Crystal and Molecular Structure of 3-(Adenin-9-yl)propiontryptamide

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The crystal structure of 3-(adenin-9-yl)propiontryptamide (3-(adenin-9-yl)-*N*-[2-(3-indolyl)ethyl]propionamide) has been investigated as a model for adenine-tryptophan interaction. The space group of the crystal is $P2_1/c$, with dimensions $a=8.512(2)$, $b=16.884(3)$, $c=12.405(3)$ Å, $\beta=105.54(2)°$, and $Z=4$. The structure was solved by the direct method and refined by a block-diagonal least-squares method. A slight overlapping between adenine and indole moieties is found, but it may not be sufficient to produce a strong π-π interaction. The adenine base is paired with that related by the centre of symmetry through two N(6)H···N(1) hydrogen bonds, and also with the other centrosymmetrically related adenine base through two N(6)H···N(7) hydrogen bonds. Adenine and indole are bound through a hydrogen bond between N(7) of adenine and imino nitrogen of indole.

Interaction between nucleic acid and protein plays an important role in several biological processes, though the precise molecular mechanism is still unknown. Some elementary binding patterns between amino acid and purine-pyrimidine base, if any, would provide a stereochemical basis for the mechanism of mutual recognition between nucleic acid and protein.

We have reported some common hydrogen bond schemes between cytosine and acidic amino acid through X-ray crystallographic studies of complexes between nucleotide bases and amino acid derivatives.[1-3] The preparation of complex crystals is very difficult owing to the physico-chemical properties of the compounds; only a few complex crystals of restricted combination of components have been obtained. We have tried to use other type of model compounds containing a nucleotide base and a side group of amino acid in a molecule. They might provide interaction modes for any combinations between nucleotide bases and amino acids.

Intermolecular stacking interaction between adenine and tryptophan was suggested from spectroscopic studies.[4-7] On the other hand, in the crystal of 9-ethyladenine–indole complex[8] there is no stacking interaction between the two components. They are bound through a hydrogen bond between N(3) of adenine and imino nitrogen of indole. We have found the same hydrogen bond in the monohydrate crystal[9] of the title compound. In the present paper, we report another mode of hydrogen bond between adenine and indole moieties.

Experimental

3-(Adenin-9-yl)propiontryptamide (3-(adenin-9-yl)-*N*-[2-(3-indolyl)ethyl]propionamide) was synthesized from 9-(β-carboxyethyl)adenine[10] and tryptamine by the dicyclohexylcarbodiimide method. Plate crystals were obtained by evaporating a solution of benzene and methanol (10: 1) at room temperature. Oscillation and Weissenberg photographs showed the space group to be $P2_1/c$ from the systematic absence of reflexions. The density was determined by flotation in a mixture of cyclohexane and carbon tetrachloride. A crystal, $0.2\times0.3\times0.4$ mm, was mounted on a Rigaku four-circle automated diffractometer. Unit-cell parameters were calculated by least-squares refinement of 2θ values for 22 high-angle reflexions (Mo$K\alpha$; $\lambda=0.71069$ Å). Crystallographic data are summarized in Table 1.

Table 1. Crystal data

3-(Adenin-9-yl)propiontryptamide	
$C_{18}H_{19}N_7O$	$F.W.=349.40$
Crystal system: monoclinic	
Systematic absences: $h0l$, $l=2n+1$; $0k0$, $k=2n+1$	
Space group: $P2_1/c$	$Z=4$
$a=8.512(2)$ Å	$D_x=1.350$ g cm^{-3}
$b=16.884(3)$	$D_m=1.34_7$ g cm^{-3}
$c=12.405(3)$	μ(Mo$K\alpha$)
$\beta=105.54(2)°$	$=0.98$ cm^{-1}
$U=1719.6(6)$ Å^3	

Intensity data were collected on the diffractometer by use of graphite-monochromated Mo$K\alpha$ radiation, with a $\omega/2\theta$ scanning technique ($2\theta\leq50°$). Five reference reflexions monitored periodically showed no significant intensity fluctuations during the course of data collection. Corrections were made for the Lorentz and polarization factors, but not for absorption. A total of 3030 independent reflexions were obtained, zero-reflexions ($I\leq\sigma(I)$) numbering 810.

Structure Determination and Refinement

The structure was solved by the symbolic addition procedure.[11] The atomic parameters were refined by the block-diagonal least-squares method; the quantity minimized was $\Sigma\omega(|F_o|-|F_c|)^2$, with $\omega=1/(\sigma^2_p+qF_o^2)$ where σ_p is due to counting statistics and q is 1.25×10^{-5} derived from the intensity variance of the monitored reflexions. In the refinement, the zero-reflexions were included by assuming $|F_o|=F_{lim}$ and $\omega=\omega(F_{lim})$ where F_{lim} is 2.43, an observational threshold value. However, zero-reflexions for which $|F_c|<F_{lim}$ were omitted. When the R value reached 0.11, a difference synthesis revealed all the hydrogen atoms. The refinement was terminated when the maximum shift of parameters for hydrogen was less than 0.49σ. The final R value was 0.088 for 2504 reflexions ($R=0.073$ for $F_o\geq3/\sqrt{\omega}$). Atomic scattering factors were taken from "International Tables for X-Ray Crystallography."[12] A comparison between observed and calculated structure factors is given in Table 2.[13] The final positional and thermal parameters are listed in Table 3.

Table 3. Final positional and thermal parameters

Standard deviations are given in parentheses. The anisotropic temperature factor has the form $\exp[-(B_{11}h^2+B_{22}k^2+B_{33}l^2+B_{12}hk+B_{13}hl+B_{23}kl)]$.

Atom	x*	y*	z*	B_{11}*	B_{22}*	B_{33}*	B_{12}*	B_{13}*	B_{23}*
N(1)	−3764(3)	−491(2)	1369(2)	83(4)	46(1)	42(2)	3(4)	29(5)	6(3)
C(2)	−3318(4)	−679(2)	2460(3)	109(6)	48(2)	53(3)	−1(6)	76(7)	2(4)
N(3)	−1841(3)	−879(2)	3110(2)	101(5)	41(1)	38(2)	11(4)	44(5)	2(3)
C(4)	−720(3)	−858(2)	2521(2)	86(5)	25(1)	38(2)	4(5)	16(6)	0(3)
C(5)	−1005(3)	−656(2)	1411(2)	70(5)	27(1)	43(2)	4(4)	27(6)	2(3)
C(6)	−2593(4)	−470(2)	816(2)	101(6)	30(1)	42(3)	−10(5)	25(6)	−4(3)
N(6)	−3003(3)	−280(2)	−273(2)	89(5)	54(2)	38(2)	8(4)	12(5)	26(3)
N(7)	438(3)	−698(2)	1079(2)	96(5)	35(1)	42(2)	13(4)	37(5)	4(3)
C(8)	1527(4)	−912(2)	2001(3)	89(5)	33(2)	51(3)	13(5)	45(6)	−2(3)
N(9)	911(3)	−1020(1)	2897(2)	88(4)	27(1)	36(2)	12(4)	15(5)	3(3)
C(9)	1851(4)	−1259(2)	4024(3)	116(6)	31(2)	43(3)	27(5)	21(6)	11(3)
C(10)	2230(4)	−555(2)	4823(2)	114(6)	29(1)	47(3)	17(5)	30(6)	0(3)
C(11)	2989(4)	126(2)	4344(2)	96(6)	35(2)	39(3)	0(5)	−2(6)	−5(3)
O(1)	3832(3)	13(1)	3692(2)	133(4)	50(1)	63(2)	−19(4)	90(5)	−34(3)
N(10)	2671(3)	841(2)	4699(2)	135(5)	33(1)	43(2)	9(4)	53(5)	1(3)
C(12)	3311(4)	1568(2)	4363(3)	156(7)	34(2)	64(3)	−30(6)	16(8)	−1(4)
C(13)	1953(5)	2167(2)	3923(3)	219(8)	32(2)	64(3)	11(6)	1(8)	−16(4)
C(14)	705(4)	1895(2)	2889(3)	191(8)	26(2)	46(3)	17(6)	26(7)	2(3)
C(15)	988(4)	1544(2)	1969(3)	161(7)	45(2)	71(3)	21(6)	28(8)	−11(4)
N(11)	−459(3)	1401(2)	1180(2)	185(6)	44(2)	54(3)	3(5)	36(6)	−16(3)
C(16)	−1726(4)	1650(2)	1582(3)	169(7)	29(2)	62(3)	0(6)	43(8)	12(4)
C(17)	−1019(4)	1969(2)	2667(3)	180(7)	24(1)	59(3)	5(5)	58(8)	19(4)
C(18)	−2064(5)	2273(2)	3262(3)	249(9)	31(2)	81(4)	3(7)	148(9)	25(4)
C(19)	−3718(5)	2258(2)	2781(4)	240(9)	38(2)	154(5)	−8(7)	233(12)	15(5)
C(20)	−4375(5)	1944(2)	1708(4)	181(9)	40(2)	175(6)	−36(7)	126(11)	20(6)
C(21)	−3410(4)	1628(2)	1096(3)	177(8)	37(2)	98(4)	−29(7)	15(9)	12(5)

*$\times 10^4$

Atom	x**	y**	z**	B/Å^2	Atom	x**	y**	z**	B/Å^2
H(2)	−422(3)	−66(2)	286(2)	1.3(0.7)	H(122)	419(3)	182(2)	504(2)	2.7(0.8)
H(61)	−412(3)	−8(2)	−67(2)	2.2(0.8)	H(131)	251(3)	268(2)	377(2)	1.5(0.7)
H(62)	−223(3)	−14(2)	−53(2)	2.1(0.8)	H(132)	132(3)	232(2)	449(2)	2.2(0.8)
H(8)	268(3)	−99(1)	203(2)	0.9(0.7)	H(15)	205(4)	143(2)	185(2)	3.4(0.9)
H(91)	288(3)	−151(2)	393(2)	1.7(0.7)	H(11)	−52(4)	114(2)	53(2)	3.6(0.9)
H(92)	115(3)	−167(2)	428(2)	1.4(0.7)	H(18)	−161(3)	248(2)	403(2)	2.1(0.8)
H(101)	310(3)	−77(2)	555(2)	2.6(0.8)	H(19)	−446(4)	248(2)	311(3)	5.6(1.1)
H(102)	120(3)	−38(1)	500(2)	1.1(0.7)	H(20)	−560(4)	194(2)	134(3)	4.4(1.0)
H(10)	219(3)	88(2)	528(2)	3.1(0.8)	H(21)	−383(4)	140(2)	30(3)	3.9(0.9)
H(121)	393(3)	146(2)	379(2)	2.2(0.8)					

**$\times 10^3$

Results and Discussion

Molecular Structure. Bond lengths and angles are given in Table 4 and those involving non-hydrogen atoms in Fig. 1. The least-squares planes of adenine, indole and amide moieties are given in Table 5, together with the displacements of atoms from the planes. The molecular structure is shown in Fig. 2, torsion angles being given in Table 6.

The bond lengths and angles of the adenine ring are in good agreement with those found in related compounds.[14] The purine base is highly planar with a maximum shift of 0.011 Å for N(1) from the least-squares plane.

In the six-membered ring of indole, the bond lengths of C(18)–C(19) and C(20)–C(21) are shorter than the others, the bond angle of C(16)–C(21)–C(20) being the smallest. This is a common feature in the related compounds.[15,16] The indole ring is highly planar with a maximum displacement of 0.010 Å for C(20) from the least-squares plane. The exocyclic atom of C(13) significantly deviates from the plane.

As shown in Fig. 2, the molecule is folded as torsions around C(9)–C(10) and C(12)–C(13) are in skew arrangement (Table 6), in contrast to the extended form in its monohydrate crystal.[9] The dihedral angle between the adenine and indole rings in the molecule is 38.3°. The shortest intramolecular contact between the adenine and indole rings is 3.612 Å for C(6)···N(11).

Crystal Structure. The crystal structure viewed along the a axis is shown in Fig. 3, and that along the

Table 4. Bond lengths and angles

Length (l/Å)					
N(1)–C(2)	1.343(4)	C(2)–N(3)	1.343(4)	N(3)–C(4)	1.350(4)
C(4)–C(5)	1.374(4)	C(5)–C(6)	1.393(4)	C(6)–N(1)	1.354(4)
C(6)–N(6)	1.340(4)	C(5)–N(7)	1.399(4)	N(7)–C(8)	1.316(4)
C(8)–N(9)	1.363(4)	N(9)–C(4)	1.370(4)	N(9)–C(9)	1.469(4)
C(9)–C(10)	1.525(4)	C(10)–C(11)	1.517(4)	C(11)–O(1)	1.232(4)
C(11)–N(10)	1.337(4)	N(10)–C(12)	1.450(4)	C(12)–C(13)	1.524(5)
C(13)–C(14)	1.501(5)	C(14)–C(15)	1.364(5)	C(15)–N(11)	1.374(5)
N(11)–C(16)	1.371(4)	C(16)–C(17)	1.424(5)	C(17)–C(14)	1.425(5)
C(17)–C(18)	1.398(5)	C(18)–C(19)	1.376(6)	C(19)–C(20)	1.401(6)
C(20)–C(21)	1.369(6)	C(21)–C(16)	1.400(5)		
C(2)–H(2)	1.02(3)	N(6)–H(61)	1.00(3)	N(6)–H(62)	0.84(3)
C(8)–H(8)	0.99(3)	C(9)–H(91)	1.01(3)	C(9)–H(92)	1.03(3)
C(10)–H(101)	1.07(3)	C(10)–H(102)	1.00(3)	N(10)–H(10)	0.93(3)
C(12)–H(121)	1.01(3)	C(12)–H(122)	1.05(3)	C(13)–H(131)	1.03(3)
C(13)–H(132)	1.03(3)	C(15)–H(15)	0.98(3)	N(11)–H(11)	0.90(3)
C(18)–H(18)	0.99(3)	C(19)–H(19)	0.93(4)	C(20)–H(20)	1.02(3)
C(21)–H(21)	1.03(3)				

Angle (ϕ/°)			
C(2)–N(1)–C(6)	118.0(3)	N(1)–C(2)–N(3)	129.1(3)
C(2)–N(3)–C(4)	110.8(3)	N(3)–C(4)–C(5)	126.0(3)
N(3)–C(4)–N(9)	127.6(3)	C(5)–C(4)–N(9)	106.4(3)
C(4)–C(5)–C(6)	118.2(3)	C(4)–C(5)–N(7)	110.5(3)
C(6)–C(5)–N(7)	131.3(3)	N(1)–C(6)–C(5)	118.0(3)
N(1)–C(6)–N(6)	119.2(3)	C(5)–C(6)–N(6)	122.8(3)
C(5)–N(7)–C(8)	103.2(2)	N(7)–C(8)–N(9)	114.2(3)
C(4)–N(9)–C(8)	105.8(2)	C(4)–N(9)–C(9)	128.6(3)
C(8)–N(9)–C(9)	125.6(3)	N(9)–C(9)–C(10)	111.8(3)
C(9)–C(10)–C(11)	112.0(3)	C(10)–C(11)–O(1)	121.6(3)
C(10)–C(11)–N(10)	114.2(3)	O(1)–C(11)–N(10)	124.2(3)
C(11)–N(10)–C(12)	123.0(3)	N(10)–C(12)–C(13)	111.0(3)
C(12)–C(13)–C(14)	113.5(3)	C(13)–C(14)–C(15)	127.2(3)
C(13)–C(14)–C(17)	126.6(3)	C(15)–C(14)–C(17)	106.2(3)
C(14)–C(15)–N(11)	110.3(3)	C(15)–N(11)–C(16)	109.3(3)
N(11)–C(16)–C(17)	106.5(3)	N(11)–C(16)–C(21)	130.6(3)
C(17)–C(16)–C(21)	122.9(3)	C(14)–C(17)–C(16)	107.7(3)
C(14)–C(17)–C(18)	134.3(3)	C(16)–C(17)–C(18)	118.0(3)
C(17)–C(18)–C(19)	119.2(3)	C(18)–C(19)–C(20)	121.4(4)
C(19)–C(20)–C(21)	121.9(4)	C(16)–C(21)–C(20)	116.7(4)
N(1)–C(2)–H(2)	116(1)	N(3)–C(2)–H(2)	115(1)
C(6)–N(6)–H(61)	122(2)	C(6)–N(6)–H(62)	116(2)
H(61)–N(6)–H(62)	117(3)	N(7)–C(8)–H(8)	122(2)
N(9)–C(8)–H(8)	124(2)	N(9)–C(9)–H(91)	106(2)
N(9)–C(9)–H(92)	106(2)	H(91)–C(9)–H(92)	110(2)
C(10)–C(9)–H(91)	111(2)	C(10)–C(9)–H(92)	112(2)
C(9)–C(10)–H(101)	105(2)	C(9)–C(10)–H(102)	109(1)
H(101)–C(10)–H(102)	111(2)	C(11)–C(10)–H(101)	109(2)
C(11)–C(10)–H(102)	111(1)	C(11)–N(10)–H(10)	120(2)
C(12)–N(10)–H(10)	116(2)	N(10)–C(12)–H(121)	111(2)
N(10)–C(12)–H(122)	111(2)	H(121)–C(12)–H(122)	104(2)
C(13)–C(12)–H(121)	111(2)	C(13)–C(12)–H(122)	109(2)
C(12)–C(13)–H(131)	106(2)	C(12)–C(13)–H(132)	115(2)
H(131)–C(13)–H(132)	105(2)	C(14)–C(13)–H(131)	111(2)
C(14)–C(13)–H(132)	106(2)	C(14)–C(15)–H(15)	127(2)
N(11)–C(15)–H(15)	123(2)	C(15)–N(11)–H(11)	123(2)
C(16)–N(11)–H(11)	127(2)	C(17)–C(18)–H(18)	120(2)
C(19)–C(18)–H(18)	121(2)	C(18)–C(19)–H(19)	123(2)
C(20)–C(19)–H(19)	115(2)	C(19)–C(20)–H(20)	122(2)
C(21)–C(20)–H(20)	117(2)	C(20)–C(21)–H(21)	125(2)
C(16)–C(21)–H(21)	118(2)		

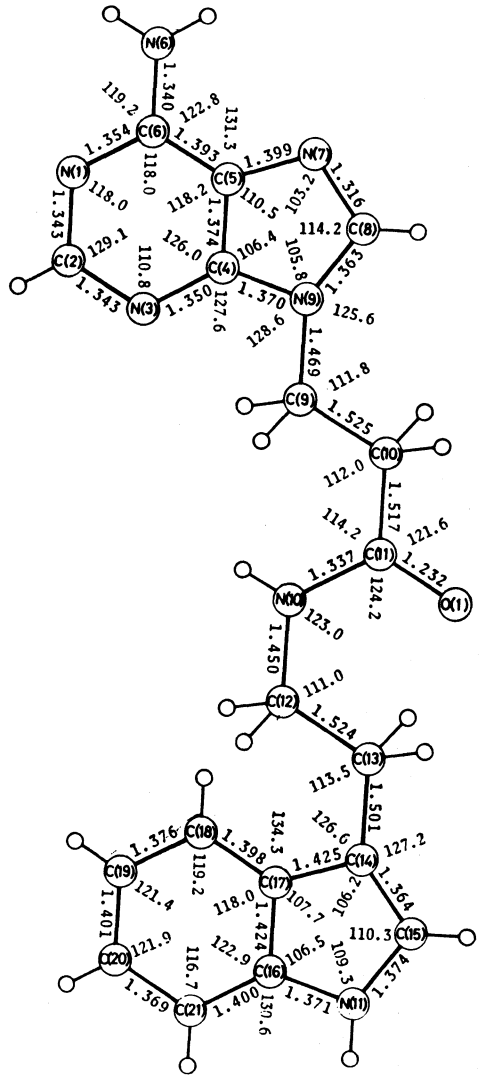

Fig. 1. Bond lenghts (l/Å) and angles (ϕ/°).

b axis in Fig. 4. As seen from Fig. 4, the folded molecules come together around the 2_1 axes, and stack along them. Short intermolecular contacts are 3.474 for N(9)···C(17), 3.479 for N(9)···C(18), and 3.129 Å for C(8)···C(18), the last one being fairly shorter than the normal van der Waals separation.[17] Figure 5 shows the stacking geometry of the adenine and indole rings, (a) being a

Table 5. Least-squares planes

X, Y, and Z are in Å along the directions **a***, **c**×**a***, and **c**, respectively.

Plane 1 (adenine ring)

$0.1902X-0.9615Y+0.2074Z+6.018=0$

Plane 2 (indole ring)

$-0.0479X-0.9007Y+0.4318Z+1.429=0$

Plane 3 (amide group)

$0.8171X-0.0635Y+0.5730Z-4.691=0$

Deviation (l/Å)

Plane 1		Plane 2		Plane 3	
N(1)*	−0.011	C(14)*	−0.003	C(10)*	0.001
C(2)*	0.009	C(15)*	−0.001	C(11)*	−0.003
N(3)*	0.001	N(11)*	−0.006	O(1)*	0.001
C(4)*	−0.004	C(16)*	0.006	N(10)*	0.001
C(5)*	0.009	C(17)*	0.004	C(9)	−0.696
C(6)*	−0.001	C(18)*	0.004	C(12)	0.029
N(7)*	0.001	C(19)*	−0.003	H(10)	0.152
C(8)*	0.001	C(20)*	−0.010		
N(9)*	−0.006	C(21)*	0.009		
N(6)	−0.014	C(13)	−0.036		
C(9)	−0.010	H(15)	−0.036		
H(2)	0.050	H(11)	0.054		
H(8)	−0.008	H(18)	0.037		
H(61)	0.095	H(19)	−0.063		
H(62)	0.220	H(20)	−0.030		
		H(21)	−0.020		

* Atoms included in the calculation of the least-squares plane.

Dihedral angles between the planes (ϕ/°)

No.	2	3
1	141.7	78.2
2		74.6

Table 6. Selected torsion angles of the molecule

C(4)-N(9)-C(9)-C(10)	−78.4°
C(8)-N(9)-C(9)-C(10)	101.4
N(9)-C(9)-C(10)-C(11)	−51.3
C(9)-C(10)-C(11)-O(1)	−29.9
C(9)-C(10)-C(11)-N(10)	150.6
O(1)-C(11)-N(10)-C(12)	−0.9
C(10)-C(11)-N(10)-C(12)	178.5
C(11)-N(10)-C(12)-C(13)	128.6
N(10)-C(12)-C(13)-C(14)	−62.9
C(12)-C(13)-C(14)-C(15)	−44.9
C(12)-C(13)-C(14)-C(17)	136.4

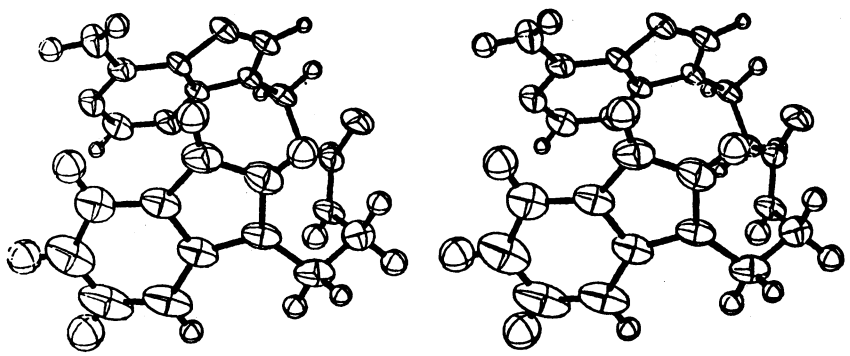

Fig. 2. A stereoscopic view of 3-(adenine-9-yl)propiontryptamide. Thermal ellipsoids are drawn at the 50% probability level.

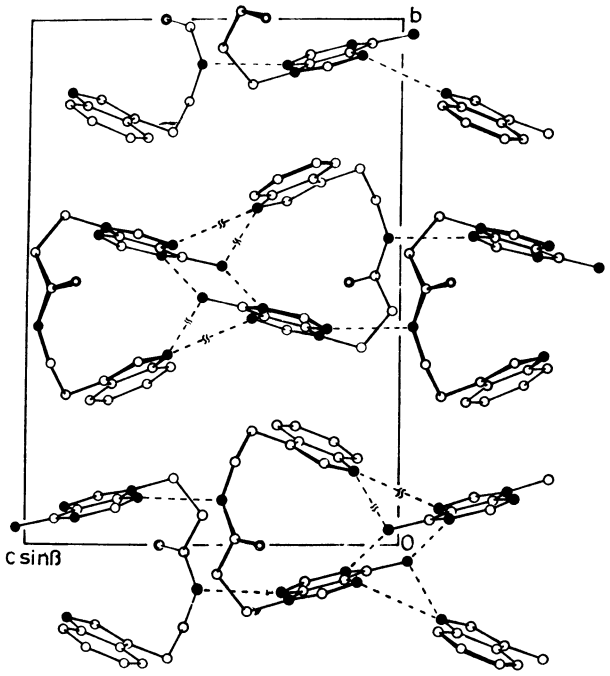

Fig. 3. The crystal structure viewed along the a axis.

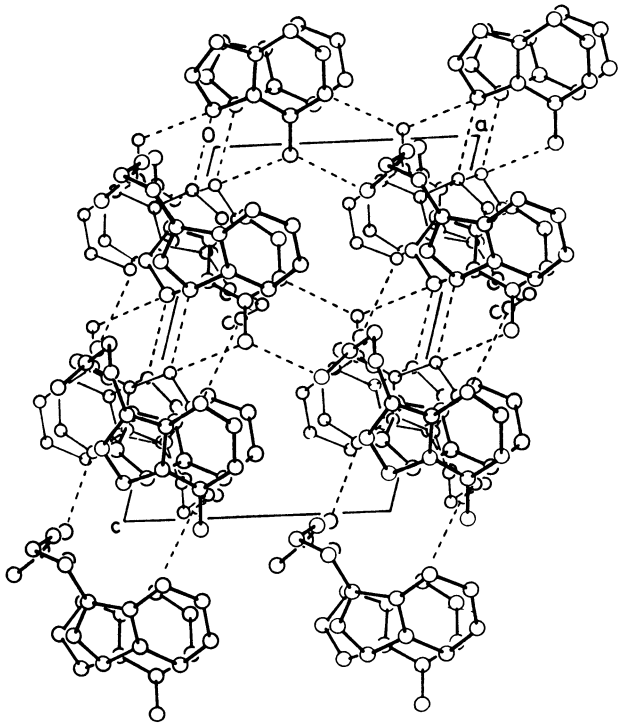

Fig. 4. The crystal structure viewed along the b axis.

projection onto the adenine plane and (b) that onto the indole. These planes make an angle of 18.7°, and the overlapping area is very small, so that there is no strong π-π interaction between them.

The hydrogen bond arrangement is shown in Fig. 6, relevant distances and angles being given in Table 7. The adenine base is paired with that related by the centre of symmetry through two N(6)H···N(1) hydrogen bonds and also with the other centrosymmetrically

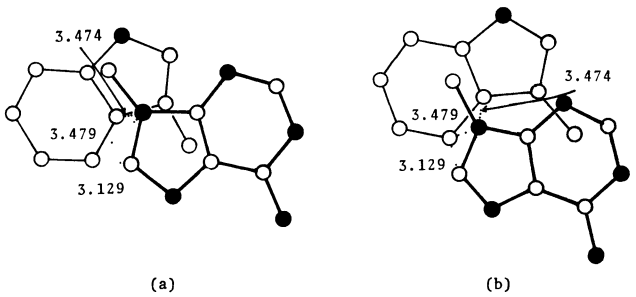

Fig. 5. The stacking geometry of adenine and indole rings. (a) is a projection onto the adenine plane and (b) is that onto the indole.

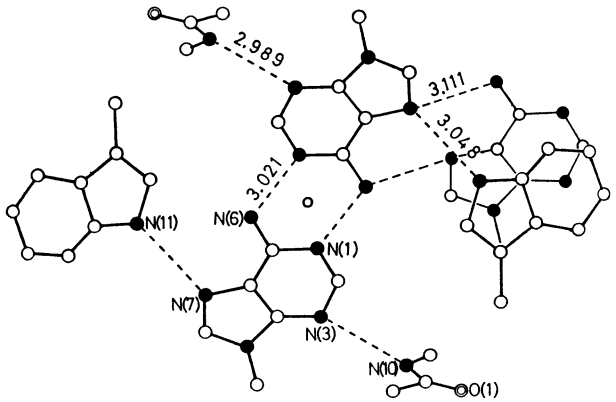

Fig. 6. Hydrogen bond arrangement in the crystal.

Table 7. Distances and angles of the hydrogen bonds (X–H···Y)

				Distance (l/Å)	Distance (l/Å)	Angle (ϕ/°)
X	H	Y		X···Y	H···Y	X–H···Y
N(6)	H(61)	N(1)	(a)	3.021	2.03	171
N(10)	H(10)	N(3)	(b)	2.987	2.09	162
N(11)	H(11)	N(7)	(c)	3.048	2.16	170
N(6)	H(62)	N(7)	(c)	3.111	2.32	158
			(a)	at $-1-x$,	$-y$,	$-z$
			(b)	at $-x$,	$-y$,	$1-z$
			(c)	at $-x$,	$-y$,	$-z$

related adenine bases through two N(6)H···N(7) hydrogen bonds. From a comparison of the hydrogen bond lengths and angles between these two pairing modes (Table 7), it is suggested that the mode by two N(6)H···N(1) hydrogen bonds is more stable than that by two N(6)H···N(7) bonds. This is consistent with the relative stability of these modes calculated by Pullman *et al.*[18] using molecular orbital methods.

N(3) of the adenine ring is hydrogen bonded with N(10) of the amide group in the molecule related by the centre of symmetry. The same kind of hydrogen bonding between nucleotide bases and amide groups is proposed by Gurskii *et al.*[19] as a model of interaction of nucleic acid with regulatory proteins. Furthermore, it is found that N(7) of the adenine ring is hydrogen bonded with N(11) of the indole. Thus N(7) acts as an acceptor

for two hydrogen bonds from N(11) of indole and N(6) of adenine. A similar situation was found for N(1) of adenine in the crystal of *N*-[3(adenin-9-yl)propyl]-3-carbamoylpyridinium bromide.[20] This would be attributable to the large basicity of the nitrogen atoms.[21] Judging from the lengths and angles (Table 7), the N(11)H···N(7) hydrogen bond should be stronger than N(6)H···N(7). The hydrogen bonded adenine and indole rings make an angle of 18.7°.

Interaction Mode between Adenine and Aromatic Moiety of Amino Acid. Crystals of 3-(adenin-9-yl)propiontyramide dihydrate,[22] 3-(adenin-9-yl)propiontryptamide (the present molecule), its monohydrate,[9] and 9-ethyladenine–indole complex[8] are systems in which adenine and aromatic moieties co-exist. Although a π-π interaction between adenine bases in nucleic acid and aromatic side groups in protein is suggested by spectroscopic studies,[4-7] these crystal structures show that there is no stacking between the two components except for the present crystal. Even in the overlapping between adenine and indole rings found in the present crystal (Fig. 5), the relative arrangement may not be sufficient to produce a strong π-π interaction. This is consistent with the calculations of Pullman and Pullman,[23] which indicate both adenine and indole to be π-electron donating. Thus, we consider that hydrogen bonding is more important than the stacking in the system of adenine and the aromatic amino acids.

Two interaction modes between adenine and indole have been found. One is the hydrogen bonding between N(3) of the former and N(11) of the latter found in the crystals of 9-ethyladenine–indole complex[8] and 3-(adenin-9-yl)propiontryptamide monohydrate.[9] The other is the hydrogen bonding between N(7) of the former and N(11) of the latter found in the present crystal. All the adenine bases interacting with indole are paired with other symmetry-related adenines in the crystals. Thus, the hydrogen bonds between adenine and indole provide models of interaction between paired adenine and the side group of tryptophan. We have tried to fit the interaction geometries found in our studies into a double helical nucleic acid (conformation B), atomic coordinates of which are taken from the work of Arnott and Hukins.[24] The indole ring bound to N(7) can be situated in the major groove of DNA without any stereochemical difficulties (Fig. 7); the shortest intermolecular contact is 4.67 Å. On the other hand, the indole ring bound to N(3) in the minor groove gives very short approach to the ribose part, so that some modification of the DNA structure might be required.

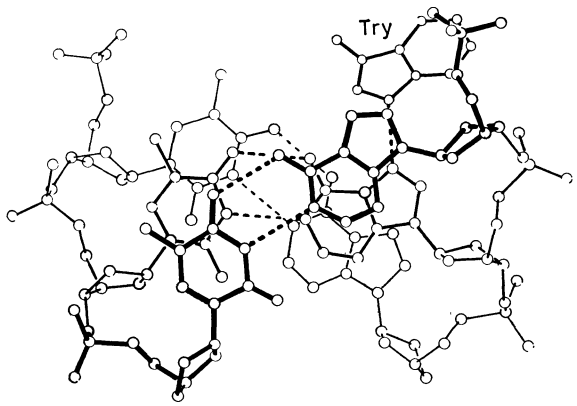

Fig. 7. Indole fitted into a double helical nucleic acid which is constituted with three adenine: thymine base pairs in the B conformation.

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