(3')	119·4 (9)	C(5)—C(6)—C(7)	121·8 (8)
O(2')—C(2')—C(3')	122·3 (9)	C(4')—C(7)—C(6)	116·9 (9)
C(2')—C(3')—C(4')	119·7 (10)	C(4')—C(7)—C(8)	120·6 (9)
C(3')—C(4')—C(7)	122·6 (10)	C(6)—C(7)—C(8)	122·4 (9)
N(2)—C(1)—C(8)	113·8 (8)	C(1)—C(8)—C(7)	116·1 (8)
N(2)—C(1)—C(9)	107·4 (8)	C(1)—C(9)—C(5)	111·4 (9)
C(8)—C(1)—C(9)	110·8 (9)	C(1)—C(9)—C(10)	113·2 (9)
C(1)—N(2)—C(3)	110·9 (7)	C(5)—C(9)—C(10)	111·1 (9)
C(1)—N(2)—C(12)	115·5 (8)	N(2)—C(12)—C(13)	116·3 (9)
C(3)—N(2)—C(12)	111·5 (9)	C(12)—C(13)—C(14)	111·2 (8)
N(2)—C(3)—C(4)	110·9 (9)	C(13)—C(14)—O(15)	108·8 (9)
C(3)—C(4)—C(5)	113·6 (10)	C(13)—C(14)—C(18)	113·5 (9)
C(4)—C(5)—C(6)	108·7 (8)	O(15)—C(14)—C(18)	105·8 (9)
C(4)—C(5)—C(9)	106·0 (8)	C(14)—O(15)—C(16)	109·1 (8)
C(4)—C(5)—C(11)	106·5 (9)	O(15)—C(16)—C(17)	107·9 (10)
C(6)—C(5)—C(9)	107·9 (8)	C(16)—C(17)—C(18)	104·2 (11)
C(6)—C(5)—C(11)	114·9 (7)	C(14)—C(18)—C(17)	102·1 (9)
C(9)—C(5)—C(11)	112·4 (9)		

matic ring connected to a half-boat six-membered ring, and perpendicular to it a piperidine in the chair conformation.

Following the N-side chain from C(1) to O(15) a (−)-synclinal [−58 (1)]/antiperiplanar [−174 (1)]/ (−)-synclinal [−60 (1)°] conformation is observed. The tetrahydrofuryl ring adopts a twist form with a local twofold axis through C(16). It has a rather moderate puckering amplitude of 0·31 (1) Å, compared with the normal value of 0·37 Å (Cremer & Pople, 1975); furthermore, the displacement factors of C(16), C(17) and C(18) are quite large. Whether this is due to minor static variations in the crystal or to dynamic behaviour remains a matter of discussion.

With respect to the N-side-chain conformation, the three-dimensional rotational space (if the different puckering forms of the tetrahydrofuryl are not taken into account) was explored using the empirical potential-energy-evaluating program *EENY* (Motherwell, 1974) with constants from Giglio (1969). The C(12)—C(13)—C(14)—O(15) dihedral angle is limited to the range 150–360° to avoid synperiplanarity between the ring and the C(12) moiety, while the H(3) and H(8) atoms make the C(1)—N(2)— C(12)—C(13) region 0–150° barely accessible. Within these restrictions, N(2)—C(12)—C(13)—C(14) can adopt several values in the range 60–360°. Within 5·0 kJ mol⁻¹ of the global energy minimum eight other possible conformers are found. All are present in the 180 and 300° sections of the C(12)—C(13)—C(14)— O(15) torsion angle (Fig. 3). One of these minima is observed in the crystal structure.

The packing of the crystal (Fig. 4) is essentially achieved by forming endless chains along a through hydrogen bonds between the piperidinium and bromide,

(a)

(b)

Fig. 3. Map of the intramolecular potential-energy calculations; the contours are in kJ mol⁻¹. The asterisk indicates the conformation adopted in the crystal. (a) Section for C(12)—C(13)—O(14)— C(15) at 180°; (b) section at 300°.
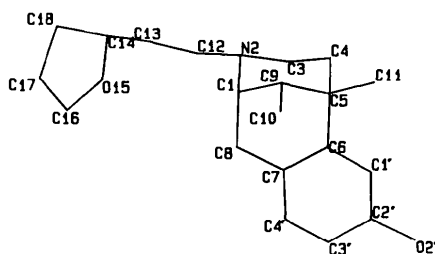

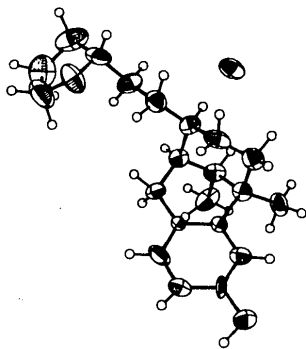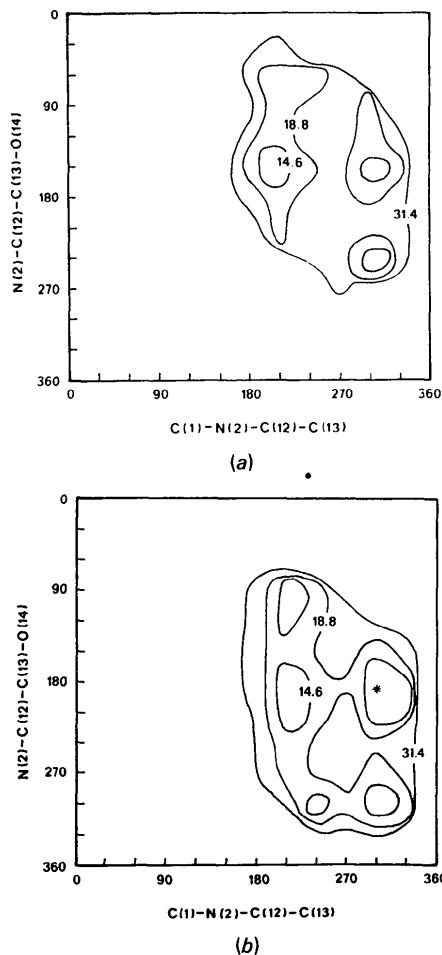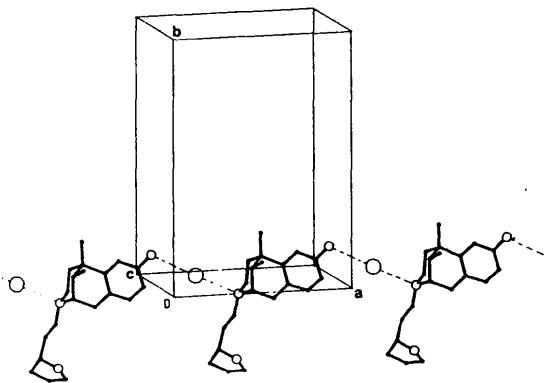Fig. 1. Atomic numbering scheme.

Fig. 2. A view of the title compound with 50% probability anisotropic displacement ellipsoids for the non-hydrogen atoms.

Fig. 4. Packing of the crystal. Hydrogen bonds are indicated by dashed lines.

and between bromide and phenol [N(2)$\cdots$Br 3·252 (7), H(2)$\cdots$Br 2·168 (2) Å, N(2)–H(2)$\cdots$Br 172·7 (5)°, O(2')$\cdots$Br^i 3·281 (6), H(2')$\cdots$Br^i 2·187 (2) Å, O(2')–H(2')$\cdots$Br^i 172·0 (3)°; (i) $x + 1, y, z$].

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Structure and Conformation of a Tightly Bound Inhibitor of Adenosine Transport, 2-Amino-6-[(4-nitrobenzyl)thio]-9-β-D-ribofuranosylpurine

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Abstract. $C_{17}H_{18}N_6O_6S$, $M_r = 434·4$, monoclinic, $P2_1$, $a = 14·577$ (4), $b = 8·820$ (2), $c = 7·304$ (2) Å, $\beta = 94·76$ (1)°, $V = 935·9$ Å^3, $Z = 2$, $D_m = 1·55$, $D_x = 1·542$ g cm^{-3}, $\lambda(Cu K\alpha) = 1·5418$ Å, $\mu = 19·66$ cm^{-1}, $F(000) = 452$, $T = 287$ K, $R = 0·029$ ($wR = 0·038$) for 1995 observed reflections. The glycosidic torsion angle, χ[C(8)–N(9)–C(1')–O(4')], is $-120·0$ (4)°, which corresponds to the *syn* nucleoside conformation with an intramolecular O(5')–H(O5')$\cdots$N(3) hydrogen bond; the ribose has the C(2')-*endo* (^2E) pucker conformation with pseudorotational parameters: $P = 158·6$ (3)° and $\tau_m = 36·7$ (3)°; C(2') is displaced 0·567 Å from the plane of C(3'), C(4'), O(4') and C(1'). The conformation of the exocyclic C(4')–C(5') bond is g^+.

Introduction. The passage of nucleoside molecules across the plasma membrane of animal cells is mediated by nucleoside-specific transport mechanisms of several types (for reviews, see Plagemann & Wohlueter, 1980; Young & Jarvis, 1983; Paterson & Cass, 1985; Paterson, Jakobs, Ng, Odegard & Adjei, 1987), including (*a*) facilitative diffusion (equilibrative) systems of high or low sensitivity to 6-[(4-nitrobenzyl)-thio]-9-β-D-ribofuranosylpurine (NBMPR) (Soriano-Garcia, Parthasarathy, Paul & Paterson, 1984; Paterson *et al.*, 1987), the potent nucleoside transport (NT) inhibitor, and (*b*) concentrative, 'secondary active' NT systems linked to fluxes of sodium ions (Paterson *et al.*, 1987; Jakobs & Paterson, 1986). Of these, the best characterized is the equilibrative NBMPR-sensitive NT system of human erythrocytes (Young & Jarvis, 1983; Jarvis, Hammond, Paterson & Clanachan, 1983; Plagemann & Wohlueter, 1984*a*, *b*). A component of that system, a membrane glycoprotein of M_r 45 000–66 000 (Young, Jarvis, Robins & Paterson, 1983), binds NBMPR at sites with high affinity [K_D 0·3 n*M* (Jarvis, Hammond, Paterson & Clanachan, 1982)] for that ligand. NBMPR-sensitive equilibrative NT systems