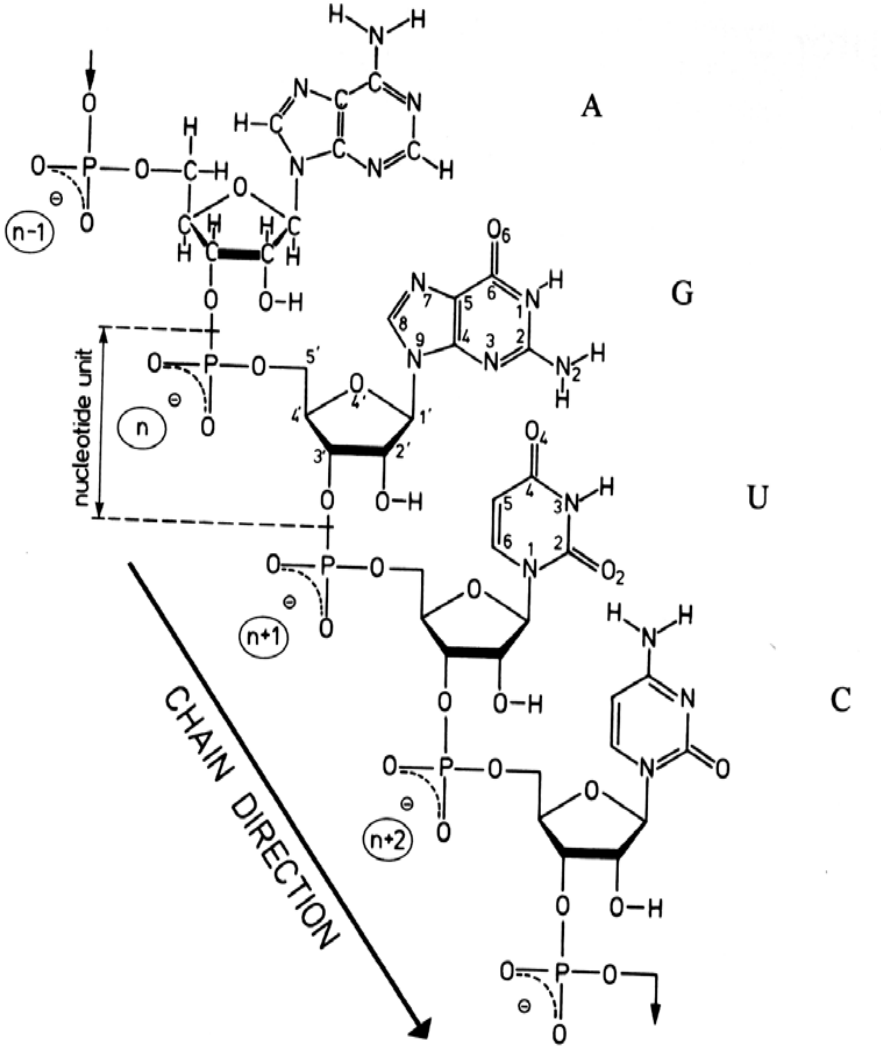


Fragment of ribonucleic acid (RNA) with sequence adenosine (A), guanosine (G), uridine (U), cytidine (C) linked by 3′,5′-phosphodiester bonds. Chain direction is from 5′- to 3′-end as shown by arrow. Atom numbering scheme is indicated in one framed nucleotide unit, 5′-GMP. All hydrogen atoms drawn in A and only functional hydrogens in other nucleotides. In short notation, this fragment would be pApGpUpCp or pAGUCp. In deoxyribonucleic acid (DNA), the hydroxyl attached to $C_{2'}$ is replaced by hydrogen and uracil, by thymine.

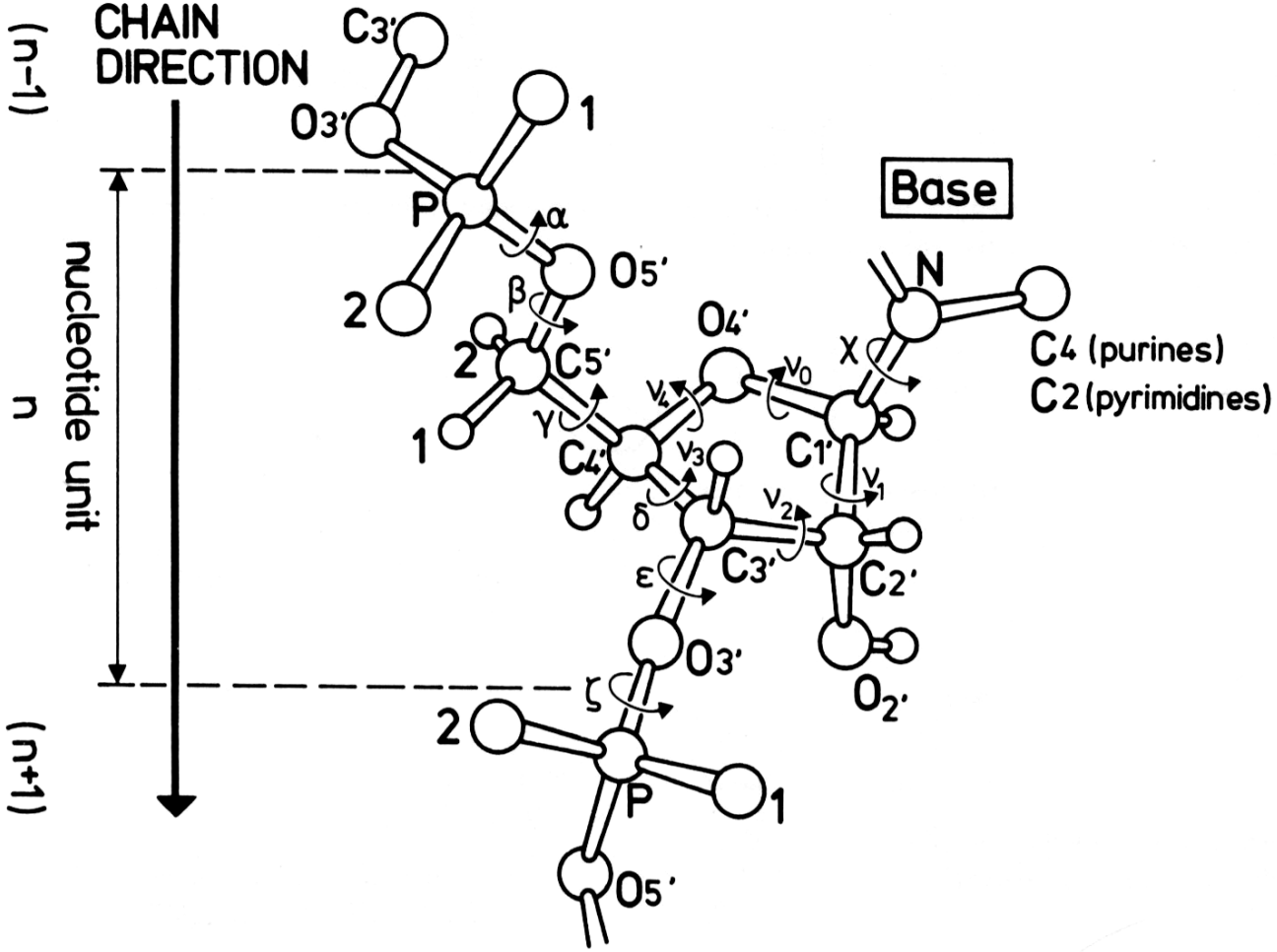
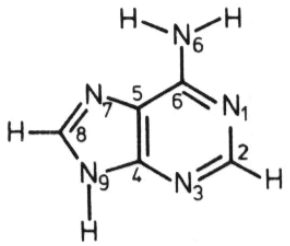
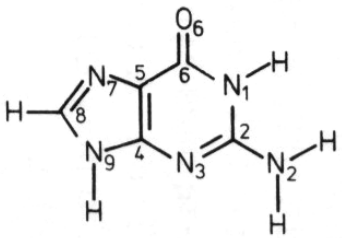


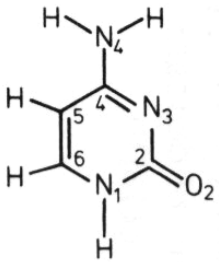
Figure 2-3. Atomic numbering scheme and definition of torsion angles for a polyribonucleotide chain. Counting of nucleotides is from top to bottom, i.e., in the direction $O_{5'} \rightarrow O_{3'}$. Hydrogens at $C_{5'}$ and oxygens at P are differentiated by 1 and 2 according to the rule given in the text. In deoxyribose, the hydrogen replacing $O_{2'}$ is labeled 1, the other one, 2. For a full description of torsion angles, see Table 2-2.



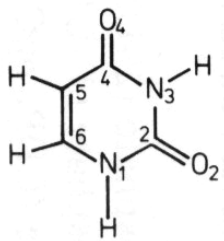
Adenine
Ade



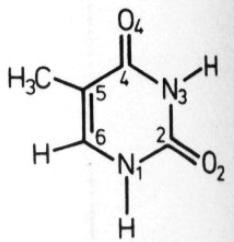
Guanine
Gua



Cytosine
Cyd

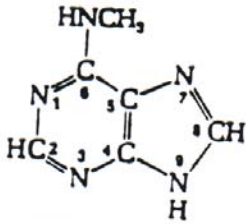


Uracil
Ura

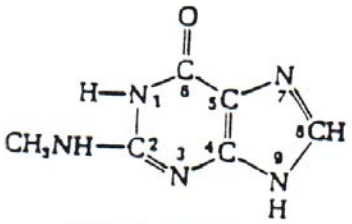


Thymine
Thy

Two minor purines

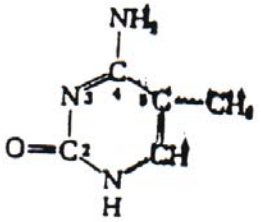


N^6-Methyladenine

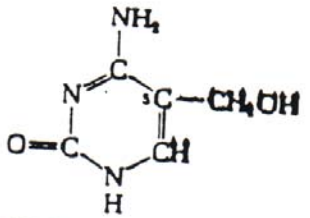


2-Methylguanine

Two minor pyrimidines



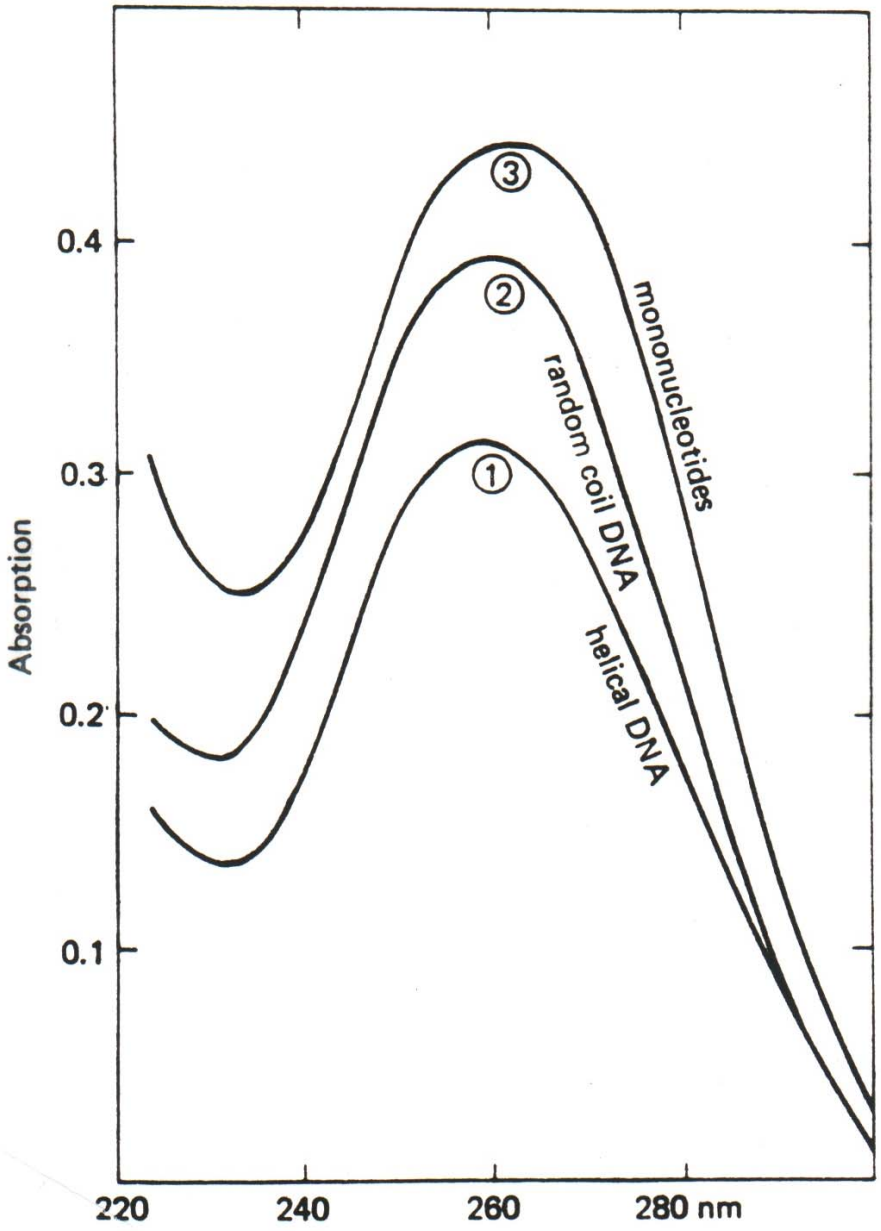
5-Methylcytosine

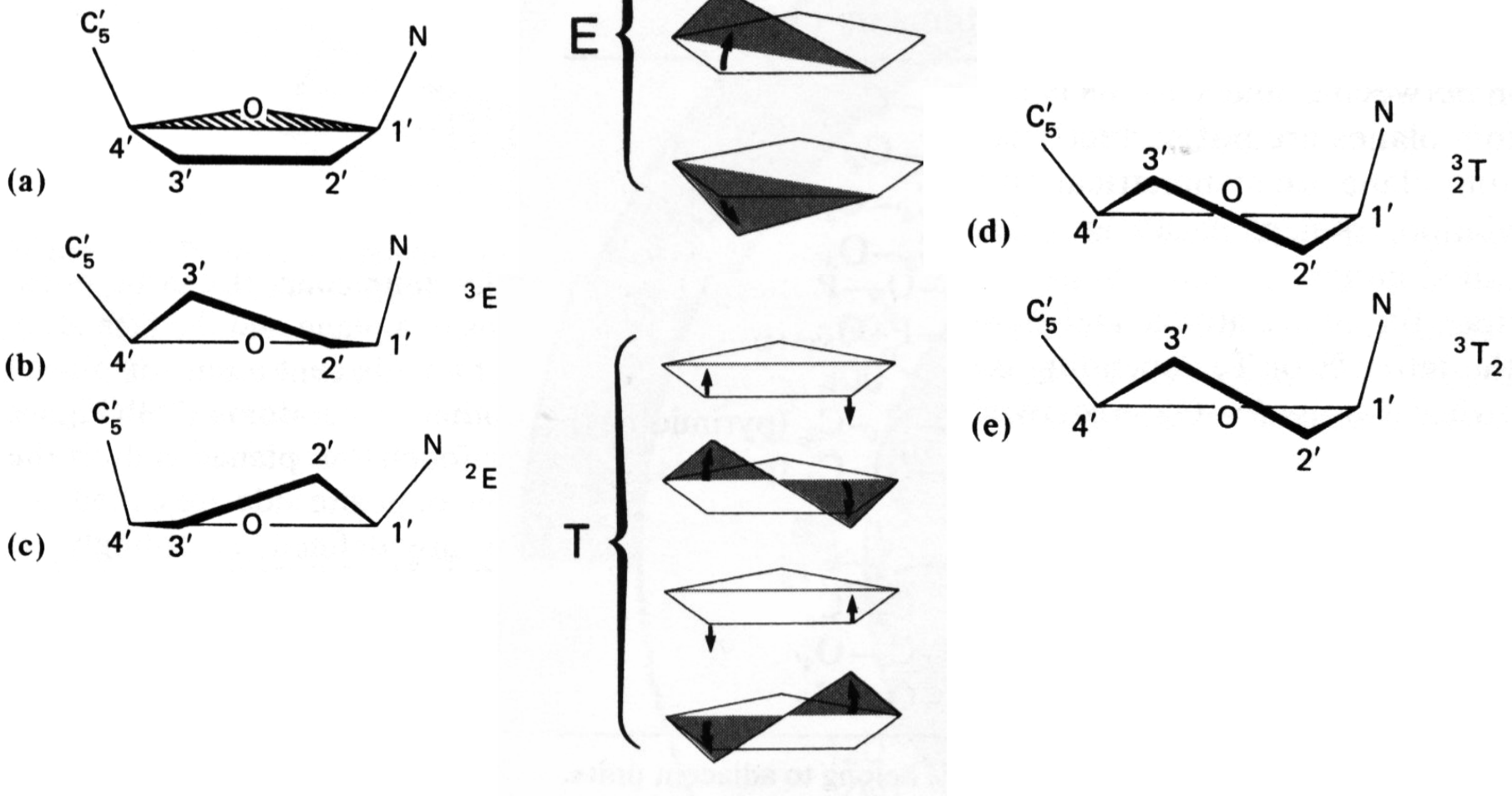


5-Hydroxymethylcytosine

Table 1 Other rare bases found in nucleic acids

5,6-Dihydrouracil
1-Methyluracil
3-Methyluracil
5-Hydroxymethyluracil
2-Thiouracil
N^4-Acetylcytosine
3-Methylcytosine
5-Methylcytosine
5-Hydroxymethylcytosine
1-Methyladenine
2-Methyladenine
7-Methyladenine
N^6-Methyladenine
N^6,N^6-Dimethyladenine
N^6-(Δ^2-Isopentenyl)adenine
1-Methylguanine
7-Methylguanine
N^2-Methylguanine
N^2,N^2-Dimethylguanine


Absorption
0.4
0.3
0.2
0.1
220
240
260
280 nm
③
②
①
mononucleotides
random coil DNA
helical DNA


(a)
C′5
N
O
4′
1′
3′
2′
(b)
C′5
3′
N
3E
4′
O
2′
1′
(c)
C′5
2′
N
2E
4′
3′
O
1′
E
T
(d)
C′5
N
3′
3T2
O
4′
1′
2′
(e)
C′5
3′
N
3T2
4′
O
1′
2′

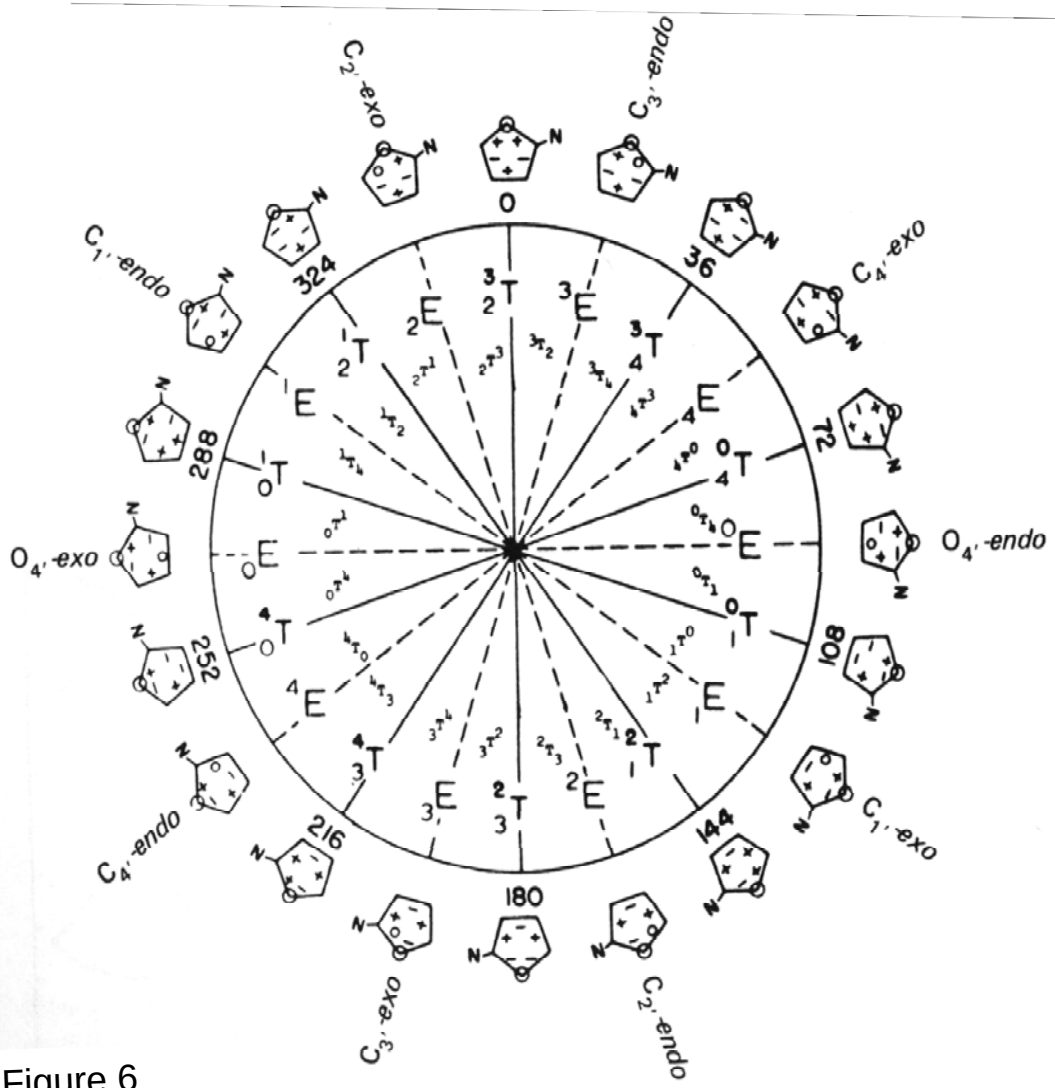
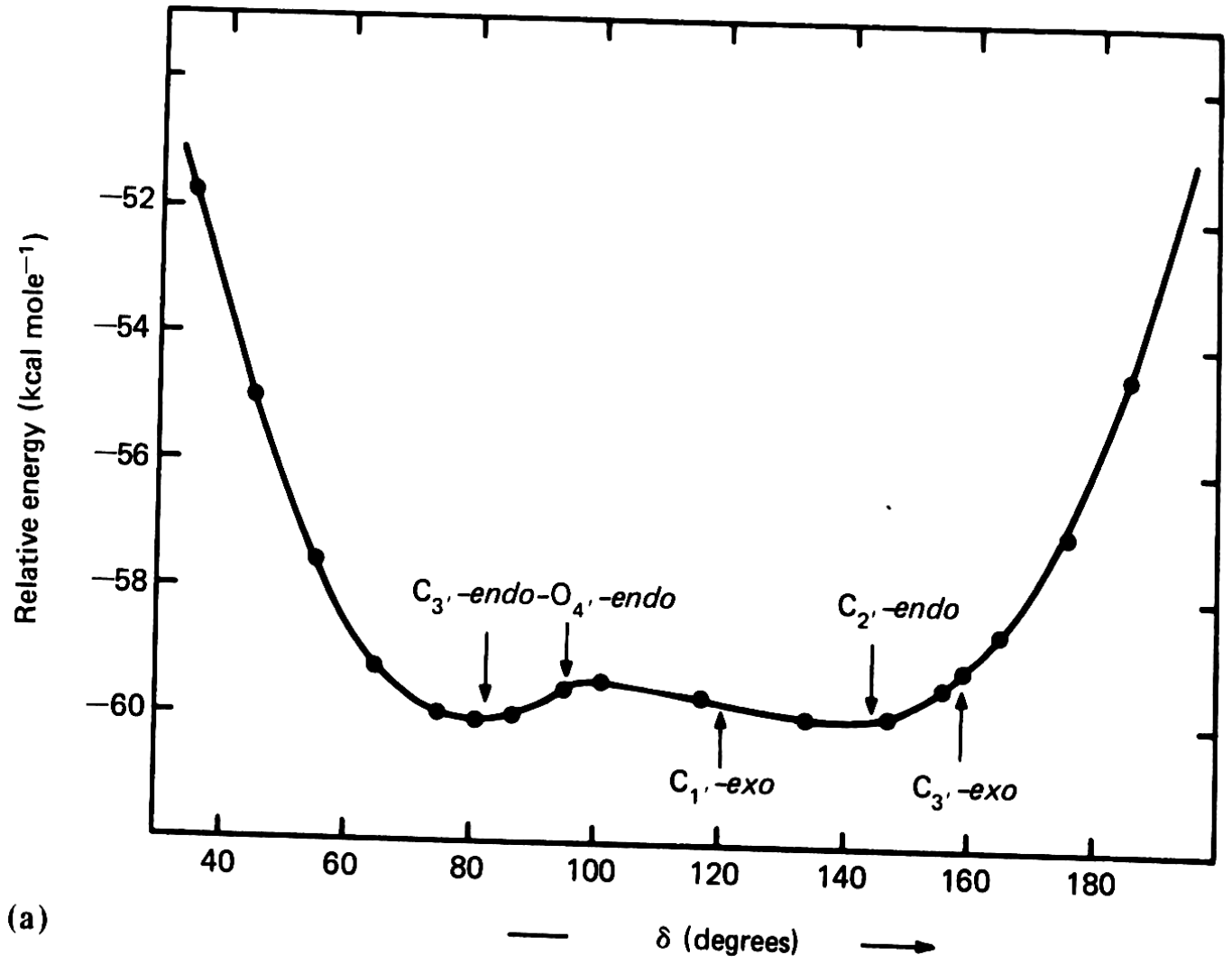


Figure 6

Pseudorotation cycle of the furanose ring in nucleosides. Values of phase angles given in multiples of 36°. Envelope E and twist T forms alternate every 18°. After rotation by 180° the mirror image of the starting position is found. On the periphery of the cycle, riboses with signs of endocyclic torsion angles are indicated. (+) Positive, (−) Negative, (0) angle at 0°. From (31).


Relative energy (kcal mole^{-1})
−52
−54
−56
−58
−60
40
60
80
100
120
140
160
180
δ (degrees)
$C_{3'}$-*endo*-$O_{4'}$-*endo*
$C_{2'}$-*endo*
$C_{1'}$-*exo*
$C_{3'}$-*exo*

(a)

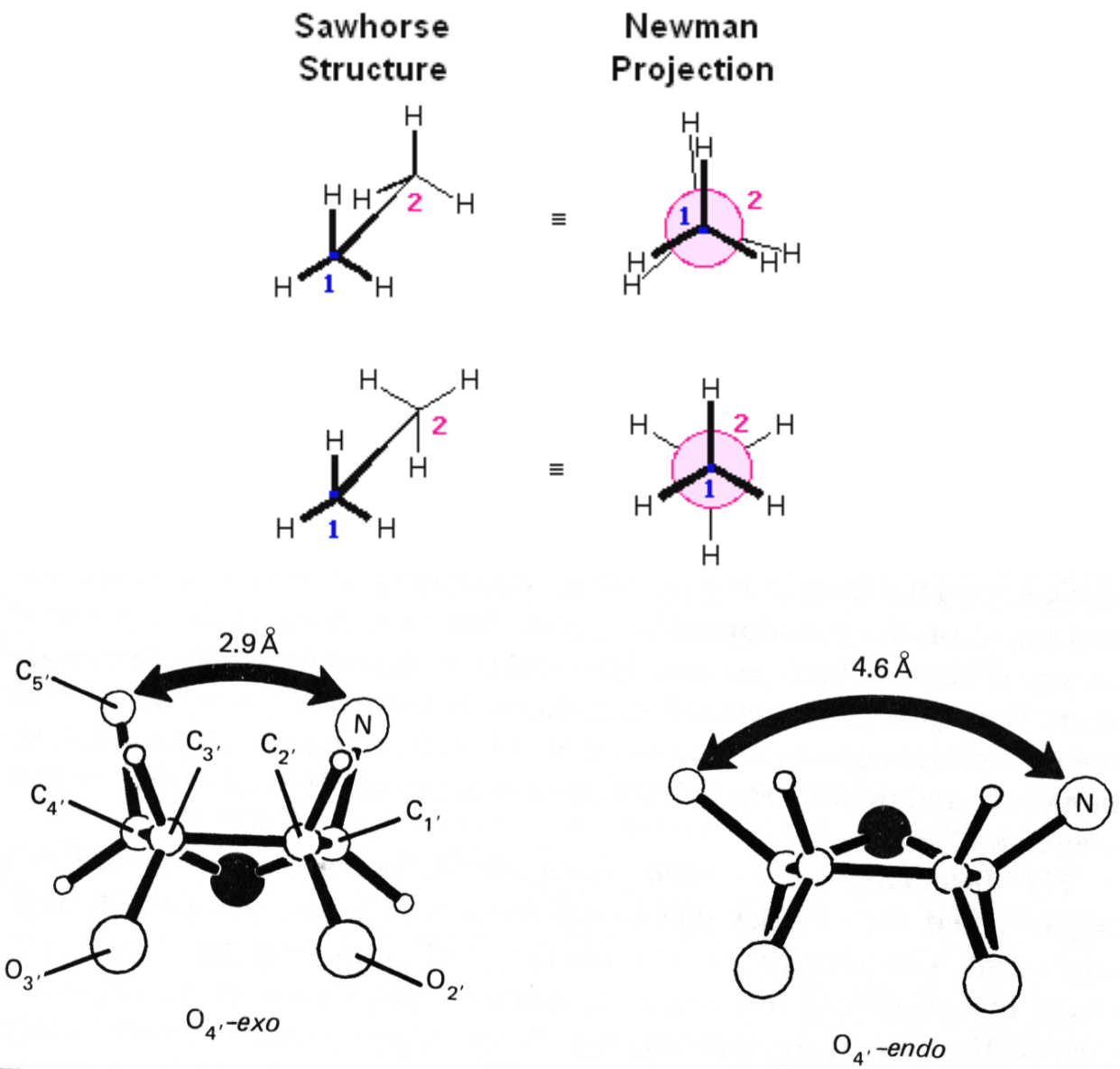
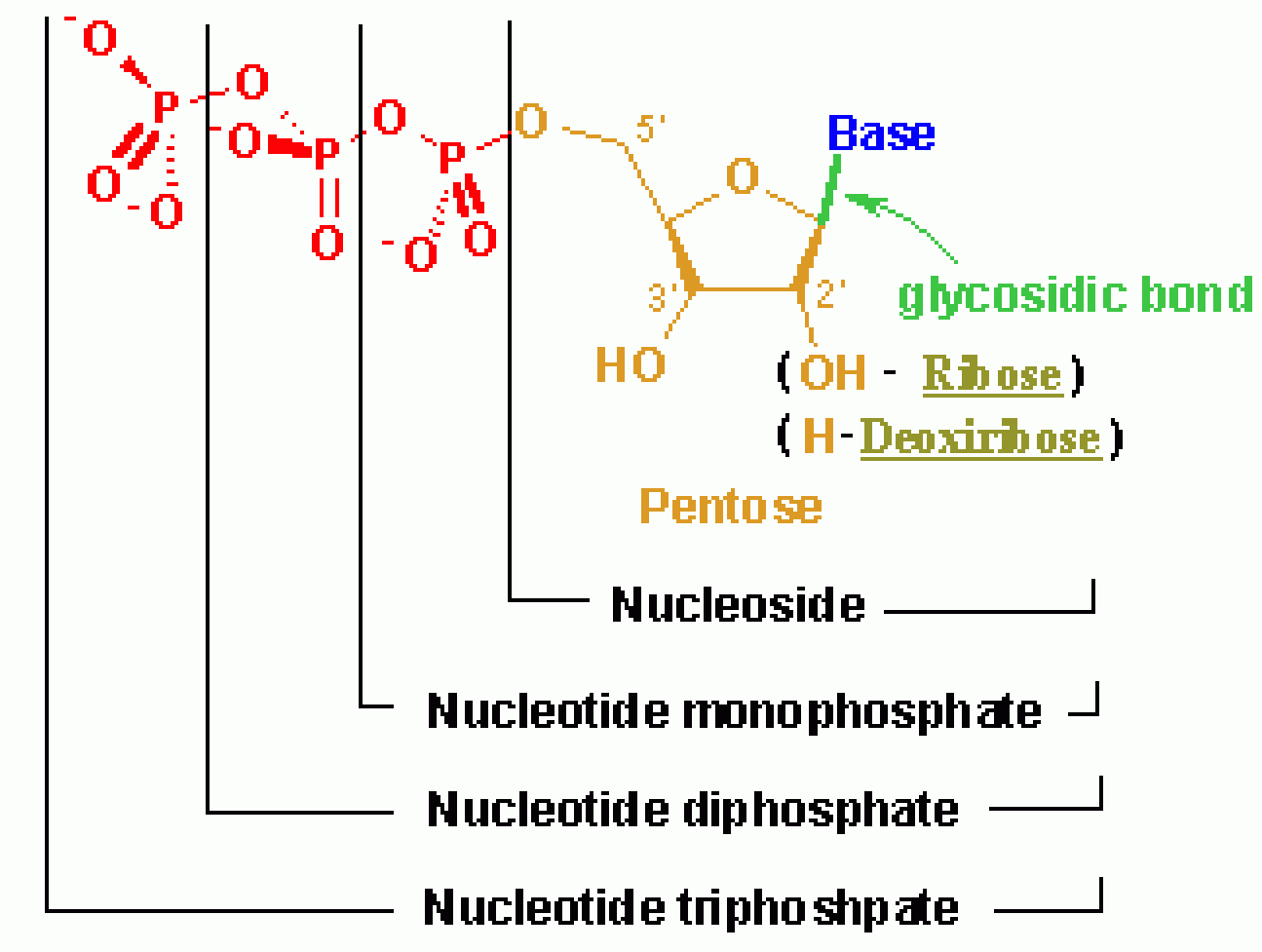


Figure 4-5. Equatorial and axial positioning of substituents N (base) and $C_{5'}$ in sugar puckering modes $O_{4'}$-*exo* (left) and $O_{4'}$-*endo* (right). In $O_{4'}$-*exo*, $C_{5'}$ and N interfere sterically and therefore the $C_{2'}$-*endo*⇌$C_{3'}$-*endo* interchange occurs via $O_{4'}$-*endo* as intermediate.


Base
glycosidic bond
HO
(OH - Ribose)
(H-Deoxiribose)
Pentose
Nucleoside
Nucleotide monophosphate
Nucleotide diphosphate
Nucleotide triphoshpate

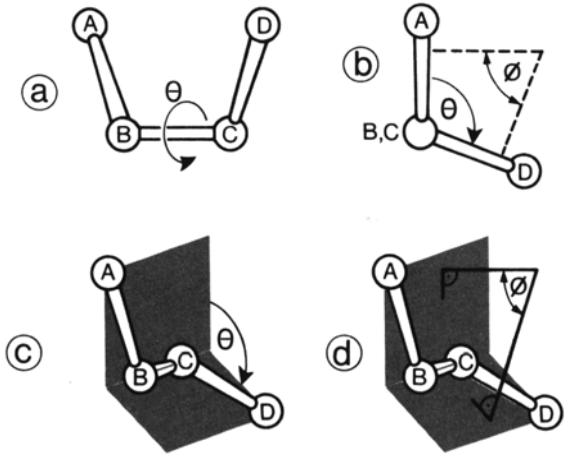
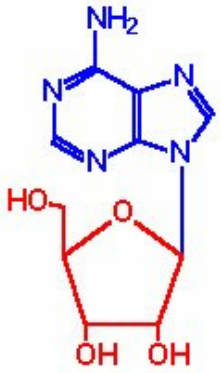
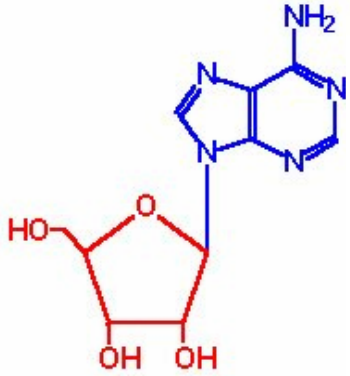


Figure 2-4. Definition of *torsion* and *dihedral angles*. (a) *Torsion angle* θ (A–B–C–D) describing orientations of bonds A–B and C–D with respect to the central bond B–C. (b) View along B→C. θ is the torsion angle between the projected bonds A–B and C–D; the complement ϕ is called the *dihedral angle*. If A–B and C–D are *cis*-planar (coinciding in projection), angles θ and ϕ are 0°; they are counted positive if the far bond C–D rotates clockwise with respect to the near bond A–B. (c) θ is defined as the angle between planes A–B–C and B–C–D. (d) The *dihedral angle* ϕ represents the angle between normals to these planes.



syn-Adenosine



anti-Adenosine