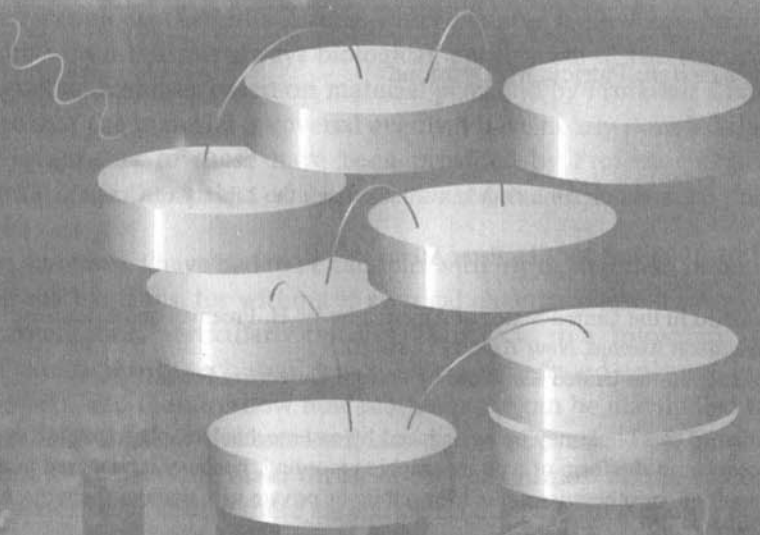
THIRD EDITION

The Elements of Physical Chemistry

With Applications in Biology

Peter Atkins

Professor of Chemistry, and Fellow of Lincoln College, Oxford



W. H. Freeman and Company
New York

Cover design: Patricia McDermond

Cataloging-in-publication data is available from the Library of Congress.

Published in the United States of America by W. H. Freeman and Company,
41 Madison Avenue, New York, NY 10010.
Published in the United Kingdom by Oxford University Press.

Printed in the United States of America

First printing 2000

This edition has been authorized by the Oxford University Press for sale in the USA and Canada only and not for export therefrom.

Chapter 16

Molecular substances

Contents

ATOMS and molecules with complete valence shells are still able to interact with one another. They attract one another over the range of several atomic diameters and they repel one another when pressed together. These residual forces are highly important. They account, for instance, for the condensation of gases to liquids and the structures of molecular solids. All organic liquids and solids, ranging from small molecules like benzene to virtually infinite cellulose and the polymers from which fabrics are made, are bound together by the forces of cohesion we explore in this chapter. These forces are also responsible for the structural organization of biological macromolecules, for they twist the long polypeptide chains of proteins into characteristic shapes and then pin them together in the arrangement essential to their function.

The origins of cohesion

A **van der Waals force** is an interaction between closed-shell molecules. The attractive contributions to these forces include the interactions between the partial electric charges of polar molecules and of polar functional groups in macromolecules. Van der Waals forces also include the repulsive interactions that prevent the complete collapse of matter to densities as high as those char-

acteristic of atomic nuclei. The repulsive interactions arise from the exclusion of electrons from regions of space where the orbitals of closed-shell species overlap.

16.1 Interactions between partial charges

Atoms in molecules in general have partial charges. Table 16.1 gives the partial charges typically found in peptides. If these charges were separated by a vacuum, they would attract or repel each other in accord with Coulomb's law, and we would write[1]

$$V = \frac{q_1 q_2}{4\pi\varepsilon_0 r} \qquad (16.1a)$$

where q_1 and q_2 are the partial charges and r is their separation. However, it is more accurate to take into account the possibility that other parts of the molecule, or other molecules, lie between the charges, and decrease the strength of the interaction (Fig 16.1). We therefore write

$$V = \frac{q_1 q_2}{4\pi\varepsilon r} \qquad (16.1b)$$

where ε is the **permittivity** of the medium lying between the charges. The permittivity is usually expressed as a multiple of the vacuum permittivity by writing $\varepsilon = \varepsilon_r\varepsilon_0$, where ε_r is the **relative permittivity**.[2] The effect of the medium can be very large: for water, $\varepsilon_r = 78$, so the potential energy of two charges separated by bulk water is reduced by nearly two orders of magnitude compared to the value it would have if the charges were separated by a vacuum. The problem is made worse in calculations on polypeptides (and nucleic acids) by the fact that two partial charges may have water and polypeptide chain lying between them. Various models have been proposed to take this awkward effect into account, the simplest being to set $\varepsilon_r = 3.5$ and to hope for the best.

Table 16.1 *Partial charges in polypeptides*

Atom	Partial charge/*e*
N	−0.36
H(-N)	+0.18
C(-CO)	+0.06
H(-C)	+0.02
C(=O)	+0.45
O	−0.38
H(-O)	+0.42

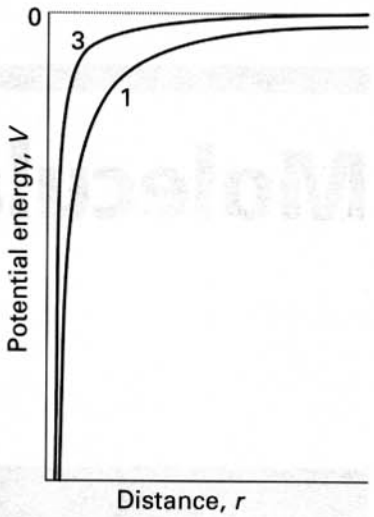


Fig 16.1 The Coulomb potential for two charges and its dependence on their separation. The two curves correspond to different relative permittivities (1 for a vacuum, 3 for a fluid).

16.2 Electric dipole moments

When the molecules or groups that we are considering are widely separated, it turns out to be simpler to express the principal features of their interaction in terms of the dipole moments associated with the charge distributions rather than with each partial charge. At its simplest, an **electric dipole** consists of two charges q and $-q$ separated by a distance l. The product ql is called the **electric di-**

[1] Equation 16.1a is for the potential energy of the interaction. The force between the two charges is inversely proportional to the square of their separation, $F \propto 1/r^2$.

[2] The relative permittivity is still widely called the *dielectric constant*.

pole moment, μ. We represent dipole moments by an arrow with a length proportional to μ and pointing from the negative charge to the positive charge (**1**).[3] Because a dipole moment is the product of a charge (in coulombs, C) and a length (in metres, m), the SI unit of dipole moment is the coulomb-metre (C m). However, it is often much more convenient to report a dipole moment in **debye**, D, where

$$1\ \text{D} = 3.335\ 64 \times 10^{-30}\ \text{C m}$$

because the experimental values for molecules are then close to 1 D (Table 16.2).[4] The dipole moment of charges e and $-e$ separated by 100 pm is 1.6×10^{-29} C m, corresponding to 4.8 D. Dipole moments of small molecules are typically smaller than that, at about 1 D.

1

A **polar molecule** is a molecule with a permanent electric dipole moment arising from the partial charges on its atoms (Section 14.17). A **nonpolar molecule** is a molecule that has no permanent electric dipole moment. All heteronuclear diatomic molecules are polar because the difference in electronegativities of their two atoms results in nonzero partial charges. Typical dipole moments are 1.08 D for HCl and 0.42 D for HI (Table 16.2). A very approximate relation between the dipole moment and the difference in Pauling electronegativities (Table 14.2) of the two atoms, $\Delta\chi$, is

$$\mu/\text{D} \approx \Delta\chi \qquad (16.2)$$

Illustration 16.1

The electronegativities of hydrogen and bromine are 2.1 and 2.8 respectively. The difference is 0.7, so we predict an electric dipole moment of about 0.7 D for HBr. The experimental value is 0.80 D.

[3] Be careful with this convention: for historical reasons the opposite convention is still widely adopted.

[4] The unit is named after Peter Debye, the Dutch pioneer of the study of dipole moments of molecules.

Table 16.2 *Dipole moments (μ) and polarizability volumes (α')*

	μ/D	$\alpha'/(10^{-30}\ \text{m}^3)$
Ar	0	1.66
CCl_4	0	10.5
C_6H_6	0	10.4
H_2	0	0.819
H_2O	1.85	1.48
NH_3	1.47	2.22
HCl	1.08	2.63
HBr	0.80	3.61
HI	0.42	5.45

The polarizability volumes are mean values over all orientations of the molecule.

Because it attracts the electrons more strongly, the more electronegative atom is usually the negative end of the dipole. However, there are exceptions, particularly when antibonding orbitals are occupied. Thus, the dipole moment of CO is very small (0.12 D) but the negative end of the dipole is on the C atom even though the O atom is more electronegative. This apparent paradox is resolved as soon as we realize that antibonding orbitals are occupied in CO (see Fig 14.30), and, because electrons in antibonding orbitals tend to be found closer to the less electronegative atom, they contribute a negative partial charge to that atom. If this contribution is larger than the opposite contribution from the electrons in bonding orbitals, the net effect will be a small negative partial charge on the *less* electronegative atom. Figure 16.2 shows a

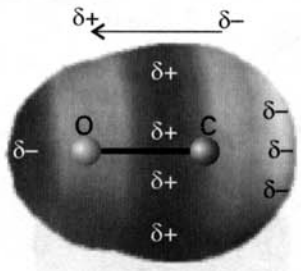
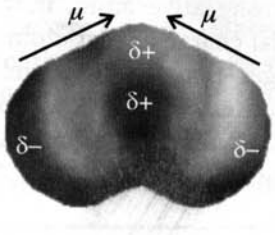


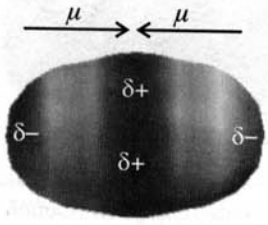
Fig 16.2 The computed charge distribution in a CO molecule. Note that, although oxygen is more electronegative than carbon, the negative end of the dipole is on carbon.

computed electron density distribution in CO, and the small charge imbalance can be seen.

Molecular symmetry is of the greatest importance in deciding whether a polyatomic molecule is polar or not. Indeed, molecular symmetry is more important than the question of whether or not the atoms in the molecule belong to the same element. Homonuclear polyatomic molecules may be polar if they have low symmetry and the atoms are in inequivalent positions. For instance, the angular molecule ozone, O_3 (**2**), is homonuclear; however, it is polar because the central O atom is different from the outer two (it is bonded to two atoms, they are bonded only to one); moreover, the dipole moments associated with each bond make an angle to each other and do not cancel. Heteronuclear polyatomic molecules may be nonpolar if they have high symmetry, because individual bond dipoles may then cancel. The heteronuclear linear triatomic molecule CO_2, for example, is nonpolar because, although there are partial charges on all three atoms, the dipole moment associated with the OC bond points in the opposite direction to the dipole moment associated with the CO bond, and the two cancel (**3**).



2 Ozone



3 Carbon dioxide

Self-test 16.1

Use the VSEPR model to judge whether ClF_3 is polar or nonpolar. (*Hint*. Predict the structure first.)

[*Answer*: polar]

To a first approximation, it is possible to resolve the dipole moment of a polyatomic molecule into contributions from various groups of atoms in the molecule and the directions in which these individual contributions lie (Fig 16.3). Thus, *p*-dichlorobenzene is nonpolar by symmetry on account of the cancellation of two equal but opposing C–Cl moments (exactly as in carbon dioxide). *o*-Dichlorobenzene has a dipole moment which is approximately the resultant of two chlorobenzene dipole moments arranged at 60° to each other. This technique of 'vector addition' can be applied with fair success

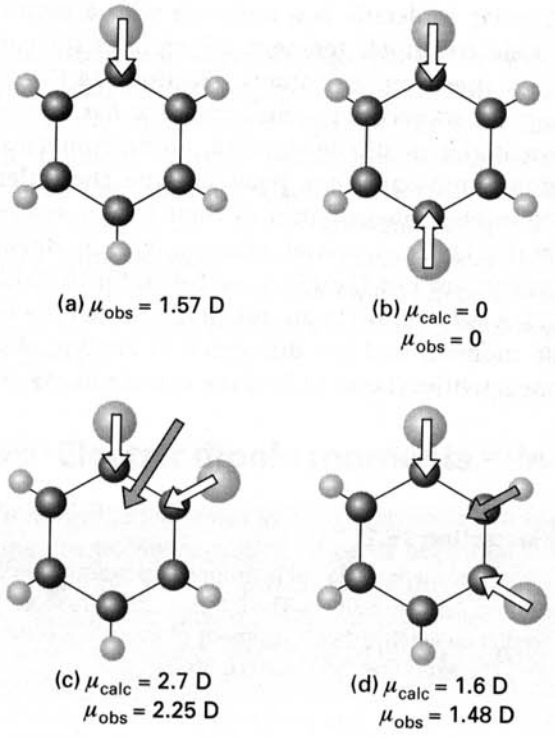
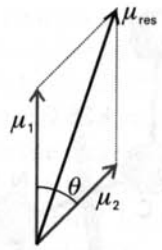


Fig 16.3 The dipole moments of the dichlorobenzene isomers can be obtained approximately by vectorial addition of two chlorobenzene dipole moments (1.57 D).



4

to other series of related molecules, and the resultant μ_{res} of two dipole moments μ_1 and μ_2 that make an angle θ to each other (4) is approximately

$$\mu_{res} \approx (\mu_1^2 + \mu_2^2 + 2\mu_1\mu_2 \cos\theta)^{1/2} \qquad (16.3)$$

Self-test 16.2

Estimate the ratio of the electric dipole moments of *ortho*- and *meta*-disubstituted benzenes.

[*Answer*: $\mu(ortho)/\mu(meta) = 1.7$]

A better approach to the calculation of dipole moments is to take into account the locations and magnitudes of the partial charges on all the atoms. These partial charges are included in the output of many molecular structure software packages. Indeed, the programs calculate the dipole moments of the molecules in the manner we now describe.

Derivation 16.1 *The dipole moment of a molecule*

An electric dipole moment is a vector, $\boldsymbol{\mu}$, with three components, μ_x, μ_y, and μ_z. The direction of $\boldsymbol{\mu}$ shows the orientation of the dipole in the molecule and the length of the vector is the magnitude, μ, of the dipole moment. In common with all vectors, the magnitude is related to the components by

$$\mu = (\mu_x^2 + \mu_y^2 + \mu_z^2)^{1/2} \qquad (16.4a)$$

Each component is related to the magnitude of the partial charges and their positions relative to a point in the molecule:

$$\mu_x = \text{Sum of (partial charge} \times \text{distance along } x\text{-axis)} \qquad (16.4b)$$

with similar expressions for the *y*- and *z*-components. For an electrically neutral molecule, the origin of the coordinates is arbitrary, so it is best chosen to simplify the measurements. For a planar molecule, there are no charges above or below the *xy*-plane, so the *z*-component (where *z* is perpendicular to the plane) is zero. The procedure is illustrated in the following example.

Example 16.1 *Calculating a molecular dipole moment*

Calculate the electric dipole moment of the peptide group using the partial charges (as multiples of *e*) in Table 16.1 and the locations of the atoms shown in Fig 16.4.

Strategy We use eqn 16.4b to calculate each of the components of the dipole moment and then eqn 16.4a to assemble the three components into the magnitude of the dipole moment. Note that the partial charges are multiples of the fundamental charge, $e = 1.609 \times 10^{-19}$ C (see inside front cover).

Solution The first few terms of the expression for μ_x are

$$\mu_x = (-0.36e) \times (-0.8 \text{ pm}) + (0.45e) \times (2.1 \text{ pm}) + \cdots$$
$$= -3.8 \times 10^{-18} \text{ C pm} = -3.8 \times 10^{-30} \text{ C m}$$

corresponding to −1.1 D. A similar calculation gives μ_y = −0.91 D and $\mu_z = 0$. Therefore,

$$\mu = [(-1.1 \text{ D})^2 + (-0.96 \text{ D})^2]^{1/2} = 1.5 \text{ D}$$

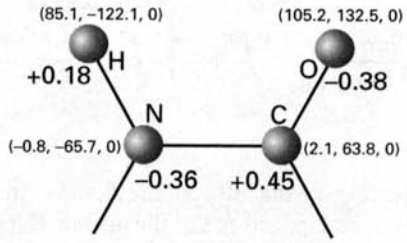


Fig 16.4 The locations of the atoms (in picometres relative to the centre of the molecule) and the partial charges (as multiples of *e*) used to calculate the dipole moment of a peptide group.

We can find the orientation of the dipole moment by arranging an arrow of length 1.5 units of length to have *x*-, *y*-, and *z*-components of −1.1, −0.96, and 0 units (**5**).

Self-test 16.3

Calculate the electric dipole moment of formaldehyde, using the information in (**6**).

[*Answer*: −3.2 D]

16.3 Interactions between dipoles

We calculate the potential energy of a dipole μ_1 in the presence of a charge q_2 by taking into account the interaction of the charge with the two partial charges of the dipole.

Derivation 16.2 *The interaction of a charge with a dipole*

For simplicity, suppose that the charge and dipole are collinear (**7**). Then the potential energy is

$$V = \frac{q_1 q_2}{4\pi\varepsilon_0 (r + \frac{1}{2}l)} - \frac{q_1 q_2}{4\pi\varepsilon_0 (r - \frac{1}{2}l)}$$
$$= \frac{q_1 q_2}{4\pi\varepsilon_0 r\left(1 + \frac{l}{2r}\right)} - \frac{q_1 q_2}{4\pi\varepsilon_0 r\left(1 - \frac{l}{2r}\right)}$$

Now we suppose that the separation of charges in the dipole is much smaller than the distance of the charge q_2 in the sense that $l/2r \ll 1$. Then we can use the expansion

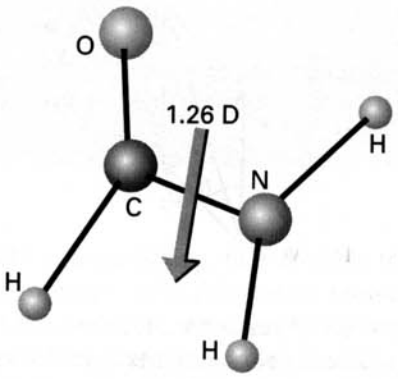
$$\frac{1}{1+x} = 1 - x + x^2 - \cdots$$

to write

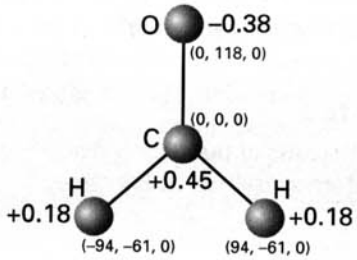
$$V = \frac{q_1 q_2}{4\pi\varepsilon_0 r}\left\{\left(1 - \frac{l}{2r} + \cdots\right) - \left(1 + \frac{l}{2r} + \cdots\right)\right\}$$
$$= -\frac{q_1 q_2 l}{4\pi\varepsilon_0 r^2} + \cdots$$

Now we recognize that $q_1 l = \mu_1$, the dipole moment of molecule 1, and ignore all but the leading term (that is, we neglect the unwritten terms in this expression as they are so small). We find

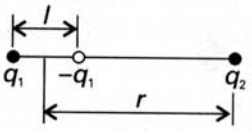
$$V = -\frac{\mu_1 q_2}{4\pi\varepsilon_0 r^2} \qquad (16.5a)$$



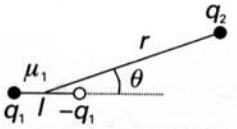
5



6 Formaldehyde, H_2CO



7



8

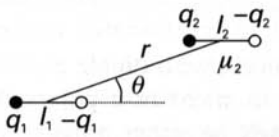
A similar calculation for the more general orientation shown in (**8**) gives

$$V = -\frac{\mu_1 q_2 \cos\theta}{4\pi\varepsilon_0 r^2} \qquad (16.5b)$$

If q_2 is positive, the energy is lowest when $\theta = 180°$ (and $\cos\theta = -1$), because then the partial negative charge of the dipole lies closer than the partial positive charge to the point charge and the attraction outweighs the repulsion. This interaction energy decreases more rapidly with distance than that be-

tween two point charges (as r^2 rather than r) because, from the viewpoint of the single charge, the partial charges of the point dipole seem to merge and cancel as the distance r increases.

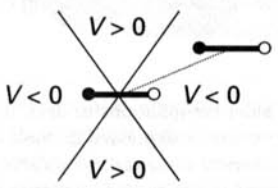
We can calculate the interaction energy between two dipoles μ_1 and μ_2 in the orientation shown in (**9**) in a similar way, taking into account all four charges of the two dipoles. The outcome is



9

$$V = \frac{\mu_1 \mu_2 (1 - 3\cos^2\theta)}{4\pi\varepsilon_0 r^3} \qquad (16.6)$$

This potential energy decreases even more rapidly than in eqn 16.5 because the charges of both dipoles seem to merge as the separation of the dipoles increases. The angular factor takes into account how the like or opposite charges come closer to one another as the relative orientation of the dipoles is changed. The energy is lowest when $\theta = 0$ or 180° (when $1 - 3\cos^2\theta = -2$), because opposite partial charges then lie closer together than like partial charges. The potential energy is negative (attractive) in some orientations when $\theta < 54.7°$ (the angle at which $1 - 3\cos^2\theta = 0$) because opposite charges are closer than like charges. It is positive (repulsive) when $\theta > 54.7°$ because then like charges are closer than unlike charges. The potential energy is zero on the line at 54.7° (and at 180 − 54.7 = 125.3°) because at that angle the two attractions and the two repulsions cancel (**10**).



10

Illustration 16.2

To calculate the molar potential energy of the dipolar interaction between two peptide links separated by 3.0 nm in different regions of a polypeptide chain with $\theta = 180°$, we take $\mu_1 = \mu_2 = 1.4$ D, corresponding to 4.7×10^{-30} C m, and find

$$V = -\frac{(4.7 \times 10^{-30}\,\text{C m})^2 \times (-2)}{4\pi \times (8.854 \times 10^{-12}\,\text{J}^{-1}\text{C}^2\text{m}^{-1}) \times (3.0 \times 10^{-9}\,\text{m})^3}$$
$$= -1.5 \times 10^{-23}\,\text{J}$$

which corresponds to -8.9 J mol^{-1}.

The average potential energy of interaction between polar molecules that are freely rotating in a fluid (a gas or liquid) is zero because the attractions and repulsions cancel. However, because the potential energy of a dipole near another dipole depends on their relative orientations, the molecules exert forces on each other and therefore do not in fact rotate completely freely, even in a gas. As a result, the lower energy orientations are marginally favoured, so there is a nonzero interaction between polar molecules (Fig 16.5). The detailed calculation of the average interaction energy is quite complicated, but the final answer is very simple:

$$V = -\frac{2\mu_1^2 \mu_2^2}{3(4\pi\varepsilon_0)^2 kTr^6} \qquad (16.7)$$

The important features of this expression are the dependence of the average interaction energy on the inverse sixth power of the separation and its inverse dependence on the temperature. The temperature-dependence reflects the way that the greater thermal motion overcomes the mutual orientating effects of the dipoles at higher temperatures.

Illustration 16.3

At 25°C the average interaction energy for pairs of molecules with $\mu = 1$ D is about -1.4 kJ mol^{-1} when the separation is 0.3 nm. This energy should be compared with the average molar kinetic energy of $\frac{3}{2}RT = 3.7$ kJ mol^{-1} at the same temperature: the two are not very dissimilar, but they are both much less than the energies involved in the making and breaking of chemical bonds.

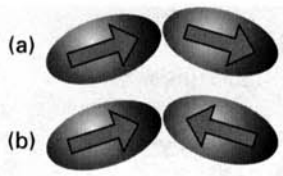


Fig 16.5 A dipole–dipole interaction. When a pair of molecules can adopt all relative orientations with equal probability, the favourable orientations (a) and the unfavourable ones (b) cancel, and the average interaction is zero. In an actual fluid, the interactions in (a) slightly predominate.

16.4 Induced dipole moments

A nonpolar molecule may acquire a temporary **induced dipole moment**, μ^*, as a result of the influence of an electric field generated by a nearby ion or polar molecule. The field distorts the electron distribution of the polarizable molecule, and gives rise to an electric dipole in it. The magnitude of the induced dipole moment is proportional to the strength of the field, $\mathscr{E}$, and we write

$$\mu^* = \alpha\mathscr{E} \tag{16.8}$$

The proportionality constant α is the **polarizability** of the molecule. The larger the polarizability of the molecule, the greater the distortion that is caused by a given electric field. If the molecule has few electrons, they are tightly controlled by the nuclear charges and the polarizability of the molecule is low. If the molecule contains large atoms with electrons some distance from the nucleus, the nuclear control is less and the polarizability of the molecule is greater. The polarizability depends on the orientation of the molecule with respect to the field unless the molecule is tetrahedral (such as CCl_4), octahedral (such as SF_6), or icosahedral (C_{60}, buckminsterfullerene). Atoms, tetrahedral, octahedral, and icosahedral molecules have isotropic (orientation-independent) polarizabilities; all other molecules have anisotropic (orientation-dependent) polarizabilities.

The polarizabilities reported in Table 16.2 are given as **polarizability volumes**, α':

$$\alpha' = \frac{\alpha}{4\pi\varepsilon_0} \tag{16.9}$$

The polarizability volume has the dimensions of volume (hence its name) and is comparable in magnitude to the volume of a molecule.[5]

Self-test 16.4

What strength of electric field is required to induce an electric dipole moment of 1.0 μD in a molecule of polarizability volume 1.1×10^{-31} m^3 (like CCl_4)?

[*Answer*: 2.7 kV cm^{-1}]

A polar molecule with dipole moment μ_1 can induce a dipole moment in a polarizable molecule (which may itself be either polar or nonpolar) because the partial charges of the polar molecule give rise to an electric field that distorts the second molecule. That induced dipole interacts with the permanent dipole of the first molecule, and the two are attracted together (Fig 16.6). The formula for the **dipole–induced-dipole interaction energy** is

$$V = -\frac{\mu_1^2\alpha_2}{\pi\varepsilon_0 r^6} \tag{16.10}$$

where α_2 is the polarizability of molecule 2. The negative sign shows that the interaction is attractive. For a molecule with $\mu = 1$ D (such as HCl) near a molecule of polarizability volume $\alpha' = 1.0 \times 10^{-31}$ m^3 (such as benzene, Table 16.2) the average interaction energy is about −33 J mol^{-1} when the separation is 0.3 nm.

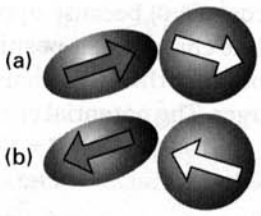


Fig 16.6 A dipole–induced-dipole interaction. The induced dipole (light arrows) follows the changing orientation of the permanent dipole (dark arrow).

[5] When using older compilations of data, it is useful to note that polarizability volumes expressed in cubic centimetres (cm^3) have the same numerical values as the 'polarizabilities' reported using c.g.s. electrical units; so the tabulated values previously called 'polarizabilities' can be used directly as polarizability volumes.

16.5 Dispersion interactions

Finally, we consider the interactions between species that have neither a net charge nor a permanent electric dipole moment (such as two Xe atoms in a gas or two nonpolar groups on the peptide residues of a protein). We know that uncharged, nonpolar species can interact because they form condensed phases, such as benzene, liquid hydrogen, and liquid xenon.

The **dispersion interaction**, or **London force**, between nonpolar species arises from the transient dipoles that they possess as a result of fluctuations in the instantaneous positions of their electrons (Fig 16.7). Suppose, for instance, that the electrons in one molecule flicker into an arrangement that results in partial positive and negative charges and thus gives it an instantaneous dipole moment μ_1. While it exists, this dipole can polarize the other molecule and induce in it an instantaneous dipole moment μ_2. The two dipoles attract each other and the potential energy of the pair is lowered. Although the first molecule will go on to change the size and direction of its dipole (perhaps within 10^{-16} s), the second will follow it; that is, the two dipoles are *correlated* in direction like two meshing gears, with a positive partial charge on one molecule appearing close to a negative partial charge on the other molecule and vice versa. Because of this correlation of the relative positions of the partial charges, and their resulting attractive interaction, the attraction between the two instantaneous dipoles does not average to zero. Instead, it gives rise to a net attractive interaction. Polar molecules interact by a dispersion interaction as well as by dipole–dipole interactions.

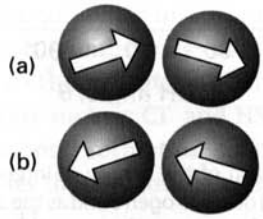


Fig 16.7 In the dispersion interaction, an instantaneous dipole on one molecule induces a dipole on another molecule, and the two dipoles then interact to lower the energy. The directions of the two instantaneous dipoles are correlated, and, although they occur in different orientations at different instants, the interaction does not average to zero.

The strength of the dispersion interaction depends on the polarizability of the first molecule because the magnitude of the instantaneous dipole moment μ_1 depends on the looseness of the control that the nuclear charge has over the outer electrons. If the control is loose, the electron distribution can undergo relatively large fluctuations. Moreover, if the control is loose, then the electron distribution can also respond strongly to applied electric fields and hence have a high polarizability. It follows that a high polarizability is a sign of large fluctuations in local charge density. The strength also depends on the polarizability of the second molecule, for that polarizability determines how readily a dipole can be induced in molecule 2 by molecule 1. We therefore expect $V \propto \alpha_1\alpha_2$. The actual calculation of the dispersion interaction is quite involved, but a reasonable approximation to the interaction energy is the **London formula**:

$$V = -\tfrac{2}{3} \times \frac{a_1' a_2'}{r^6} \times \frac{I_1 I_2}{I_1 + I_2} \qquad (16.11)$$

where I_1 and I_2 are the ionization energies of the two molecules. Once again, the interaction turns out to be proportional to the inverse sixth power of the separation. For two CH_4 molecules, $V \approx -5$ kJ mol^{-1} when $r = 0.3$ nm.

16.6 Hydrogen bonding

The strongest intermolecular interaction arises from the formation of a **hydrogen bond**, in which a hydrogen atom lies between two strongly electronegative atoms and binds them together. The bond is normally denoted X—H···Y, with X and Y being nitrogen, oxygen, or fluorine. Unlike the other interactions we have considered, hydrogen bonding is not universal, but is restricted to molecules that contain these atoms.

The most elementary description of the formation of a hydrogen bond is that it is the result of a Coulombic interaction between the partly exposed positive charge of a proton bound to an electron-withdrawing X atom (in the fragment X–H) and the negative charge of a lone pair on the second atom Y, as in $^{\delta-}X—H^{\delta+}\cdots:Y^{\delta-}$.

Example 16.2 *Assessing a hydrogen bond energy*

Given that the partial charges on H and O are 0.45*e* and −0.83*e*, respectively, calculate the hydrogen bond energy for an O–H group next to an O atom in the arrangement shown in (**11**), and plot the molar energy as a function of the OOH angle. Take $R = 200$ pm and $r = 95.7$ pm.

Strategy The potential energy of two charges z_1e and z_2e separated by a distance r is given by the Coulomb law. We need to evaluate all the distances between pairs of atoms on different molecules and plot the result as a function of the two angles.

Solution The O–O distance is R, so the contribution to the molar potential energy is

$$V_{OO} = \frac{N_A z_O^2 e^2}{4\pi\varepsilon_0 R}$$

By trigonometry, the O–H distance, d, is given by

$$d^2 = R^2 + r^2 - 2Rr\cos\theta$$

Therefore, the contribution of the O–H interaction to the molar energy is

$$V_{OH} = \frac{N_A z_O z_H e^2}{4\pi\varepsilon_0 d} = \frac{N_A z_O z_H e^2}{4\pi\varepsilon_0 (R^2 + r^2 - 2Rr\cos\theta)^{1/2}}$$

The total molar potential energy is the sum:

$$V = V_{OO} + V_{OH}$$

To plot V as a function of angle, we use

$$\frac{N_A e^2}{4\pi\varepsilon_0} = \frac{(6.02214\times10^{23}\,\text{mol}^{-1})\times(1.6022\times10^{-19}\,\text{C})^2}{4\pi\times(8.85419\times10^{-12}\,\text{J}^{-1}\,\text{C}^2\,\text{m}^{-1})}$$

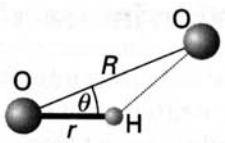
$$= 1.389\times10^{-4}\,\text{J m}$$

The graph of V is shown in Fig 16.8. We see that at $\theta = 0$, a line of atoms, $V = -19$ kJ mol^{-1}. Note how sharply the energy depends on angle: it is negative only within ±12° of linearity.

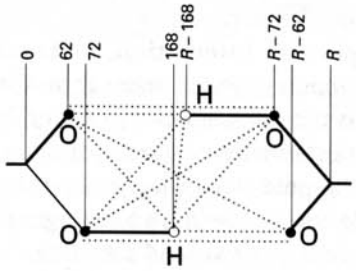
Self-test 16.5

Calculate the energy of interaction between two acetic acid molecules in a dimer, as depicted in (**12**). Consider only the Coulombic interactions indicated by the dotted lines and their symmetry-related equivalents. At what distance R does the interaction become attractive?

[*Answer*: 271 pm]



11



12 Acetic acid dimer

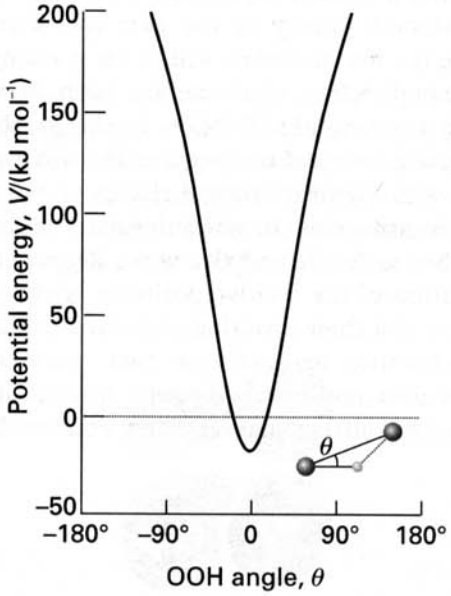


Fig 16.8 The variation of the energy of interaction (on the electrostatic model) of a hydrogen bond as the angle between the O–H and :O groups is changed.

A slightly more sophisticated version of the electrostatic description is to regard hydrogen bond formation as the formation of a Lewis acid–base complex in which the partly exposed proton of the

X–H group is the Lewis acid and :Y, with its lone pair, is the Lewis base:

$$X–H + :Y \rightarrow X–H\cdots Y$$

Molecular orbital theory provides an alternative description that is more in line with the concept of delocalized bonding and the ability of an electron pair to bind more than one pair of atoms (Section 14.18). Thus, if the X–H bond is regarded as formed from the overlap of an orbital on X, ψ_X, and a hydrogen 1*s* orbital, ψ_H, and the lone pair on Y occupies an orbital on Y, ψ_Y, then when the two molecules are close together, we can build three molecular orbitals from the three basis orbitals:

$$\psi = c_1\psi_X + c_2\psi_H + c_3\psi_Y$$

One of the molecular orbitals is bonding, one almost nonbonding, and the third antibonding (Fig 16.9). These three orbitals need to accommodate four electrons (two from the original X–H bond and two from the lone pair of Y), and they may do so if two enter the bonding orbital and two enter the nonbonding orbital. Because the antibonding orbital remains empty, the net effect is a lowering of energy.

Hydrogen bond formation, which has a typical strength of the order of 20 kJ mol^{-1},[6] dominates all other van der Waals interactions when it can occur. It accounts for the rigidity of molecular solids such as sucrose and ice, the secondary structure of proteins (the formation of helices and sheets of polypeptide chains), the low vapour pressure of liquids such as water, and their high viscosities and surface tensions. Hydrogen bonding also contributes to the solubility in water of species such as ammonia and compounds containing hydroxyl groups and to the hydration of anions. In this last case, even ions such as Cl^- and HS^- can participate in hydrogen bond formation with water, for their charge enables them to interact with the hydroxylic protons of H_2O.

[6] This figure is approximately half the enthalpy of vaporization of water: in water, there is an average of two hydrogen bonds per H_2O molecule.

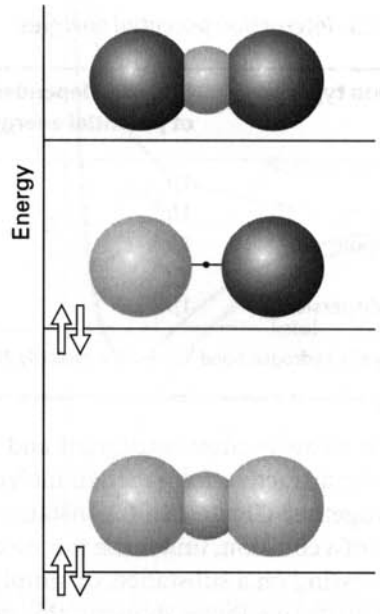


Fig 16.9 A schematic portrayal of the molecular orbitals that can be formed from an X, H, and Y orbital and which gives rise to an X–H···Y hydrogen bond. The lowest energy combination is fully bonding, the next nonbonding, and the uppermost is antibonding. The antibonding orbital is not occupied by the electrons provided by the X–H bond and the :Y lone pair, so the configuration shown may result in a net lowering of energy in certain cases (namely when the X and Y atoms are N, O, or F).

Table 16.3 summarizes the strengths and distance dependences of the attractive forces that we have considered so far.

16.7 The total interaction

The total attractive interaction energy between rotating molecules that cannot participate in hydrogen bonding is the sum of the contributions from the dipole–dipole, dipole–induced-dipole, and dispersion interactions. Only the dispersion interaction contributes if both molecules are nonpolar. All three interactions vary as the inverse sixth power of the separation, so we may write

$$V = -\frac{C}{r^6} \qquad (16.12)$$

where *C* is a coefficient that depends on the identity of the molecules.

Table 16.3 *Interaction potential energies*

Interaction type	Distance dependence of potential energy	Typical energy/ (kJ mol^{-1})	Comment
Ion–ion	$1/r$	250	Only between ions
Ion–dipole	$1/r^2$	15	
Dipole–dipole	$1/r^3$	2	Between stationary polar molecules
	$1/r^6$	0.3	Between rotating polar molecules
London (dispersion)	$1/r^6$	2	Between all types of molecules

The energy of a hydrogen bond X—H· · ·Y is typically 20 kJ mol^{-1} and occurs on contact for X, Y = N, O, or F.

Repulsive terms become important and begin to dominate the attractive forces when molecules are squeezed together (Fig 16.10), for instance, during the impact of a collision, under the force exerted by a weight pressing on a substance, or simply as a result of the attractive forces drawing the molecules together. These repulsive interactions arise in large measure from the Pauli exclusion principle, which forbids pairs of electrons being in the same region of space. The repulsions increase steeply with decreasing separation in a way that can be deduced only by very extensive, complicated molecular structure calculations. In many cases, however, progress can be made by using a greatly simplified representation of the potential energy, where the details are ignored and the general features expressed by a few adjustable parameters.

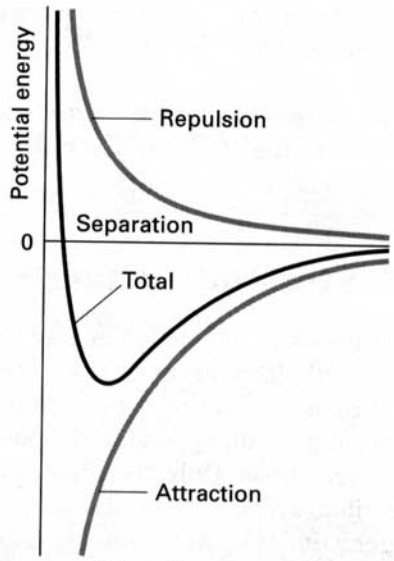


Fig 16.10 The general form of an intermolecular potential energy curve (the graph of the potential energy of two closed-shell species as the distance between them is changed). The attractive (negative) contribution has a long range, but the repulsive (positive) interaction increases more sharply once the molecules come into contact. The overall potential energy is shown by the heavy line.

One such approximation is the **hard-sphere potential**, in which it is assumed that the potential energy rises abruptly to infinity as soon as the particles come within some separation σ (Fig 16.11):

$$V = \begin{cases} \infty & \text{for } r \leq \sigma \\ 0 & \text{for } r > \sigma \end{cases} \qquad (16.13)$$

This very simple potential is surprisingly useful for assessing a number of properties.

Another widely used approximation is to express the short-range repulsive potential energy as inversely proportional to a high power of r:

$$V = +\frac{C^*}{r^n} \qquad (16.14)$$

where C^* is another constant (the star signifies repulsion). Typically, n is set equal to 12, in which case the repulsion dominates the $1/r^6$ attractions strongly at short separations because then $C^*/r^{12} >> C/r^6$. The sum of the repulsive interaction with $n = 12$ and the attractive interaction given by eqn 16.12 is called the **Lennard-Jones (12,6) potential**. It is normally written in the form

$$V = 4\varepsilon\left\{\left(\frac{\sigma}{r}\right)^{12} - \left(\frac{\sigma}{r}\right)^{6}\right\} \qquad (16.15)$$

and is drawn in Fig 16.12. The two parameters are now ε, the depth of the well, and σ, the separation

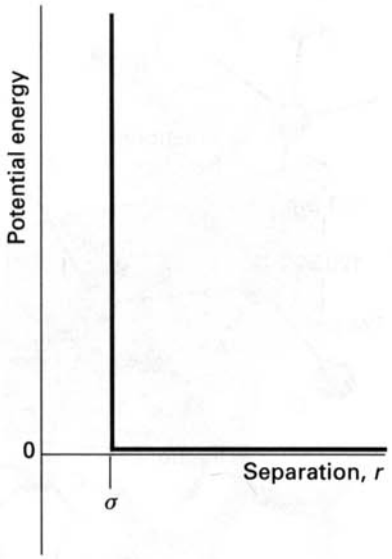


Fig 16.11 The true intermolecular potential can be modelled in a variety of ways. One of the simplest is this *hard-sphere potential*, in which there is no potential energy of interaction until the two molecules are separated by a distance σ when the potential energy rises abruptly to infinity as the impenetrable hard spheres repel each other.

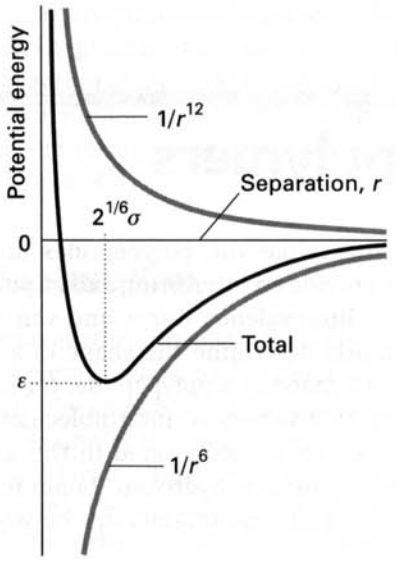


Fig 16.12 The Lennard-Jones potential is another approximation to the true intermolecular potential energy curves. It models the attractive component by a contribution that is proportional to $1/r^6$, and the repulsive component by a contribution that is proportional to $1/r^{12}$. Specifically, these choices result in the Lennard-Jones (12,6)-potential. Although there are good theoretical reasons for the former, there is plenty of evidence to show that $1/r^{12}$ is only a very poor approximation to the repulsive part of the curve.

at which $V = 0$. Some typical values are listed in Table 16.4. Although the (12,6)-potential has been used in many calculations, there is plenty of evidence to show that $1/r^{12}$ is a very poor representation of the repulsive potential, and that the exponential form $e^{-r/\sigma}$ is superior. An exponential function is more faithful to the exponential decay of atomic wavefunctions at large distances, and hence to the distance-dependence of the overlap that is responsible for repulsion. However, a disadvantage of the exponential form is that it is slower to compute, which is important when considering the interactions between the large numbers of atoms in polypeptides and nucleic acids.[7]

Table 16.4 *Lennard–Jones parameters for the (12,6) potential*

	ε/(kJ mol^{-1})	σ/pm
Ar	128	342
Br_2	536	427
C_6H_6	454	527
Cl_2	368	412
H_2	34	297
He	11	258
Xe	236	406

Self-test 16.6

At what separation does the minimum of the potential energy curve occur for a Lennard-Jones potential?

[*Answer*: $r = 2^{1/6}\sigma$]

[7] A further computational advantage of the (12,6)-potential is that, once r^6 has been calculated, r^{12} is obtained by taking the square.

Biopolymers

BIOPOLYMERS like the polypeptides and nucleic acids provide an interesting and important illustration of how valence forces and van der Waals forces jointly determine the shape of a molecule. The overall shape of a polypeptide, for instance, is sustained by a variety of intermolecular forces of the kind we have encountered in this and earlier chapters, including hydrogen bonding, the hydrophobic effect, and interactions between partial charges.

16.8 Polypeptide structures

The **primary structure** of a biopolymer is the sequence of its monomer units: this sequence is determined by valence forces in the sense that the monomers are linked by covalent bonds. For polypeptides, which we consider here, the primary structure is an ordered list of the amino acid residues. The **secondary structure** of a polypeptide is the spatial arrangement of the polypeptide chain—its twisting into a specific shape—under the influence of interactions between the various peptide residues (the amino acid groups).

We can rationalize the secondary structures of proteins in large part in terms of the hydrogen bonds between the –NH– and –CO– groups of the peptide links (Fig 16.13). These bonds lead to two principal structures. One, which is stabilized by hydrogen bonding between peptide links of the same chain, is the **α helix**. The other, which is stabilized by hydrogen bonding links to different chains or more distant parts of the same chain, is the **β-sheet**.[8]

The α helix is illustrated in Fig 16.14. Each turn of the helix contains 3.6 amino acid residues, so there are 18 residues in 5 turns of the helix. The pitch of a single turn is 544 pm. The N–H···O bonds lie parallel to the axis and link every fifth group (so residue i is linked to residues $i - 4$ and $i + 4$). There is freedom for the helix to be arranged as either a right- or a left-handed screw, but the overwhelming majority of natural polypeptides are right-handed on account of the preponderance of the L-configuration of the naturally occurring amino acids. It turns out, in agreement with experience, that a right-handed α helix of L-amino acids has a marginally lower energy than a left-handed helix of the same acids.

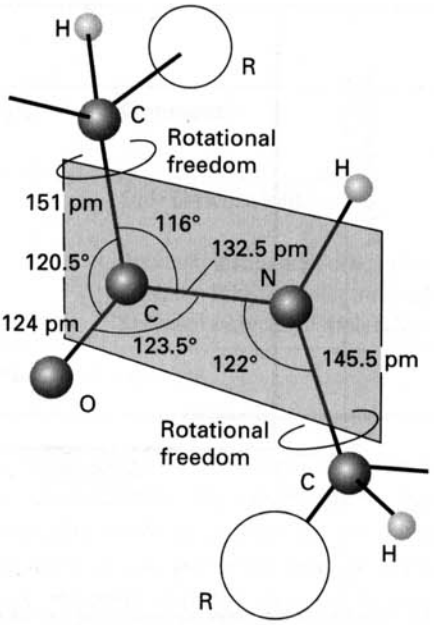


Fig 16.13 The dimensions of a typical peptide link. The C–CO–NH–C atoms define a plane (the C–N bond has partial double-bond character), but there is rotational freedom around the C–CO and N–C bonds.

Helical polypeptide chains are folded into a **tertiary structure** if there are other bonding influences between the residues of the chain that are strong enough to overcome the interactions responsible for the secondary structure. The folding influences include –S—S– **disulfide links**, ionic interactions (which depend on the pH), and strong hydrogen bonds (such as O—H···O–).

Proteins with $M > 50$ kg mol^{-1} (50 kDa) are often found to be aggregates of two or more polypeptide chains. The possibility of such **quaternary structure** often confuses the determination of their molar masses, because different techniques might

[8] The β-sheet is still widely known by its former name, the *β-pleated sheet*.

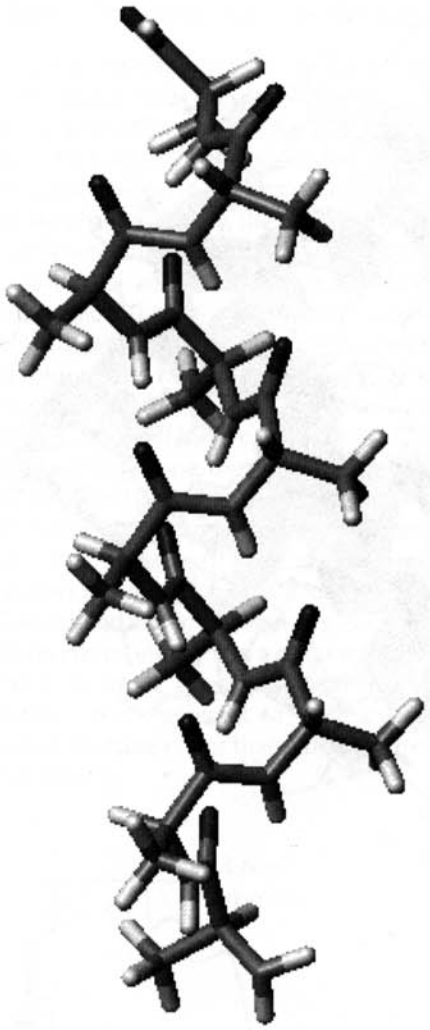


Fig 16.14 A tube representation of an α helix (polyalanine). There are 3.6 residues per turn, and a translation along the helix of 150 pm per residue, giving a pitch of 540 pm. The diameter (ignoring side chains) is about 600 pm.

give values differing by factors of 2 or more. Haemoglobin, which consists of four myoglobin-like chains (Fig 16.15), is an example of a quaternary structure. Myoglobin is an oxygen-storage protein. The subtle differences that arise when four such molecules coalesce to form haemoglobin result in the latter being an oxygen transport protein, able to load O_2 cooperatively and to unload it cooperatively too.

In contemporary physical chemistry and molecular biophysics, a great deal of work is being done on the rationalization and prediction of the structures of biomolecules such as polypeptides and nucleic acids using the interactions we have described in this section (Box 16.1).

16.9 Denaturation

Protein **denaturation**, or loss of structure, can be caused by several means, and different aspects of structure may be affected. The 'permanent waving' of hair, for example, is reorganization at the quaternary level. Hair is a form of the protein keratin, and its quaternary structure is thought to be a multiple helix, with the α helices bound together by disulfide links and hydrogen bonds. The process of permanent waving consists of disrupting these links, unravelling the keratin quaternary structure, and then reforming it into a more fashionable disposition. The 'permanence' is only temporary, however, because the structure of the newly formed hair is genetically controlled. Incidentally, normal hair grows at a rate that requires at least 10 twists of the keratin helix to be produced each second, so very close inspection of the human scalp would show it to be literally writhing with activity.

Denaturation at the secondary level is brought about by agents that destroy hydrogen bonds. Thermal motion may be sufficient, in which case denaturation is a kind of intramolecular melting. When eggs are cooked the albumin is denatured irreversibly, and the protein collapses into a structure resembling a random coil. The **helix–coil transition** is sharp, like ordinary melting, because it is a cooperative process in the sense that when one hydrogen bond has been broken it is easier to break its neighbours, and then even easier to break theirs, and so on.[9] The disruption cascades down the helix, and the transition occurs sharply. Denaturation may also be brought about chemically. For instance, a solvent that forms stronger hydrogen bonds than those within the helix will compete successfully for the NH and CO groups. Acids and bases can cause

[9] This cooperative process is described more fully in Box 20.1.

Fig 16.15 The molecular structure of myoglobin. A haemoglobin molecule consists of four units like this one. The O_2 molecule attaches to the iron atom indicated.

denaturation by protonation or deprotonation of various groups.

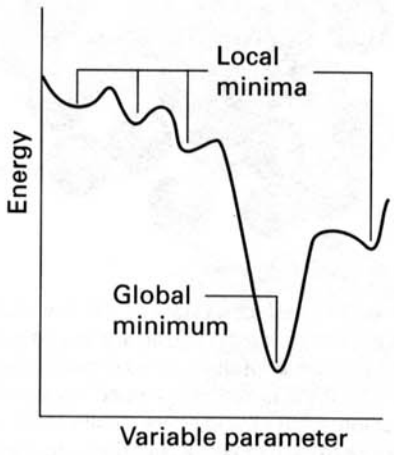
Liquids

THE starting point for the discussion of gases is the totally chaotic distribution of the molecules of a perfect gas. The starting point for the discussion of solids is the well ordered structure of perfect crystals. The liquid state is between these two extremes: there is some structure and some disorder. The particles of a liquid are held together by intermolecular forces, but their kinetic energies are comparable to their potential energies. As a result, although the molecules are not free to escape completely from the bulk, the whole structure is very mobile. The flow of molecules is like a crowd of spectators leaving a stadium.

Box 16.1 *The prediction of protein structure*

A polypeptide chain adopts a conformation corresponding to a minimum Gibbs energy. That simple perception, though, conceals a great deal of complexity. A part of the difficulty is that the Gibbs energy depends on the entropy as well as the energy of interaction between different parts of the chain. Secondly, the protein molecule is not isolated: its outer surface is covered by a mobile sheath of water molecules, and its interior contains pockets of water molecules. These water molecules play an important role in determining the conformation that the chain adopts through the hydrogen bonding in which it can participate and the hydrophobic effect (Box 4.1).

Even if we disregard these complications and concentrate on the energy alone, the problems are still severe. A simple view would be that the polypeptide adopts a conformation that corresponds to minimum energy. However, there is no guarantee that as the protein is formed in a cell it does not get trapped in a *local* minimum and, once fully formed and in the aqueous environment of a cell, it is unable to wriggle into a *global* minimum (see illustration). In other words, the conformation of a polypeptide may represent a kinetically trapped metastable structure rather than a true thermodynamically stable state.



The variation of potential energy with the conformation of a molecule showing various local minima and a single global minimum.

To calculate the energy of a conformation we need to make use of many of the interactions described earlier in the chapter. The calculation is an elaboration of the one illustrated in Example 16.2, with several additional interactions taken into account:

1 *Bond stretch*. Bonds are not rigid, and it may be advantageous for some bonds to stretch and others to be compressed slightly as parts of the chain press against one another. If we liken a bond to a spring, then the potential energy depends on the displacement from equilibrium as

$$V_{\text{stretch}} = \tfrac{1}{2}k_{\text{stretch}}(R - R_e)^2$$

where R_e is the equilibrium bond length and k_{stretch} is the force constant (a measure of the stiffness of the bond in question).

2 *Bond bend*. An O-C-H bond angle (or some other angle) may open out or close up slightly to enable the molecule as a whole to fit together better. If the equilibrium bond angle is θ_e, we write

$$V_{\text{bend}} = \tfrac{1}{2}k_{\text{bend}}(\theta - \theta_e)^2$$

3 *Interaction between partial charges*. The calculation is based on eqn 16.1. In some models of structure, the interaction between partial charges is judged to take into account the effect of hydrogen bonding; in other models, hydrogen bonding is added as another very short range interaction. The interaction between partial charges does away with the need to take dipole–dipole interactions into account, for they are taken care of by dealing with each partial charge explicitly.

4 *Dispersion interactions*. The London forces between atoms are taken into account by using the London formula, eqn 16.11, and its inverse-sixth power dependence on the separation.

5 *Repulsive interactions*. Other than the repulsion between like partial charges, which is taken into account by the charge–charge contribution, we need to take into account the effect of overlap of wavefunctions when two closed-shell atoms come into contact. That can be done by using a $1/r^{12}$ term, as in the Lennard-Jones (6,12)-potential, eqn 16.15.

These interactions—with a number of enhancements and modifications—are built into commercially available software packages. These packages also include schemes for modifying the locations of the atoms in a systematic way and searching for local and global minima.

Exercise 1 Theoretical studies have estimated that the lumiflavin isoalloazine ring system has an energy minimum at the bending angle of 15°, but that it requires only 8.5 kJ mol^{-1} to increase the angle to 30°. If there are no other compensating forces, what is the force constant for lumiflavin bending?

Exercise 2 The equilibrium bond length of a carbon–carbon single bond is 152 pm. Given a C–C force constant of 400 N m^{-1}, how much energy, in kilojoules per mole, would it take to stretch the bond to 165 pm?

16.10 The relative positions of molecules

We describe the average locations of the particles in the liquid in terms of the **pair distribution function**, g. This function is defined so that $g\delta r$ is the probability that a molecule will be found at a distance between r and $r + \delta r$ from another molecule.[10] It follows that, if g passes through a maximum at a radius of, for instance, 0.5 nm, then the most probable distance (regardless of direction) at which a second molecule will be found will be at 0.5 nm from the first molecule.

In a crystal, g is an array of sharp spikes, representing the certainty (in the absence of defects and thermal motion) that particles lie at definite locations. This regularity continues out to large distances (to the edge of the crystal, billions of molecules away), so we say that crystals have **long-range order**. When the crystal melts, the long-range order is lost and wherever we look at long distances from a given particle there is equal probability of finding a second particle. Close to the first particle, though, there may be a remnant of order (Fig 16.16). Its nearest neighbours might still adopt approximately their original positions, and even if they are displaced by newcomers the new particles might adopt their vacated positions. It may still be possible to detect, on average, a sphere of nearest neighbours at a distance r_1, and perhaps beyond them a sphere of next-nearest neighbours at r_2. The existence of this **short-range order** means that g can be expected to have a broad but pronounced peak at r_1, a smaller and broader peak at r_2, and perhaps some more structure beyond that.

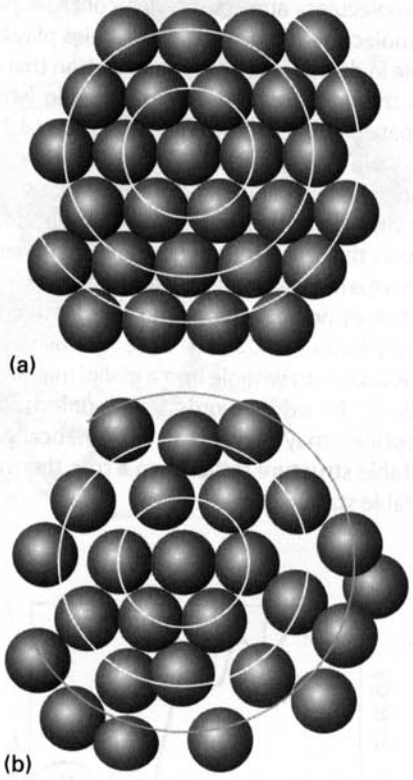


Fig 16.16 (a) In a perfect crystal at $T = 0$, the distribution of molecules (or ions) is highly regular, and the pair distribution function shows a series of sharp peaks showing the regular organization of rings of neighbours around any selected central molecule or ion. (b) In a liquid, there remain some elements of structure close to each molecule, but the further the distance, the less the correlation. The pair distribution function now shows a pronounced (but broadened) peak corresponding to the nearest neighbours of the molecule of interest (which are only slightly more disordered than in the solid), and a suggestion of a peak for the next ring of molecules, but little structure at greater distances.

The pair distribution function can be determined experimentally by X-ray diffraction, for g can be extracted from the diffuse diffraction pat-

[10] Recall the analogous quantity used to describe the distance of an electron from an atom, Section 13.4.

tern characteristic of liquid samples in much the same way as a crystal structure is obtained from X-ray diffraction of crystals (see Section 15.8). The shells of local structure shown in the example in Fig 16.17 (for water) are unmistakable. Closer analysis shows that any given H_2O molecule is surrounded by other molecules at the corners of a tetrahedron, similar to the arrangement in ice (Fig 16.18). The form of g at 100°C shows that the intermolecular forces (in this case, largely hydrogen bonds) are strong enough to affect the local structure right up to the boiling point.

16.11 Molecular motion in liquids

A molecule in a liquid is surrounded by other molecules, and it can move only a fraction of a diameter, perhaps because its neighbours move aside momentarily, before colliding. Molecular motion in liquids is a series of short steps, with incessantly changing directions, like people in an aimless, milling crowd.

The process of migration by means of a random jostling motion though a liquid is called **diffusion**. We can think of the motion of the molecule

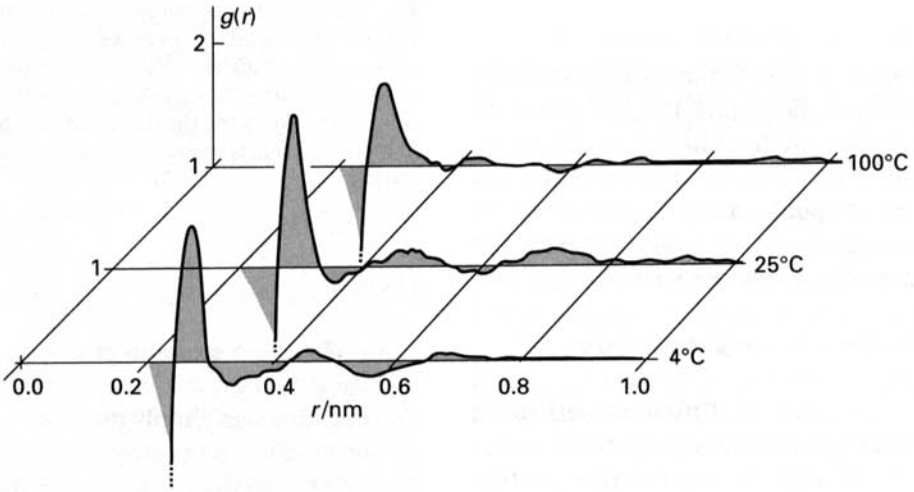


Fig 16.17 The experimentally determined radial distribution function of the oxygen atoms in liquid water at three temperatures. Note the expansion as the temperature is raised.

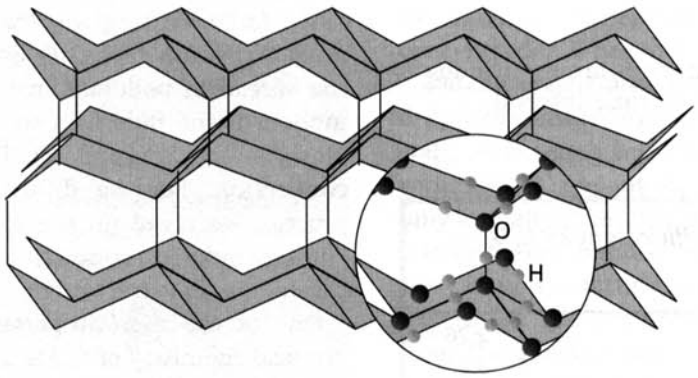


Fig 16.18 A fragment of the crystal structure of ice. Each O atom is at the centre of a tetrahedron of four O atoms at a distance of 276 pm. The central O atom is attached by two short O–H bonds to two H atoms and by two relatively long O···H bonds to two neighbouring H_2O molecules. Overall, the structure consists of planes of hexagonal puckered rings of H_2O molecules (like the chair form of cyclohexane).

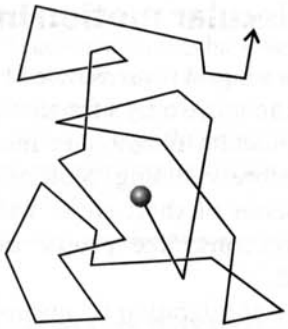


Fig 16.19 One possible path of a random walk in three dimensions. In this general case, the step length is also a random variable.

as a series of short jumps in random directions, a so-called **random walk** (Fig 16.19). If there is an initial concentration gradient in the liquid (for instance, a solution may have a high concentration of solute in one region), then the rate at which the molecules spread out is proportional to the concentration gradient, and we write

$$\text{Rate of diffusion} = D \times \text{concentration gradient}$$

The coefficient D is called the **diffusion coefficient**: if it is large, molecules diffuse rapidly. Some values are given in Table 16.5. To express this relation mathematically, we introduce the **flux**, J, which is the number of particles passing through an imaginary window in a given time interval, divided by the area of the window and the duration of the interval:

$$\text{Flux, } J = \frac{\text{number of particles passing through window}}{\text{area of window} \times \text{time interval}}$$

Table 16.5 *Diffusion coefficients at 25°C, D/(10^{-9} m^2 s^{-1})*

H_2O in water	2.26
Ar in tetrachloromethane	3.63
CH_3OH in water	1.58
$C_{12}H_{22}O_{11}$ (sucrose) in water	0.522
NH_2CH_2COOH in water	0.673
O_2 in tetrachloromethane	3.82

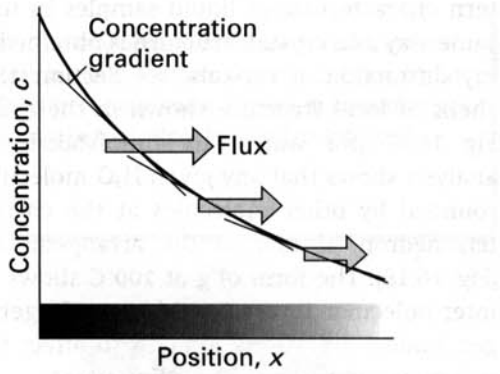


Fig 16.20 The flux of solute particles is proportional to the concentration gradient. Here we see a solution in which the concentration falls from left to right (as depicted by the shaded band and the curve). The gradient is negative (down from left to right) and the flux is positive (towards the right). The greatest flux is found where the gradient is steepest (at the left).

Then,

$$J = -D \times \text{concentration gradient} \qquad (16.16)$$

The negative sign simply means that, if the concentration gradient is negative (down from left to right, Fig 16.20), then the flux is positive (flowing from left to right). To get the number passing through a given window in a given time, we multiply the flux by the area of the window and the time interval.

Diffusion coefficients are of the greatest importance for discussing the spread of pollutants in lakes and through the atmosphere. In both cases, the spread of pollutant may be assisted by bulk motion of the fluid as a whole (as when a wind blows in the atmosphere). This motion is called **convection**. Because diffusion is often a slow process, we speed up the spread of solute molecules by inducing convection by stirring a fluid or turning on an extractor fan.

One of the most important equations in the physical chemistry of fluids is the *diffusion equation*, which enables us to predict the rate at which the concentration of a solute changes in a nonuniform solution. In essence, the diffusion equation expresses the fact that wrinkles in the concentration tend to disperse.

Derivation 16.3 *The diffusion equation*

To express this idea quantitatively, we consider the arrangement in Fig 16.21. The number of solute particles passing through the window of area A located at x in an interval dt is $J(x)Adt$, where $J(x)$ is the flux at the location x. The number of particles passing out of the region through a window of area A at $x + dx$ is $J(x + dx)Adt$, where $J(x + dx)$ is the flux at the location of this window. The flux in and the flux out will be different if the concentration gradients are different at the two windows. The net change in the number of solute particles in the region between the two windows is

$$\text{Net change in number} = J(x)Adt - J(x + dx)Adt = \{J(x) - J(x + dx)\}Adt$$

Now we express the two fluxes in terms of the concentration gradients at the locations of the two windows by using eqn 16.16, which gives

$$\text{Net change in number} = \left\{-D\left(\frac{dc}{dx}\right)_{\text{at } x} + D\left(\frac{dc}{dx}\right)_{\text{at } x+dx}\right\} Adt$$

Now we come to the only tricky part of the calculation. The concentration gradients are slightly different at x and $x + dx$, so we write

$$\left(\frac{dc}{dx}\right)_{\text{at } x+dx} = \left(\frac{dc}{dx}\right)_{\text{at } x} + \left(\frac{d^2c}{dx^2}\right)_{\text{at } x} dx$$

where d^2c/dx^2 is the 'second derivative' of the concentration; in effect, the second derivative is just the curvature of the graph of the concentration. When we substitute this expression into the preceding one, the concentration gradients at x cancel and we are left with

$$\text{Net change in number} = D\left(\frac{d^2c}{dx^2}\right) A\, dx\, dt$$

The change in concentration inside the region between the two windows is the net change in number divided by the volume of the region (which is Adx):

$$\text{Change in concentration} = D\left(\frac{d^2c}{dx^2}\right) dt$$

The rate of change in concentration, dc/dt, is therefore[11]

$$\frac{dc}{dt} = D\frac{d^2c}{dx^2} \qquad (16.17)$$

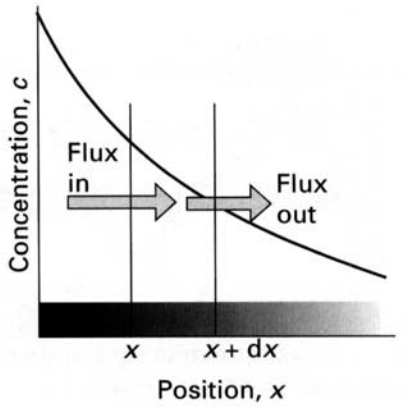


Fig 16.21 To calculate the change in concentration in the region between the two walls, we need to consider the net effect of the influx of particles from the left and their efflux towards the right. Only if the slope of the concentration is different at the two walls will there be a net change.

The **diffusion equation**, eqn 16.17, tells us that the rate of change of concentration in a small region is proportional to the curvature of the concentration there. A uniform concentration and a concentration with unvarying slope through the region results in no net change in concentration because the rate of influx through one wall is equal to the rate of efflux through the opposite wall. Only if the slope of the concentration varies through the region—only if the concentration is wrinkled—is there a change in concentration. Where the curvature is positive (a dip, Fig 16.22) the change in concentration is positive: the dip tends to fill. Where the curvature is negative (a heap), the change in concentration is negative: the heap tends to spread.

We can understand the nature of diffusion more deeply by considering it as the outcome of a random walk. Although a molecule undergoing a random walk may take many steps in a given time, it has only a small probability of being found far from its starting point because some of the steps lead it away from the starting point but others lead it back (Fig 16.23). The net distance travelled in a time t from the starting point is measured by the **root mean square distance**, d, with

[11] Because the concentration is a function of both time and location, the derivatives are in fact *partial* derivatives; but we are not using that notation in this book.

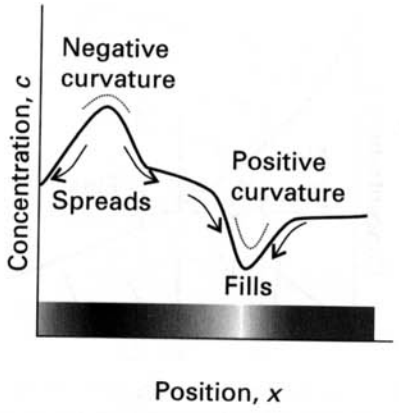


Fig 16.22 Nature abhors a wrinkle. The diffusion equation tells us that peaks in a distribution (regions of negative curvature) spread and troughs (regions of positive curvature) fill in.

$$d = (2Dt)^{1/2} \qquad (16.18)$$

Thus, the net distance increases only as the square root of the time, so for a particle to be found twice as far (on average) from its starting point, we must wait four times as long.

Self-test 16.7

The diffusion coefficient of H_2O in water is 2.26×10^{-9} $m^2 s^{-1}$ at 25°C. How long does it take for an H_2O molecule to travel (a) 1.0 cm, (b) 2.0 cm from its starting point in a sample of unstirred water?

[*Answer*: (a) 6.1 h, (b) 25 h]

The relation between the diffusion coefficient and the rate at which the molecule takes its steps and the distance of each step is called the **Einstein–Smoluchowski equation**:

$$D = \frac{\lambda^2}{2\tau} \qquad (16.19)$$

where λ is the length of each step and τ (tau) is the time each step takes. This equation tells us that a molecule that takes rapid, long steps has a high diffusion coefficient. We can interpret τ as the average lifetime of a molecule near another molecule before it makes a sudden jump to its next position.

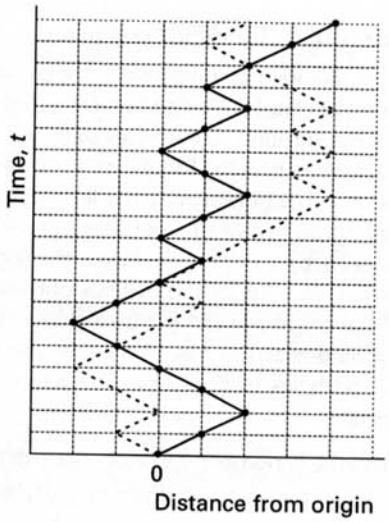


Fig 16.23 The directions of a typical sequence of steps in a one-dimensional random walk. Note how the walker might still be close to the origin after many steps. Two walks are shown here. The equations in the text refer to an average outcome of many such walks.

Self-test 16.8

Suppose an H_2O molecule moves through one molecular diameter (about 200 pm) each time it takes a step in a random walk. What is the time for each step at 25°C?

[*Answer*: 9 ps]

The diffusion coefficient increases with temperature because an increase in temperature enables a molecule to escape more easily from the attractive forces exerted by its neighbours. If we suppose that the rate $(1/\tau)$ of the random walk follows an Arrhenius temperature dependence with an activation energy E_a, then the diffusion coefficient will follow the relation

$$D = D_0 \, e^{-E_a/RT} \qquad (16.20)$$

The rate at which particles diffuse through a liquid is related to the viscosity, and we should expect a high diffusion coefficient to be found for fluids that have a low viscosity. That is, we can suspect that $\eta \propto 1/D$, where η (eta) is the **coefficient of viscosity**. In fact, the **Einstein relation** states that

$$D = \frac{kT}{6\pi h a} \qquad (16.21)$$

where a is the radius of the molecule. It follows that[12]

$$\eta = \eta_0 \, e^{E_a/RT} \qquad (16.22)$$

This temperature dependence is observed, at least over reasonably small temperature ranges (Fig 16.24). The intermolecular potentials govern the magnitude of E_a, but the problem of calculating it is immensely difficult and still largely unsolved.

Self-test 16.9

Estimate the activation energy for the viscosity of water from the graph in Fig 16.24, by using the viscosities at 40°C and 80°C. (*Hint*. Use an equation like eqn 16.22 to formulate an expression for the logarithm of the ratio of the two viscosities.)

[*Answer*: 14 kJ mol^{-1}]

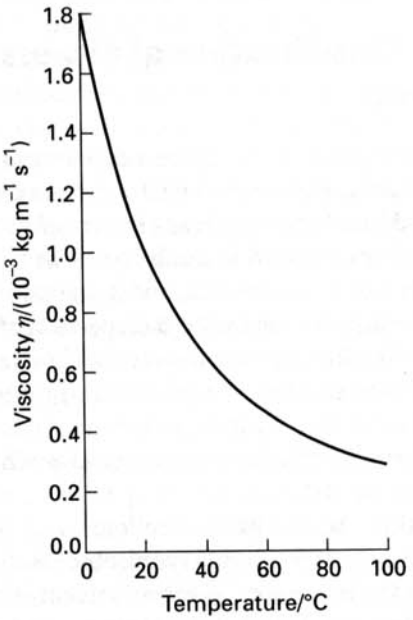


Fig 16.24 The experimental temperature dependence of the viscosity of water. As the temperature is increased, more molecules are able to escape from the potential wells provided by their neighbours, so the liquid becomes more fluid.

[12] Note the change in sign of the exponent: viscosity decreases as the temperature is raised. We are supposing that the strong temperature dependence of the exponential term dominates the weak linear dependence on T in the numerator of eqn 16.21.

Mesophases and disperse systems

A **mesophase** is a bulk phase that is intermediate in character between a solid and a liquid. The most important type of mesophase is a **liquid crystal**, which is a substance having liquid-like imperfect short-range order in some directions but some aspects of crystal-like long-range order in other directions. Liquid crystals can be used as models of biological cell walls and studied to gain insight into the process of transport through membranes. They are also of considerable technological importance for their use in liquid-crystal displays on electronic equipment. A **disperse system** is a dispersion of small particles of one material in another. The small particles are commonly called **colloids**. In this context, 'small' means something less than about 500 nm in diameter (about the wavelength of light). In general, they are aggregates of numerous atoms or molecules, but are too small to be seen with an ordinary optical microscope. They pass through most filter papers, but can be detected by light-scattering, sedimentation, and osmosis.

16.12 Liquid crystals

There are three important types of liquid crystal; they differ in the type of long-range order that they retain. One type of retained long-range order gives rise to a **smectic phase** (from the Greek word for soapy), in which the molecules align themselves in layers (Fig 16.25). Other materials, and some smectic liquid crystals at higher temperatures, lack the layered structure but retain a parallel alignment (Fig 16.26): this mesophase is the **nematic phase** (from the Greek for thread). The strongly anisotropic optical properties of nematic liquid crystals, and their response to electric fields, is the basis of their use as data displays. In the **cholesteric phase**, which is so-called because some derivatives of cholesterol form them, the molecules lie

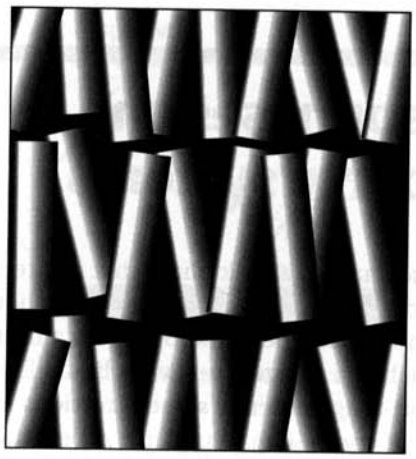


Fig 16.25 The arrangement of molecules in the smectic phase of a liquid crystal.

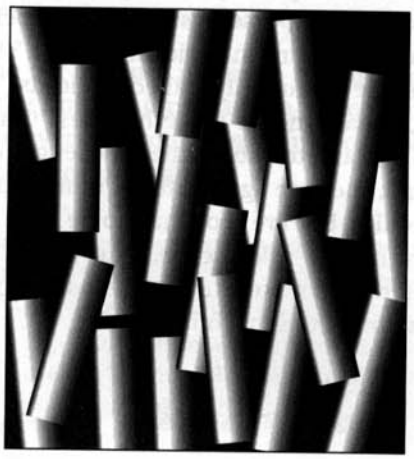


Fig 16.26 The arrangement of molecules in the nematic phase of a liquid crystal.

in sheets at angles that change slightly between neighbouring sheets (Fig 16.27), so forming helical structures. The pitch of the helix varies with temperature and, as a result, cholesteric liquid crystals diffract light and appear to have colours that depend on the temperature. They are used for detecting temperature distributions in living material, including human patients, and have even been incorporated into fabrics.

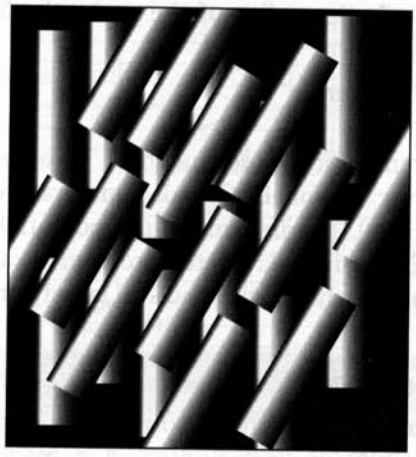


Fig 16.27 The arrangement of molecules in the cholesteric phase of a liquid crystal. Two layers are shown; the relative orientation of these layers is repeated in successive layers, to give a helical array of molecules.

16.13 Classification of disperse systems

The name given to the system depends on the nature of the substances involved. A **sol** is a dispersion of a solid in a liquid (such as clusters of gold atoms in water) or of a solid in a solid (such as ruby glass, which is a gold-in-glass sol, and achieves its colour by scattering). An **aerosol** is a dispersion of a liquid in a gas (like fog and many sprays) and of a solid in a gas (such as smoke): the particles are often large enough to be seen with a microscope. An **emulsion** is a dispersion of a liquid in a liquid (such as milk and some paints).

A further classification of colloids is as **lyophilic** (solvent attracting) and **lyophobic** (solvent repelling); in the case of water as solvent, the terms **hydrophilic** and **hydrophobic** are used instead. Lyophobic colloids include the metal sols. Lyophilic colloids generally have some chemical similarity to the solvent, such as OH groups able to form hydrogen bonds. A **gel** is a semirigid mass of a lyophilic sol in which all the dispersion medium has been absorbed by the sol particles.

The preparation of aerosols can be as simple as sneezing (which produces an aerosol). Laboratory and commercial methods make use of several tech-

niques. Material (for example, quartz) may be ground in the presence of the dispersion medium. Passing a heavy electric current through a cell may lead to the crumbling of an electrode into colloidal particles; arcing between electrodes immersed in the support medium also produces a colloid. Chemical precipitation sometimes results in a colloid. A precipitate (for example, silver iodide) already formed may be converted to a colloid by the addition of **peptizing agent**, a substance that disperses a colloid. An example of a peptizing agent is potassium iodide, which provides ions that adhere to the colloidal particles and cause them to repel one another. Clays may be peptized by alkalis, the OH^- ion being the active agent.

Emulsions are normally prepared by shaking the two components together, although some kind of **emulsifying agent** has to be used in order to stabilize the product. This emulsifier may be a soap (a long-chain fatty acid), a surfactant, or a lyophilic sol that forms a protective film around the dispersed phase. In milk, which is an emulsion of fats in water, the emulsifying agent is casein, a protein containing phosphate groups. That casein is not completely successful in stabilizing milk is apparent from the formation of cream: the dispersed fats coalesce into oily droplets, which float to the surface. This separation may be prevented by ensuring that the emulsion is dispersed very finely initially: violent agitation with ultrasonics or extrusion through a very fine mesh brings this about, the product being 'homogenized' milk.

Aerosols are formed when a spray of liquid is torn apart by a jet of gas. The dispersal is aided if a charge is applied to the liquid, for then the electrostatic repulsions blast the jet apart into droplets. This procedure may also be used to produce emulsions, for the charged liquid phase may be squirted into another liquid.

Disperse systems are often purified by dialysis (recall Box 6.2). The aim is to remove much (but not all, for reasons explained later) of the ionic material that may have accompanied their formation. A membrane (for example, cellulose) is selected that is permeable to solvent and ions, but not to the bigger colloid particles. Dialysis is very slow, and is normally accelerated by applying an electric field and making use of the charge carried by many colloids; the technique is then called **electrodialysis**.

16.14 Surface, structure, and stability

The principal feature of colloids is the very great surface area of the dispersed phase in comparison with the same amount of ordinary material. For example, a cube of side 1 cm has a surface area of 6 cm^2. When it is dispersed as 10^{18} little 10 nm cubes the total surface area is 6×10^6 cm^2 (about the size of a tennis court). This dramatic increase in area means that surface effects are of dominating importance in the chemistry of disperse systems.

As a result of their great surface area, colloids are thermodynamically unstable with respect to the bulk: that is, colloids have a thermodynamic tendency to reduce their surface area (like a liquid). Their apparent stability must therefore be a consequence of the kinetics of collapse: disperse systems are kinetically nonlabile, not thermodynamically stable. At first sight, though, even the kinetic argument seems to fail: colloidal particles attract one another over large distances by the dispersion interaction, so there is a long-range force tending to collapse them down into a single blob.

Several factors oppose the long-range dispersion attraction. There may be a protective film at the surface of the colloid particles that stabilizes the interface and cannot be penetrated when two particles touch. For example, the surface atoms of a platinum sol in water react chemically and are turned into $-Pt(OH)_3H_3$, and this layer encases the particle like a shell. A fat can be emulsified by a soap because the long hydrocarbon tails penetrate the oil droplet but the $-CO_2^-$ head groups (or other hydrophilic groups in detergents) surround the surface, form hydrogen bonds with water, and give rise to a shell of negative charge that repels a possible approach from another similarly charged particle.

By a **surfactant** we mean a species that accumulates at the interface of two phases or substances (one of which may be air) and modifies the properties of the surface. A typical surfactant consists of a long hydrocarbon tail that dissolves in hydrocarbon and other nonpolar materials, and a hydrophilic

head group, such as a carboxylate group, $-CO_2^-$, that dissolves in a polar solvent (typically water). In other words, a surfactant is an **amphipathic** substance,[13] meaning that it has both hydrophobic and hydrophilic regions. Soaps, for example, consist of the alkali metal salts of long-chain carboxylic acids, and the surfactant in detergents is typically a long-chain benzenesulfonic acid ($R-C_6H_4SO_3H$). The mode of action of a surfactant in a detergent, and of soap, is to dissolve in both the aqueous phase and the hydrocarbon phase where their surfaces are in contact, and hence to solubilize the hydrocarbon phase so that it can be washed away (Fig 16.28).

Surfactant molecules can group together as **micelles**, colloid-sized clusters of molecules, even in the absence of grease droplets, for their hydrophobic tails tend to congregate, and their hydrophilic heads provide protection (Fig 16.29). Micelles form only above the **critical micelle concentration** (CMC) and above the **Krafft temperature**. Nonionic surfactant molecules may cluster together in swarms of 1000 or more, but ionic species tend to be disrupted by the Coulombic repulsions between head groups and are normally limited to groups of between 10 and 100 molecules. The shapes of the individual micelles vary with concentration. Although spherical micelles do occur, they are more commonly flattened spheres close to the CMC, and rod-like at higher concentrations. The interior of a micelle is like a droplet of oil, and magnetic resonance shows that the hydrocarbon tails are mobile, but slightly more restricted than in the bulk.

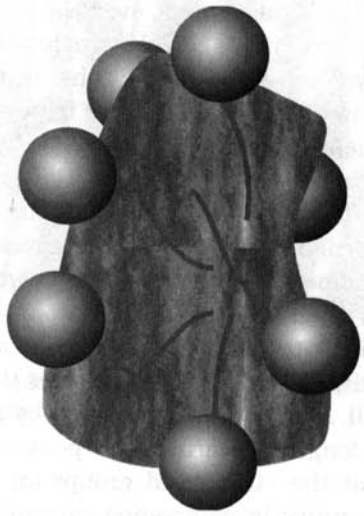


Fig 16.28 A surfactant molecule in a detergent or soap acts by sinking its hydrophobic hydrocarbon tail into the grease, so leaving its hydrophilic head groups on the surface of the grease where they can interact attractively with the surrounding water.

Micelles are important in industry and biology on account of their solubilizing function: matter can be transported by water after it has been dissolved in their hydrocarbon interiors. For this reason, micellar systems are used as detergents and drug carriers, and for organic synthesis, froth flotation, and petroleum recovery. They can be perceived as a part of a family of similar structures formed when amphipathic substances are present in water (Fig 16.30). A **monolayer** forms at the air–water interface, with the hydrophilic head groups facing the water. Micelles are like monolayers that enclose a region. A **bilayer vesicle** is like a double-micelle, with an inward pointing inner surface of molecules surrounded by and outward pointing outer layer. The 'flat' version of a bilayer vesicle is the analogue of a cell membrane (Box 16.2).

The thermodynamics of micelle formation shows that the enthalpy of formation in aqueous systems is probably positive (that is, that they are endothermic) with $\Delta H \approx 1$–2 kJ per mole of surfactant. That

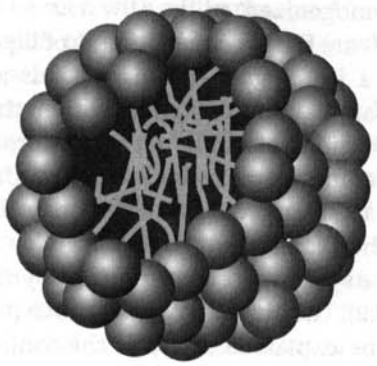


Fig 16.29 A representation of a spherical micelle. The hydrophilic groups are represented by spheres, and the hydrophobic hydrocarbon chains are represented by the stalks: the latter are mobile.

[13] The *amphi-* part of the name is from the Greek word for 'both', and the *-pathic* part is from the same root as sympathetic (meaning 'feeling').

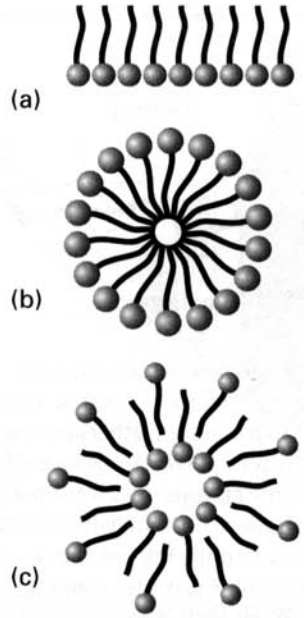


Fig 16.30 Amphipathic molecules form a variety of related structures in water: (a) a monolayer; (b) a spherical micelle; (c) a bilayer vesicle.

they do form above the CMC indicates that the entropy change accompanying their formation must then be positive (in order for the Gibbs energy accompanying the formation process to be negative), and measurements suggest a value of about +140 $J K^{-1} mol^{-1}$ at room temperature. That the entropy change is positive even though the molecules are clustering together shows that there must be a contribution to the entropy from the solvent and that its molecules must be more free to move once the solute molecules have herded into small clusters. This interpretation is plausible, because each individual solute molecule is held in an organized solvent cage (Fig 16.31), but once the micelle has formed the solvent molecules need form only a single (admittedly larger) cage. The increase in entropy when hydrophobic groups cluster together and reduce their structural demands on the solvent is the origin of the **hydrophobic interaction** that tends to stabilize groupings of hydrophobic groups in biological macromolecules (see Box 4.1). The hydrophobic interaction is an example of an ordering process that is stabilized by a tendency toward greater disorder of the solvent.

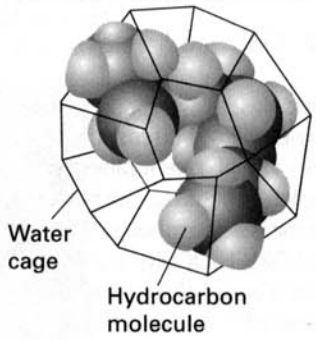


Fig 16.31 When a hydrocarbon molecule is surrounded by water, the water molecules form a clathrate cage. As a result of this acquisition of structure, the entropy of the water decreases, so the dispersal of the hydrocarbon into water is entropy-opposed; the coalescence of many hydrocarbon molecules into a single large blob is entropy-favoured.

16.15 The electric double layer

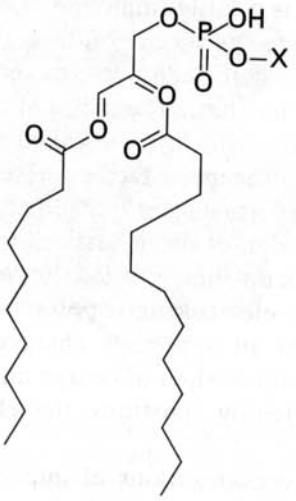
Apart from the physical stabilization of disperse systems, a major source of kinetic stability is the existence of an electric charge on the surfaces of the colloidal particles. On account of this charge, ions of opposite charge tend to cluster nearby.

Two regions of charge must be distinguished. First, there is a fairly immobile layer of ions that stick tightly to the surface of the colloidal particle, and which may include water molecules (if that is the support medium). The radius of the sphere that captures this rigid layer is called the **radius of shear**, and is the major factor determining the mobility of the particles (Fig 16.32). The electric potential at the radius of shear relative to its value in the distant, bulk medium is called the **zeta potential**, ζ (zeta), or the **electrokinetic potential**. The charged unit attracts an oppositely charged ionic atmosphere. The inner shell of charge and the outer atmosphere jointly constitute the **electric double layer**.

At high concentrations of ions of high charge number, the atmosphere is dense and the potential falls to its bulk value within a short distance. In this case there is little electrostatic repulsion to hinder the close approach of two colloid particles. As a result, **flocculation**, the coalescence of the colloidal particles, occurs as a consequence of the van der

Box 16.2 *Cell membranes*

Although micelles, bilayers, and vesicles are convenient starting points for the discussion of the nature of cell membranes, actual membranes are highly sophisticated, complex structures. The basic structural element of a membrane is a phospholipid (**13**), which has the formula $CH_2(OCOR)CH(OCOR)CH_2OPO(OH)OX$, where R is a long hydrocarbon chain (typically in the range C_{14}–C_{24}) and X is one of a variety of polar groups, such as $-CH_2CH_2NH_2$ or $-CH_2CH(NH_2)COOH$. These twin-tailed amphipathic molecules stack together to form an extensive bilayer; the head groups are different on the outside of the cell from those on the inside, so the wall is asymmetric. The membrane is about 5 nm across, and each layer of the bilayer is called a *leaflet*. The lipid molecules form layers rather than micelles because the hydrocarbon chains are too bulky to allow packing into nearly spherical clusters. Interspersed among the phospholipids are sterols, such as cholesterol (**14**), which are also amphipathic: the –OH group is hydrophilic and the rest of the molecule hydrophobic. The presence of the sterols—which are present in different proportions in different types of cell—prevents the phospholipid tails freezing into a solid array and, by disrupting the packing of these tails, spreads the melting point of the membrane over a range of temperatures.



13 A phospholipid

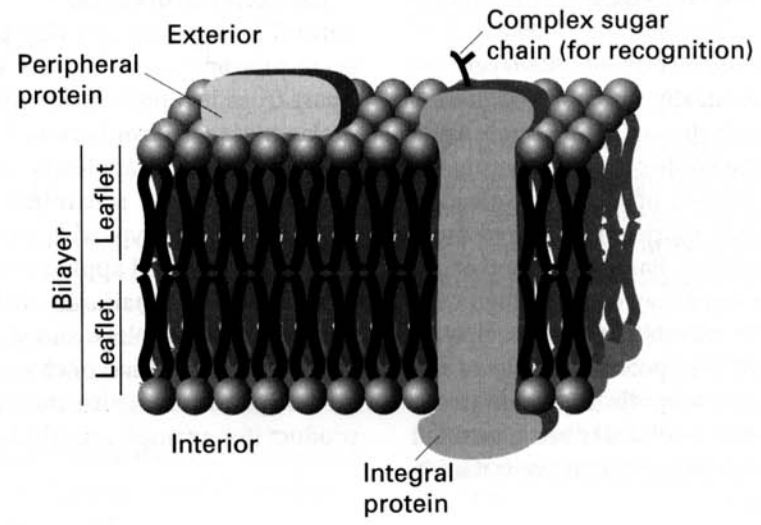
The bilayer is a highly mobile structure. Not only are the hydrocarbon tails ceaselessly twisting and turning in the region between the two leaflets, but the phospholipid and cholesterol molecules are migrating over the

14 Cholesterol

surface. It is better to think of the membrane as a viscous fluid rather than a permanent structure, with a viscosity about 100 times that of water, rather like olive oil. The average distance, l, a phospholipid molecule diffuses in two dimensions in a time t is given by the formula $l = (4Dt)^{1/2}$, where D is the diffusion constant (which is of the order of 10^{-12} m^2 s^{-2}). This formula implies that a molecule migrates through about 1 μm (the diameter of a cell) in about 1 min. There is very little likelihood that a phospholipid molecule will undergo the process called *flip-flop* and migrate from one leaflet to another: estimates of the rate of this process suggest that one flip-flop requires several hours. Certain specialized enzymes, however, can accelerate this process.

The mobile but viscous lipid bilayer is like a sea in which there are immersed *integral proteins* that may span one or both leaflets of the bilayer and on which there float *peripheral proteins* that remain largely outside the outer leaflet. The structure of an integral protein is typically a sequence of hydrophilic residues, which remain outside the leaflet, followed by a helix of about 20 hydrophobic residues that sit comfortably within the hydrocarbon region of the bilayer, and then another sequence of hydrophilic residues reaching into the interior of the cell. Several of these units may form a quaternary structure; others are monomers with a more complex folded structure with a preponderance of hydrophobic regions in the interleaflet region of the bilayer (see the structure of rhodopsin in Box 18.1). The *fluid mosaic model* shown in the illustration, suggests how the proteins and lipids are organized. Once again, the proteins are mobile, but their diffusion constants are much smaller than those of the lipids.

The mobility of the bilayer enables it to flow round a molecule close to the outer surface, to engulf it, and incorporate it into the cell by the process called *endocytosis* (like an amoeba feeding). Alternatively, material from the cell interior wrapped in cell membrane may coalesce with the cell wall itself, which then withdraws and ejects the material in the process called *exocytosis*. The function of the proteins embedded in the bilayer, though, is



The mosaic model of a bilayer showing the various types of associated proteins.

to act as devices for transporting matter into and out of the cell in a more subtle manner. By providing hydrophilic channels through an otherwise alien hydrophobic environment, these proteins act as *ion channels* and *ion pumps* (see Box 9.2 on chemiosmotic theory).

Exercise 1 Lipid diffusion in a cell plasma membrane has a diffusion constant of 1.0×10^{-8} cm^2 s^{-1} and the same lipid in a lipid bilayer has a diffusion constant of 1.0×10^{-7} cm^2 s^{-1}. How long will it take the lipid to diffuse 10 nm in a plasma membrane and a lipid bilayer?

Exercise 2 Diffusion constants of proteins are often used as a measure of molar mass. For a spherical protein $D \propto M^{-1/2}$. Considering only two-dimensional diffusion, compare the length of time it would take ribonuclease (M = 13.683 kDa) to diffuse 10 nm to the length of time it would take the enzyme catalase (M = 250 kDa) to diffuse the same distance.

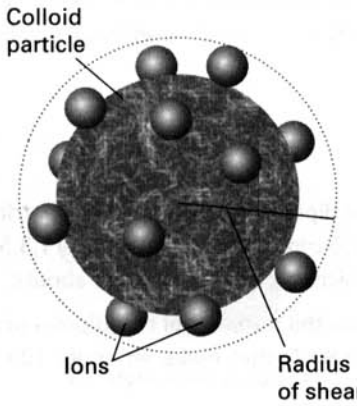


Fig 16.32 The definition of the radius of shear for a colloidal particle. The spheres are ions attached to the surface of the particle.

Waals forces. Flocculation is often reversible, and should be distinguished from **coagulation**, which is the irreversible collapse of the colloid into a bulk phase. When river water containing colloidal clay flows into the sea, the brine induces coagulation and is a major cause of silting in estuaries.

Metal oxide sols tend to be positively charged whereas sulfur and the noble metals tend to be negatively charged. Naturally occurring macromolecules also acquire a charge when dispersed in water, and an important feature of proteins and other natural macromolecules is that their overall charge depends on the pH of the medium. For instance, in acid environments protons attach to basic groups, and the net charge of the macromolecule is positive; in basic media the net charge is negative as a result of proton loss. At the **isoelectric point**, the

pH is such that there is no net charge on the macromolecule.

The primary role of the electric double layer is to render the colloid kinetically nonlabile. Colliding colloidal particles break through the double layer and coalesce only if the collision is sufficiently energetic to disrupt the layers of ions and solvating molecules, or if thermal motion has stirred away the surface accumulation of charge. This kind of disruption of the double layer may occur at high temperatures, which is one reason why sols precipitate when they are heated. The protective role of the double layer is the reason why it is important not to remove all the ions when a colloid is being purified by dialysis, and why proteins coagulate most readily at their isoelectric point.

The presence of charge on colloidal particles and natural macromolecules also permits us to control their motion, as in dialysis and electrophoresis. Apart from its application to the determination of molar mass, electrophoresis has several analytical and technological applications. One analytical application is to the separation of different macromolecules, and a typical apparatus is illustrated in Fig 16.33. Technical applications include silent inkjet printers, the painting of objects by airborne charged paint droplets, and electrophoretic rubber forming by deposition of charged rubber molecules on anodes formed into the shape of the desired product (for example, surgical gloves).

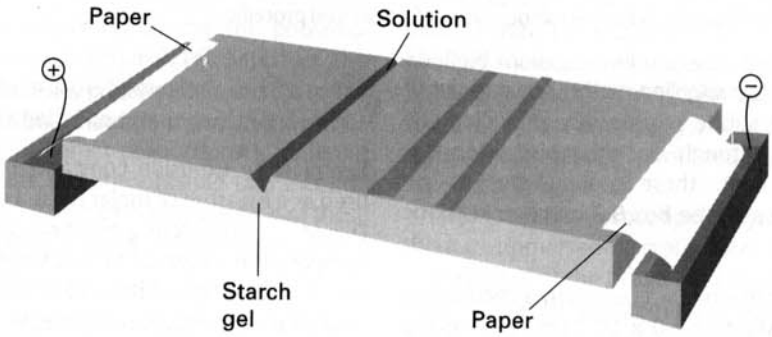


Fig 16.33 The layout of a simple electrophoresis apparatus. The sample is introduced into the trough in the gel, and the different components form separated bands under the influence of the potential difference.

Exercises

16.1 Estimate the dipole moment of an HCl molecule from the electronegativities of the elements and express the answer in debye and coulomb-metres.

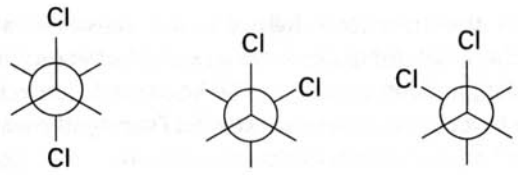
16.2 Use the VSEPR model to judge whether SF_4 is polar.

16.3 The electric dipole moment of toluene (methylbenzene) is 0.4 D. Estimate the dipole moments of the three xylenes (dimethylbenzenes). Which value can you be sure about?

16.4 From the information in the preceding problem, estimate the dipole moments of (a) 1,2,3-trimethylbenzene, (b) 1,2,4-trimethylbenzene, and (c) 1,3,5-trimethylbenzene. Which value can you be sure about?

16.5 Calculate the resultant of two dipoles of magnitude 1.5 D and 0.80 D that make an angle 109.5° to each other.

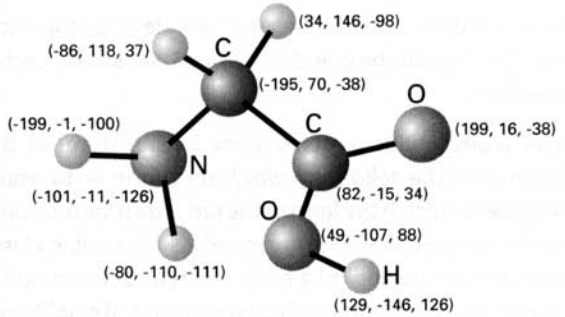
16.6 At low temperatures a substituted 1,2-dichloroethane molecule can adopt the three conformations (**15**), (**16**), and (**17**) with different probabilities. Suppose that the dipole moment of each bond is 1.5 D.



15 **16** **17**

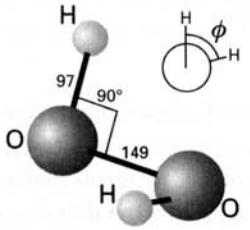
Calculate the mean dipole moment of the molecule when (a) all three conformations are equally likely, (b) only conformation (**16**) occurs, (c) the three conformations occur with probabilities in the ratio 2:1:1 and (d) 1:2:2.

16.7 Calculate the electric dipole moment of a glycine molecule using the partial charges in Table 16.1 and the locations of the atoms shown in (**18**).



18 Glycine

16.8 (a) Plot the magnitude of the electric dipole moment of hydrogen peroxide as the H–OO–H (azimuthal) angle ϕ changes. Use the dimensions shown in (**19**). (b) Devise a way for depicting how the angle as well as the magnitude changes.



19 Hydrogen peroxide

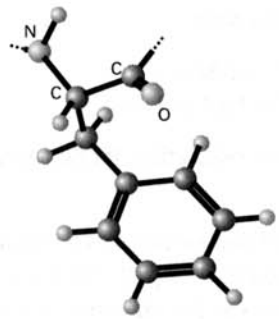
16.9 Calculate the molar energy required to reverse the direction of a water molecule located (a) 100 pm, (b) 300 pm from a Li^+ ion. Take the dipole moment of water as 1.85 D.

16.10 Show, by following the procedure in Derivation 16.2, that eqn 16.6 describes the potential energy of two electric dipole moments in the orientation shown in structure (**9**).

16.11 What is the contribution to the total molar energy of (a) the kinetic energy, (b) the potential energy of interaction between hydrogen chloride molecules in a gas at 298 K when 1.00 mol of molecules is confined to 10 L? Is the kinetic theory of gases justifiable in this case?

16.12 The electric field at a distance r from a point charge q is equal to $q/4\pi\varepsilon_0 r^2$. How close to a water molecule (of polarizability volume 1.48×10^{-30} m^3) must a proton approach before the dipole moment it induces is equal to the permanent dipole moment of the molecule (1.85 D)?

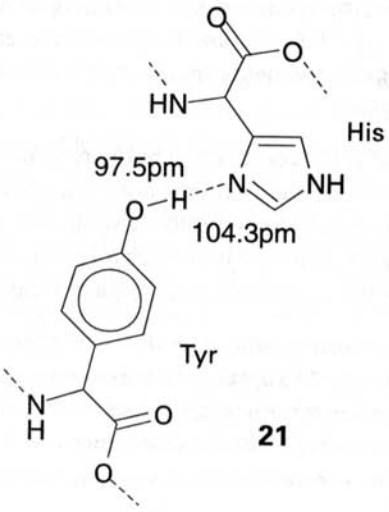
16.13 Phenylanine (Phe, **20**) is a naturally occurring amino acid with a benzene ring. What is the maximum energy of interaction between its benzene ring and the electric dipole moment of a neighbouring peptide group? Take the distance between the groups as 4.0 nm and treat the benzene ring as benzene itself. The dipole moment of the peptide group is 1.26 D.



20 Phe

16.14 Now consider the London interaction between the benzene rings of two Phe residues (see Exercise 16.13). Estimate the potential energy of attraction between two such rings (treated as benzene molecules) separated by 4.0 nm. For the ionization energy, use $I = 5.0$ eV.

16.15 In a region of the oxygen-storage protein myoglobin, the OH group of a tyrosine residue is hydrogen bonded to the N atom of a histidine residue in the geometry shown in (**21**). Use the partial charges in Table 16.1 to estimate the potential energy of this interaction.



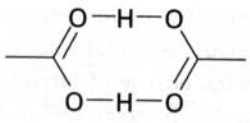
21

16.16 Given that force is the negative slope of the potential, calculate the distance-dependence of the force acting between two nonbonded groups of atoms in a polypeptide chain that have a London dispersion interaction with each other. What is the separation at which the force is zero? (*Hint*. Calculate the slope by considering the potential energy at R and $R + \delta R$, with $\delta R << R$, and evaluating $[V(R + \delta R) - V(R)]/\delta R$. You should use the expansion in Derivation 16.2 together with

$$(1 \pm x + \cdots)^6 = 1 \pm 6x + \cdots$$
$$(1 \pm x + \cdots)^{12} = 1 \pm 12x + \cdots$$

At the end of the calculation, let δR become vanishingly small.)

16.17 Acetic acid vapour contains a proportion of planar, hydrogen-bonded dimers (**22**). The apparent dipole moment of molecules in pure gaseous acetic acid increases with increasing temperature. Suggest an interpretation of the latter observation.



22

16.18 The potential energy of a CH_3 group in ethane as it is rotated around the C–C bond can be written $V = \frac{1}{2}V_0(1 + \cos 3\phi)$, where ϕ is the azimuthal angle (**23**) and $V_0 = 11.6$ kJ mol^{-1}. (a) What is the change in potential energy between the *trans* and fully eclipsed conformations? (b) Show that, for small variations in angle, the torsional (twisting) motion around the C–C bond can be expected to be that of a harmonic oscillator. (c) Estimate the vibrational frequency of this torsional oscillation.

23

16.19 Suppose you distrusted the Lennard-Jones (12,6)-potential for assessing a particular polypeptide conformation, and replaced the repulsive term by an exponential function of the form $e^{-r/\sigma}$. Sketch the form of the potential energy and locate the distance at which it is a minimum.

16.20 A diffuse 'spherical crystal' was described in Exercise 15.6. Sketch the pair distribution function for such a substance.

16.21 Many liquids preserve some local features of the structure of the solid from which they form or to which they freeze. Sketch the form of the radial distribution function for a liquid that locally resembles (a) a cubic close-packed structure and (b) a body-centred cubic structure. In each case, show only the first two spheres of neighbours (the nearest and the next nearest).

16.22 What is (a) the flux of nutrient molecules down a concentration gradient of 0.10 mol L^{-1} m^{-1}, (b) the amount of molecules (in moles) passing through an area of 5.0 mm^2 in 1.0 min? Take for the diffusion coefficient the value for sucrose in water (5.22×10^{-10} m^2 s^{-1}).

16.23 How long does it take a sucrose molecule in water at 25°C to diffuse (a) 1 mm, (b) 1 cm, (c) 1 m from its starting point?

16.24 The mobility of species through fluids is of the greatest importance for nutritional processes. (a) Estimate the diffusion coefficient for a molecule that leaps 150 pm each 1.8 ps. (b) What would be the diffusion coefficient if the molecule travelled only half as far on each step?

16.25 How long will it take a small molecule of radius 200 pm to diffuse across a phospholipid bilayer of thickness 0.50 nm at 37°C if the viscosity within the bilayer is 0.010 kg m^{-1} s^{-1}?

16.26 Pollutants spread through the environment by convection (winds and currents) and by diffusion. How many steps must a molecule take to be 1000 step lengths away from its origin if it undergoes a one-dimensional random walk?

16.27 Suppose a toxin is injected into one end of a horizontal tube full of water, so initially there is a uniform concentration of the toxin for the first 5 mm of the tube. Sketch a sequence of illustrations to show how the concentration profile of the toxin changes with time. Ignore convection.

16.28 (a) Combine eqns 16.18 and 16.19 to obtain an expression for the total path length of a molecule that diffuses to a distance d in a series of steps of length λ. (b) Use the expression you derive to estimate the total journey length of a lysozyme molecule ($D = 1.2 \times 10^{-6}$ cm^2 s^{-1}) in water given that each step takes 10 ps and in the interval in question the molecule diffuses through a total path length of 1.0 cm.

16.29 In the technique called *isoelectric focusing* (IEF), buffers are used to establish a pH gradient in a gel between two electrodes. High pH is established at the negative electrode and low pH at the positive electrode. The sample of protein is introduced into the gel at the negative electrode. What will be observed?