## e) Consequences of Watson-Crick base pair geometry for double helix geometry

Features 1), 2) and 3) in the previous paragraph c) indicate that:

- i) base pairs are nearly isomorphous, no matter whether we have A:T(U), T(U):A, G:C or C:G. They can therefore substitute each other without disturbing the geometry of the double helix
- ii) the pseudo-dyad symmetry axis requires that the direction of the sugar-phosphate backbone attached to the C1' of one base is opposite to that attached to the C1' of the other base. This implies that the two strands of a double helix are antiparallel, and that they are related by (pseudo)-dyad symmetry axes located within each base pair and also (for geometrical reasons) between all base pairs
- iii) because the glycosyl bonds are positioned on the same side of the base pair, the sugars are closer together on the (purine N3, pyrimidine O2) side than on the (purine O6/N6, pyrimidine N4/O4) side. This gives rise to a minor groove and a major groove which determine macroscopically the picture of a double helix (Fig. 14). The dimensions of the grooves can be given in Å units, as defined in chapter 2.2.

Fig. 14. Schematic description for A:U(T) and G:C base pairs occurring in RNA (DNA). Hydrogen bonds N-H---N and N-H---O indicated by dashed lines. Minor and major groove sides of base pairs are defined [84S1].

## f) Base pair propeller, twist, roll, tilt, dislocation, slide

The geometry of a base pair and its position in a double helix and relative to the helix axis is characterized by several parameters. These are all defined in chapter 2.2 and therefore not described here.

## 1.4 Geometry of bases, sugars, and phosphate groups

The binding geometry of a molecule is defined by bond angles and bond distances. These parameters were averaged for the base, sugar and phosphate moieties in the four common nucleosides. They are given in Fig. 15a...c, with details indicated in the respective legends. For the phosphate group, Fig. 15c, data are given for (i) deprotonated monophosphate group, (ii) protonated monophosphate group, (iii) phosphodiester group, (iv) protonated pyrophosphate ester group as it occurs in ADP etc. Figs. 15a...c were taken from [84S1].

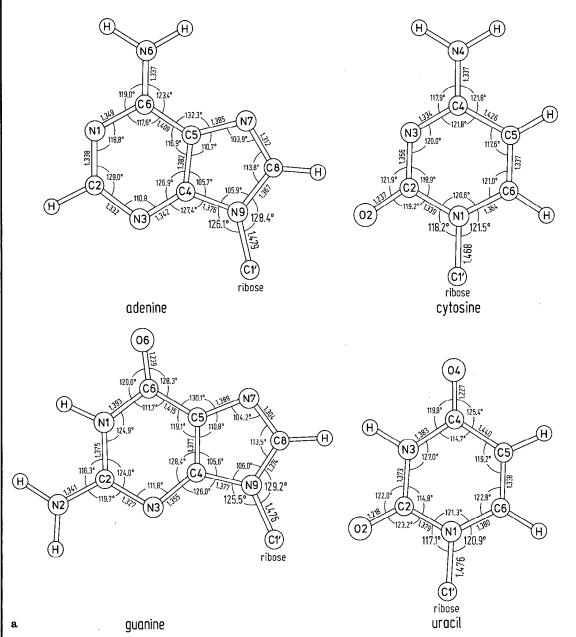
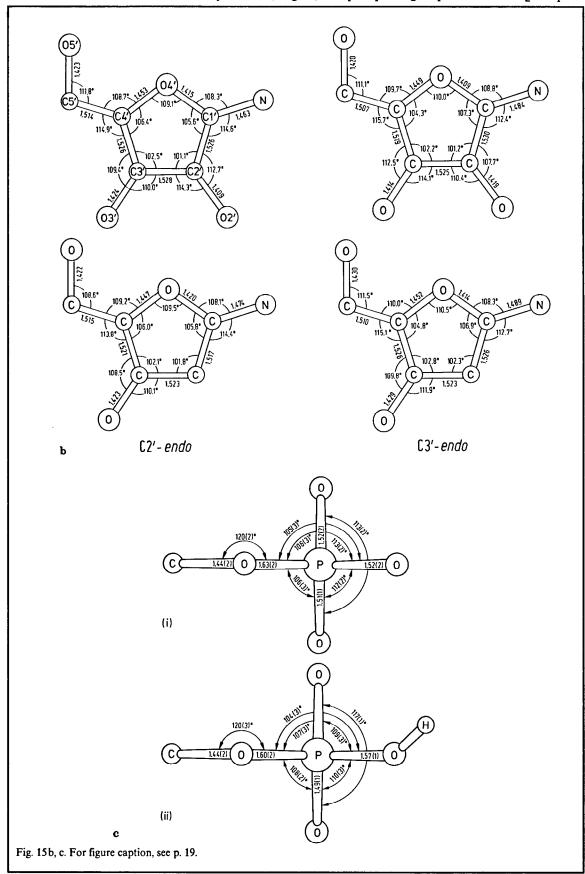


Fig. 15a···c. Average bond angles (in degrees) and distances (in Å) for the constituents of nucleotides. (a) Geometrical data for 1-substituted cytosine and uracil and for 9-substituted adenine and guanine. Data are from [82T1]; standard deviations are defined as  $\sigma = [\Sigma(X_i - \bar{X})^2/(N-1)]^{1/2}$ , where  $X_i$  and  $\bar{X}$  denote individual and mean values, and N is the number of observations. For angles,  $\sigma$ 's are in the range  $0.3^{\circ} \cdots 1^{\circ}$ , and for distances,  $0.005 \cdots 0.016$  Å. N is 32 for uracil, 14 for cytosine, 21 for adenine, and 7 for guanine. Data in capital numbers involve glycosyl C-N linkages taken from [70V1]. They are less accurate because they depend on orientation of base and on furanose pucker [84S1]. (b) Geometrical data for ribose and deoxyribose in nucleosides with C2'-endo and C3'-endo puckering. For other averaged data, see [72A1]. Data are averages obtained from well-refined crystal structures (R < 0.08); standard deviations  $\sigma$  calculated according to formula given in legend to (a). For C2'-endo and C3'-endo riboses, N = 35,  $\sigma_{\text{distances}} = 0.006 \cdots 0.014$  Å,  $\sigma_{\text{angles}} = 0.6 \cdots 2.3^{\circ}$ , for C2'-endo deoxyribose, N = 7,  $\sigma_{\text{distances}} = 0.009 \cdots 0.018$  Å,  $\sigma_{\text{angles}} = 0.5^{\circ} \cdots 3.2^{\circ}$ , for C3'-endo deoxyribose, N = 8,  $\sigma_{\text{distances}} = 0.007 \cdots 0.024$  Å,  $\sigma_{\text{angles}} = 0.5^{\circ} \cdots 2.1^{\circ}$  [84S1]. (c) Geometrical data for phosphate mono- and diesters and pyrophosphate. Data for monoesters from [82T1]; those for diesters and pyrophosphate ester from [79A1]. Standard deviations  $\sigma$  obtained with formula given in legend to (a) are presented in parentheses. Numbers of observations, N, are 11 and 15 for monoester di- and monoanion (i) and (ii), respectively, 33 for diester (iii), and 4 for pyrophosphate ester (iv) [84S1].



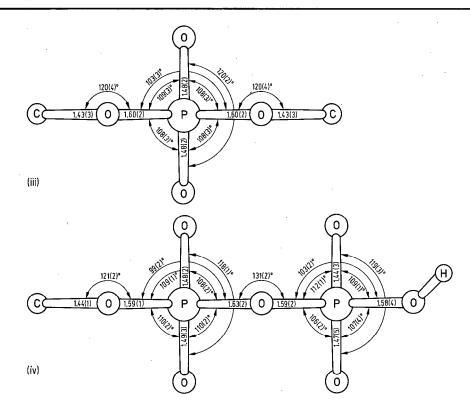


Fig. 15c, continued.

## 1.5 References for 1

- 60K1 Klyne, W., Prelog, V.: Experientia 16 (1960) 521.
- 70A1 Arnott, S.: Prog. Biophys. Mol. Biol. 21 (1970) 267.
- 70I1 IUPAC-IUB Commission on Biochemical Nomenclature (CBN): Eur. J. Biochem. 15 (1970) 203; for correction, see Eur. J. Biochem. 25 (1972) 1.
- 70V1 Voet, D., Rich, A.: Prog. Nucleic Acid Res. Mol. Biol. 10 (1970) 183.
- 72A1 Arnott, S., Hukins, D.W.L.: Biochem. J. 130 (1972) 453.
- 72A2 Altona, C., Sundaralingam, M.: J. Amer. Chem. Soc. 94 (1972) 8205.
- 73A1 Altona, C., Sundaralingam, M.: J. Amer. Chem. Soc. 95 (1973) 2333.
- 73F1 Frey, M.N., Koetzle, T.F., Lehmann, M.S., Hamilton, W.C.: J. Chem. Phys. 59 (1973) 915.
- 73S1 Sundaralingam, M.: Conformations of Biological Molecules and Polymers, Bergmann, E.D., Pullman, B. (eds.), New York: Academic Press 1973, 417.
- 76R1 Rosenberg, J.M., Seeman, N.C., Day, R.O., Rich, A.: J. Mol. Biol. 104 (1976) 145.
- 76S1 Seeman, N.C., Rosenberg, J.M., Suddath, F.L., Kim, J.J.P., Rich, A.: J. Mol. Biol. 104 (1976) 109.
- 79A1 Allen, F.H., Bellard, S., Brice, M.D., Cartwright, B.A., Doubleday, A., Higgs, H., Hummelink, T., Hummelink-Peters, B.G., Kennard, O., Motherwell, W.D.S., Rodgers, J.R., Watson, D.G.: Acta Crystallogr. Sect. B 35 (1979) 2331.
- 81R1 Rao, S.T., Westhof, E., Sundaralingam, M.: Acta Crystallogr. Sect. B 37 (1981) 1670.
- 82T1 Taylor, R., Kennard, O.: J. Mol. Struct. 78 (1982) 1.
- 83I1 IUPAC-IUB Joint Commission on Biochemical Nomenclature (JCBN): Eur. J. Biochem. 131 (1983) 9.
- 84S1 Saenger, W.: Principles of Nucleic Acid Structure, New York: Springer 1984.
- 85M1 Merritt, E.A., Sundaralingam, M.: J. Biomol. Struct. Dynamics 3 (1985) 559.