Covalent and Non-Covalent Bonds; Chemistry of Aqueous Solutions; Ionization of Weak Acids (Buffers); Functional Groups

CHEM 420 – Principles of Biochemistry Instructor – Anthony S. Serianni

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A "folded" protein



Myoglobin: An O₂ binding protein (153 amino acid polypeptide)

1958 – Kendrew X-ray crystallography

TABLE 1-1Strengths of Bonds Commonin Biomolecules

Type of bond	Bond dissociation energy* (kJ/mol)	Type of bond	Bond dissociation energy (kJ/mol)
Single	bonds	Double	e bonds
0—Н	470	C==0	712
H—H	435	C=N	615
P—0	419	C=C	611
C—H	414	P==0	502
N—H	389		
C—0	352	Triple	bonds
C—C	348	C≡C	816
S—H	339	N≡N	930
C—N	293		
C—S	260		
N—0	222		
S—S	214		

*The greater the energy required for bond dissociation (breakage), the stronger the bond.

4.18 kJ = 1 kcal



Weak electrostatic interactions between two macromolecules with complementary surfaces; non-covalent interactions



associate.

Bond Type	Bond Strength (kcal mol ⁻¹)
Covalent	>50
Noncovalent	0.6-7
Hydrophobic (i.e., two benzyl side chain groups of Phe)	2-3
Hydrogen	1-7
Ionic (low dielectric environment)	1-6
van der Waals	<1
Average energy of kinetic motion $(37^{\circ}C)$	0.6

Types of non-covalent (reversible) bonds in biological systems

Type of Interaction	Model	Example	Dependence of Energy on Distance
(a) Charge-charge Longest-range force; nondirectional	+=	-NH ₃ -)c-	1/ <i>r</i>
(b) Charge-dipole Depends on orientation of dipole	+q^+	$-\overset{*}{\mathrm{NH}_3}$ $q^{-} \overset{H}{\overset{q^+}{\overset{H}{\overset{H}{\overset{H}}}}}$	1/r ²
(c) Dipole-dipole Depends on mutual orientation of dipoles	q q q	$q = \begin{pmatrix} H^{+} & q = \begin{pmatrix} H^{+} & q \\ q^{+} & q = \begin{pmatrix} H^{+} & q \\ H^{+} & H \end{pmatrix}$	1/r ³
(d) Charge-induced dipole Depends on polarizability of molecule in which dipole is induced	+ q q	-ŇH ₃	1/r ⁴
(e) Dipole-induced dipole Depends on polarizability of molecule in which dipole is induced	a a a	q_0_+ H	1/r ⁵
(f) Dispersion Involves mutual synchronization of fluctuating charges		and a second sec	1/r ⁶
(g) van der Waals repulsion Occurs when outer electron orbitals overlap	XSX	2	1/r ¹²
(h) Hydrogen bond Charge attraction + partial covalent bond	Donor Acceptor	N-H···O=C Hydrogen bond length	Length of bond fixed

From Mathews and van Holde, Biochemistry, Third Edition. Copyright © Addison Wesley Longman, Inc.

$$E_{\rm el} \approx \frac{Z_{\rm A} \cdot Z_{\rm B} \cdot \varepsilon^2}{D \cdot r_{\rm ab}}$$

Figure 3.49. Strength of electrostatic interactions.

$E_{\rm VDW} = -\frac{A}{\frac{6}{r_{\rm ab}^6}} + \frac{B}{\frac{12}{r_{\rm ab}^{12}}}$

Figure 3.50. Strength of van der Waals interactions.



the excess negative charge (q^-) on the oxygen together with corresponding positive charge (q^+) on the carbon produces a dipole moment directed along the C—O axis. (b) Water: the excess negative charge on O together with the excess positive charge on each H produces two moments, μ_1 and μ_2 , directed along the H—O bonds. Their vector sum (μ) represents the dipole moment of the molecule.





Figure 3.52. π -Electron- π -electron interactions between two aromatic rings.



Figure 3.51. van der Waals–London dispersion interaction energies between two hydrogen atoms and two (tetrahedral) carbon atoms. Redrawn from Fersht, A. *Enzyme Structure and Mechanism*. San Francisco: Freeman, 1977, p. 228.



$$E_{\rm VDW} = -\frac{A}{r_{\rm ab}^6} + \frac{B}{r_{\rm ab}^{12}}$$

Figure 3.50. Strength of van der Waals interactions.

TABLE 2.2 van der Waals some atoms an of atoms	radii of d groups
	<i>R</i> (nm)
Atoms	
Н	0.12
0	0.14
N	0.15
С	0.17
S	0.18
Р	0.19
Groups	
-OH	0.14
$-NH_2$	0.15
$-CH_2-$	0.20
—CH ₃	0.20
Half-thickness of aromatic ring	0.17



(c) © Irving Geis.

Table 2–1 Covalent and Noncovalent Chemical Bonds

BOND TYPE	LENGTH (nm)	STRENGTH (IN VACUUM	kcal/mole) IN WATER
Covalent	0.15	90	90
Noncovalent: ionic*	0.25	80	3
hydrogen	0.30	4	1
van der Waals attraction (per atom)	0.35	0.1	0.1

*An ionic bond is an electrostatic attraction between two fully charged atoms.

Table 2-1 Molecular Biology of the Cell 5/e (© Garland Science 2008)

$$E_{\rm el} \approx rac{Z_{\rm A} \cdot Z_{\rm B} \cdot \varepsilon^2}{D \cdot r_{\rm ab}}$$

Figure 3.49. Strength of electrostatic interactions.

Substance	Dielectric Constant	Dipole Moment (debye)
Formamide	110.0	3.37
Water	78.5	1.85
Dimethyl sulfoxide	48.9	3.96
Methanol	32.6	1.66
Ethanol	24.3	1.68
Acetone	20.7	2.72
Ammonia	16.9	1.47
Chloroform	4.8	1.15
Diethyl ether	4.3	1.15
Benzene	2.3	0.00
Carbon tetrachloride	2.2	0.00
Hexane	1.9	0.00

Source: Brey, W.S., *Physical Chemistry and Its Biological Applications*, p. 26, Academic Press (1978).

Dielectric constants and permanent molecular dipole moments of some common solvents



Structure of the water molecule





The polar water molecule red = δ^- region blue = δ^+ region

View: HOH atoms in viewing plane; both oxygen lone-pairs eclipsed and perpendicular to the viewing plane.

> D. Chipman, 2007 ND Radiation Laboratory



The hydrogen bond. The figure shows an idealized H bond that might exist, for example, in $-O-H\cdots O=$. Although the H bond is between H and the acceptor, the H-bond length is defined as the distance between donor and acceptor.



Hydrogen bonding between two water molecules



Structure of ice: 4 H-bonds per water molecule (two as donor, two as acceptor)

General characteristics of H-bonds

Hydrogen covalently attached to an electronegative atom
Partial positive (+) charge of hydrogen on donor
Partial negative (-) charge on the electronegative donor atom
At least one lone-pair of electrons on the acceptor atom
The partial positive hydrogen is strongly attracted to the lone-pair electrons on the acceptor



H - F

Interaction much stronger than dipole-dipole interaction

ethanol (bp = 78.5 °C)
 methoxymethane (bp = -24.8 °C)
 ~100° elevation of bp







Figure 1.4. Representative hydrogen bonds of importance in biological systems.

Different types of H-bonds

- · Common elements that form H-bonds: S, O, N, F
- H-bonds involving C-H donors (proteins)

Summary of H-bond properties

	Strong	Moderate	Weak
interaction type	strongly covalent	mostly electrostatic	electrostat./ dispers.
bond lengths [Å]			
$H \cdots A$	1.2 - 1.5	1.5 - 2.2	> 2.2
lengthening of X–H [Å]	0.08 - 0.25	0.02 - 0.08	< 0.02
X–H versus $H \cdots A$	$X – H \approx H \cdots A$	$X – H < H \cdots A$	$X – H \ll H \cdots A$
$X \cdots A [Å]$	2.2 - 2.5	2.5 - 3.2	> 3.2
directionality	strong	moderate	weak
bond angles [°]	170 - 180	>130	> 90
bond energy [kcalmol ⁻¹]	15 - 40	4-15	< 4
relat. IR shift $\Delta \tilde{\nu}_{XH}$ [cm ⁻¹]	25 %	10 - 25 %	<10%
¹ H downfield shift	14-22	< 14	

For an X-H-MA H-bond

Low-barrier hydrogen bonds (LBHB)

- H-bond strength depends on its length, linearity, microenvironment and pK_a values of the H-sharing components.
- H-bonds in water are relatively weak because of the pKa mismatch between H₃O⁺ (-1.7) and H₂O (15.7).
 - The proton in the structure is tightly associated with OH⁻ as a water molecule.
- In the gas phase, the dielectric constant is low.
 - Hydrogen bonds between heteroatoms with matched pK_a values can be ≅ 2.5 Å and very strong (25-30 kcal/mol)



H-bonds in proteins

I. H-bonds contribute to structure and folding.
 II. H-bonds contribute to catalysis.

Structure/folding - Protein B-sheets

Anti-parallel β-sheets

- 10-14 atoms in a ring
- H-bonds linear
- Stability?



Parallel β-sheets

- 12 atoms in a ring
- H-bonds not 180°
- Stability?





Enzyme Catalysis: Catalytic mechanism of a Serine protease



Solvation of ions (salts) by oriented solvent water molecules



Ordering of water molecules around hydrophobic residues on the surface of a protein (clathrate) plays a key role in the <u>hydrophobic</u> <u>effect</u>



Examples of amphipathic (amphiphilic) compounds



Spontaneous self-assembly of <u>amphipathic</u> <u>compounds</u> in aqueous solution



Spontaneous self-association of <u>amphipathic</u> <u>molecules</u> in aqueous solutions



Hydronium ion migration in aqueous solution via proton jumps



Relative concentrations of acetic acid and acetate ion in aqueous solution as a function of solution pH

TABLE 2.6 Some weak acids and their conjugate bases

pK _a) Conjugate Base (Proton Accepto	К _а (м)	
3.75	HCOO ⁻ Formate ion	1.78×10^{-4}	
4.76	$\stackrel{\longrightarrow}{\longleftrightarrow} CH_3COO^-$ Acetate ion	1.74×10^{-5}	
3.86	$ \stackrel{OH}{=} CH_{3}CH - COO^{-}$ Lactate ion	1.38×10^{-4}	
2.14	H ₂ PO ₄ ⁻ Dihydrogen phosphate ion	7.24×10^{-3}	
6.86	$\stackrel{\longrightarrow}{\longrightarrow} HPO_4^{2-}$	1.38×10^{-7}	
12.4	$\stackrel{\longrightarrow}{\longrightarrow} PO_4^{3-}$	3.98×10^{-13}	
6.37	$\stackrel{\longrightarrow}{\longleftrightarrow} HCO_3^-$ Bicarbonate ion	4.27×10^{-7}	
10.25	$\iff CO_3^{2-}$ Carbonate ion	5.62×10^{-11}	
9.89	\leftarrow $C_6H_5O^-$ Phenolate ion	1.29×10^{-10}	
9.25	\implies NH ₃ Ammonia	5.62×10^{-10}	
	Phenolate ion \longrightarrow NH ₃ Ammonia Carbonic acid series	9.25	9.25 5.62×10^{-10}

Acid dissociation constants and pK_a s for some weak acids commonly used as biochemical buffers



Acid-base titration curves of 1 liter solutions of 1*M* acetic acid, H₂PO₄⁻, and NH₄⁺ by a strong base



Titration curve of a 1 liter aqueous solution of $1M H_3PO_4$ (phosphoric acid; a triprotic weak acid with three buffering ranges)



Ratio of conjugate [base]/[acid] as a function of pH

Note specifically how this ratio changes for each unit of pH change in either direction from the pK_a. 10. Citric acid, a tricarboxylic acid important in intermediary metabolism, can be symbolized as H₃A. Its dissociation reactions are

$H_{3}A \not \subset H^+ + H_2A^-$	$pK_1 = 3.13$
H_2A - $\neq H^+ + HA^{2-}$	$pK_2 = 4.76$
$HA^{2-} \rightleftharpoons H^+ + A^{3-}$	$pK_3 = 6.40$

If the total concentration of the acid and its anion forms is 0. (2 M, what are the individual concentrations of $H_{3}A$, $H_{2}A^{-}$, HA^{2-} , and A^{3-} at pH 5.2?

Answer: For citric acid

H₃A \overrightarrow{z} H⁺ + H₂A⁻ \overrightarrow{z} H⁺ + HA²⁻ \overrightarrow{z} H⁺ + A³⁻ 3.13 4.76 6.40 At pH = 5.2 the predominant equilibrium will involve H₂A⁻ \overrightarrow{z} H⁺ + HA²⁻ The ratio of their concentrations is:

 $\frac{[\text{HA}^{2}]}{[\text{H}_{2}\text{A}]} = 2.754 \text{ (from Henderson-Hasselbach equation)}$ (1)

Likewise for the other two equilibria we can write:

$$\frac{[H_2A]}{[H_3A]} = 117.5$$
 (2)
and,

 $\frac{[A^{3}]}{[HA^{2}]} = 0.063 \qquad (3)$

Each of the terms are related as follows

 $[A^{3-}] + [HA^{2-}] + [H_2A^-] + [H_3A] = 0.2$ (4) Using equations (1), (2) and (3) we can relate the concentration of any one species to any other.

For example,

$$[A^{3-}] = 0.063 [HA^{2-}]$$
 (from 3)
 $[H_2A^{-}] = \frac{[HA^{2-}]}{2.754}$ (from 1)

and,

 $[H_{3}A] = \frac{[H_{2}A^{-}]}{117.5} = \frac{[HA^{2}-]}{2.754 \times 117.5} (\text{from 1 and 2})$ Substituting these expressions into (4), we find: $[HA^{2}-] = 0.140$ From (1) $[H_{2}A^{-}] = [HA^{2}-]/2.754 = 0.140/2.754 = 0.051$ From (2) $[H_{3}A] = [HA^{2}-]/117.5 = 0.001$ From (3) $[A^{3}-] = 0.063 \times 0.140 = 0.009$

We could have anticipated these results because the pH is far from two of the pK_as. Only the equilibrium between H₂A⁻ and HA²⁻ with a pK_a = 4.76 will be significant at pH = 5.2.

An example of a buffer problem involving a tricarboxylic acid with three pK_a values that are very similar in magnitude (unlike inorganic phosphate, H₃PO₄).



Figure 1.10. Major chemical constituents of blood plasma and cell fluid. Adapted from Gregersen, M. I. In: P. Bard (Ed.), *Medical Physiology*, 11th ed. St. Louis: Mosby, 1961, p. 307.

The Bicarbonate Buffer System of Blood Plasma

The important buffer system of blood plasma is the bicarbonate/ carbonic acid couple:

$$H_2CO_3 \rightleftharpoons H^+ + HCO_3^-$$

The relevant pK_{a} , pK_{l} for carbonic acid, has a value far removed from the normal pH of blood plasma (pH 7.4). (The pK_{l} for H₂CO₃ at 25°C is 3.77 [Table 2.4], but at 37°C, pK_{l} is 3.57.) At pH 7.4, the concentration of H₂CO₃ is a minuscule fraction of the HCO₃⁻ concentration; thus the plasma appears to be poorly protected against an influx of OH⁻ ions.

$$pH = 7.4 = 3.57 + \log_{10} \frac{[HCO_3^-]}{[H_2CO_3]}$$
$$\frac{[HCO_3^-]}{[H_2CO_4]} = 6761$$

For example, if $[\text{HCO}_3^-] = 24 \text{ mM}$, then $[\text{H}_2\text{CO}_3]$ is only $3.55 \ \mu$ M ($3.55 \times 10^{-6} \text{ M}$), and an equivalent amount of OH⁻ (its usual concentration in plasma) would swamp the buffer system, causing a dangerous rise in the plasma pH. How, then, can this bicarbonate system function effectively? The bicarbonate buffer system works well because the critical concentration of H₂CO₃ is maintained relatively constant through equilibrium with dissolved CO₂ produced in the tissues and available as a gaseous CO₂ reservoir in the lungs.*

Gaseous CO_2 from the lungs and tissues is dissolved in the blood plasma, symbolized as $CO_2(d)$, and hydrated to form H_2CO_3 :

$$CO_{2}(g) \rightleftharpoons CO_{2}(d)$$

$$CO_{2}(d) + H_{2}O \rightleftharpoons H_{2}CO_{3}$$

$$H_{2}CO_{3} \rightleftharpoons H^{+} + HCO_{3}^{-}$$

Thus, the concentration of H_2CO_3 is itself buffered by the available pools of CO_2 . The hydration of CO_2 is actually mediated by an enzyme, *carbonic anhydrase*, which facilitates the equilibrium by rapidly catalyzing the reaction

$$H_2O + CO_2(d) \rightleftharpoons H_2CO_3$$

Under the conditions of temperature and ionic strength prevailing in mammalian body fluids, the equilibrium for this reaction lies far to the left, such that more than 300 CO₂ molecules are present in solution for every molecule of H₂CO₃. Because dissolved CO₂ and H₂CO₃ are in equilibrium, the proper expression for H₂CO₃ availability is $[CO_2(d)] + [H_2CO_3]$, the so-called total carbonic acid pool, consisting primarily of CO₂(d). The overall equilibrium for the bicarbonate buffer system then is

$$CO_{2}(d) + H_{2}O \xleftarrow{K_{n}} H_{2}CO_{3}$$
$$H_{2}CO_{3} \xleftarrow{K_{n}} H^{+} + HCO_{3}^{-}$$

An expression for the ionization of H_2CO_3 under such conditions (that is, in the presence of dissolved CO_2) can be obtained from

*Well-fed humans exhale about 1 kg of CO₂ daily. Imagine the excretory problem if CO₂ were not a volatile gas.

 $K_{\rm h}$, the equilibrium constant for the hydration of CO₂, and from $K_{\rm a}$, the first acid dissociation constant for H₂CO₃:

$$K_{\rm h} = \frac{[\rm H_2\rm CO_3]}{[\rm CO_2(\rm d)]}$$

Thus,

$$[H_2CO_3] = K_b[CO_2(d)]$$

Putting this value for $[H_2CO_3]$ into the expression for the first dissociation of H_2CO_3 gives

$$K_{a} = \frac{[H^{+}][HCO_{3}^{-}]}{[H_{2}CO_{3}]}$$
$$= \frac{[H^{+}][HCO_{3}^{-}]}{K_{h}[CO_{2}(d)]}$$

Therefore, the overall equilibrium constant for the ionization of H_2CO_3 in equilibrium with $CO_2(d)$ is given by

$$K_{a}K_{h} = \frac{[\mathrm{H}^{+}][\mathrm{HCO}_{3}^{-}]}{\mathbf{K}_{a}[\mathrm{CO}_{2}(\mathrm{d})]}$$

and $K_a K_h$, the product of two constants, can be defined as a new equilibrium constant, $K_{overall}$. The value of K_h is 0.003 at 37°C and K_a , the ionization constant for H_2CO_3 , is $10^{-3.57} = 0.000269$. Therefore,

$$K_{\text{overall}} = (0.000269) (0.003)$$

= 8.07 × 10⁻⁷
p $K_{\text{overall}} = 6.1$

which yields the following Henderson-Hasselbalch relationship:

$$pH = pK_{overall} + \log_{10} \frac{[HCO_3^{-}]}{[CO_2(d)]}$$

Although the prevailing blood pH of 7.4 is more than 1 pH unit away from $pK_{overall}$, the bicarbonate system is still an effective buffer. Note that, at blood pH, the concentration of the acid component of the buffer will be less than 10% of the conjugate base component. One might imagine that this buffer component could be overwhelmed by relatively small amounts of alkali, with consequent disastrous rises in blood pH. However, the acid component is the total carbonic acid pool, that is, $[CO_2(d)] +$ $[H_2CO_3]$, which is stabilized by its equilibrium with $CO_2(g)$. Gaseous CO_2 serves to buffer any losses from the total carbonic acid pool by entering solution as $CO_2(d)$, and blood pH is effectively maintained. Thus, the bicarbonate buffer system is an *open system*. The natural presence of CO_2 gas at a partial pressure of 40 mm Hg in the alveoli of the lungs and the equilibrium

$CO_2(g) \rightleftharpoons CO_2(d)$

keep the concentration of $CO_2(d)$ (the principal component of the total carbonic acid pool in blood plasma) in the neighborhood of 1.2 m*M*. Plasma [HCO₃⁻⁻] is about 24 m*M* under such conditions.

Definitions of Buffer Capacity



The number of moles of H⁺ that must be added to one liter of buffer in order to decrease the pH by 1 unit = the buffer capacity in the <u>acid</u> direction

and

The number of moles of OH⁻ that must be added to one liter of buffer in order to increase the pH by one unit = the buffer capacity in the <u>alkaline</u> direction.

Characteristics important to buffers used in biochemical experiments

- $\square pK_a$ value
- Variation of pK_a with temperature and ionic strength
- Anionic, cationic, or multiple charges on buffer species
- Interaction with other components (e.g., metal ions)
- Solubility
- Expense
- UV absorption

FIGURE 2.21

Dependence of protein solubility on pH. (a) Most proteins are very soluble at high pH, where all of their molecules are negatively charged. (b) At the isoelectric point, where a protein has no *net* charge, its molecules retain regions of positive and negative charge on their surfaces, resulting in aggregation and precipitation. (c) At low pH the proteins are soluble because of their positive charge. (d) The solubility of β -lactoglobulin with varying pH; the lowest solubility occurs at the isoelectric point.



(a) High pH: protein soluble (deprotonated) (b) Isoelectric point: protein aggregates





(c) Low pH: protein soluble (protonated)



Some ionizable amino acid sidechains found in proteins

> One or more of these groups can be found in the active site of an enzyme.



Effect of pH on enzyme catalytic activity



Schematic representation of the effect of pH on the velocity of an enzyme-catalyzed reaction if only the protonated form of a single ionizing group is catalytically active. The solid curve represents the experimental data.

The pK_a of this group can be estimated by extrapolating the linear portions of the curve as shown.

<i>Ionization properties of some amino acta stae chain</i>	niza	atio	n	properties	of	some	amino	acid	side	chain
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Group	р <i>К</i> _а (298 К)	$\Delta H_{\rm i}({\rm kJ\ mol}^{-1})$
β -Carboxyl (Asp) γ -Carboxyl (Glu)	~4	$\sim \pm 4$
Imidazole (His)	~6	~29
ε -Amino (Lys)	~10	~46
Phenolic OH (Tyr)	~10	~25

The assignment of pK_as to specific amino acid sidechains is not straightforward since these pK_as are affected by local protein structure. For example, in pepsin, an Asp residue involved in the mechanism (pepsin is an aspartic protease) has a pK_a of 1.1, whereas this sidechain has a pK_a of ~ 4 in the free amino acid.

If the rate dependence on pH is known as a function of temperature, then enthalpies of ionization (ΔH_i) can sometimes help to make the correlation between the measured p K_a and the functional group. Two <u>functionally important</u> ionizable groups in the active site of an enzyme





The effect of pH on the velocity of an enzyme-catalyzed reaction when **two** ionizing groups are involved. The solid line is the experimental data.

Extrapolation of the appropriate linear portions of the plot yield values of pK_{a1} and pK_{a2} as shown.

Review of key functional groups in biochemistry: Structure and properties

alcohol aldehyde carboxyl amine ketone amide oxyester thioester thiol disulfide imine phosphoanhydride mixed anhydride