

Kód předmětu: C8980



MASARYKOVA UNIVERZITA

Protein expression and purification

II. Calculation in the molecular biosciences

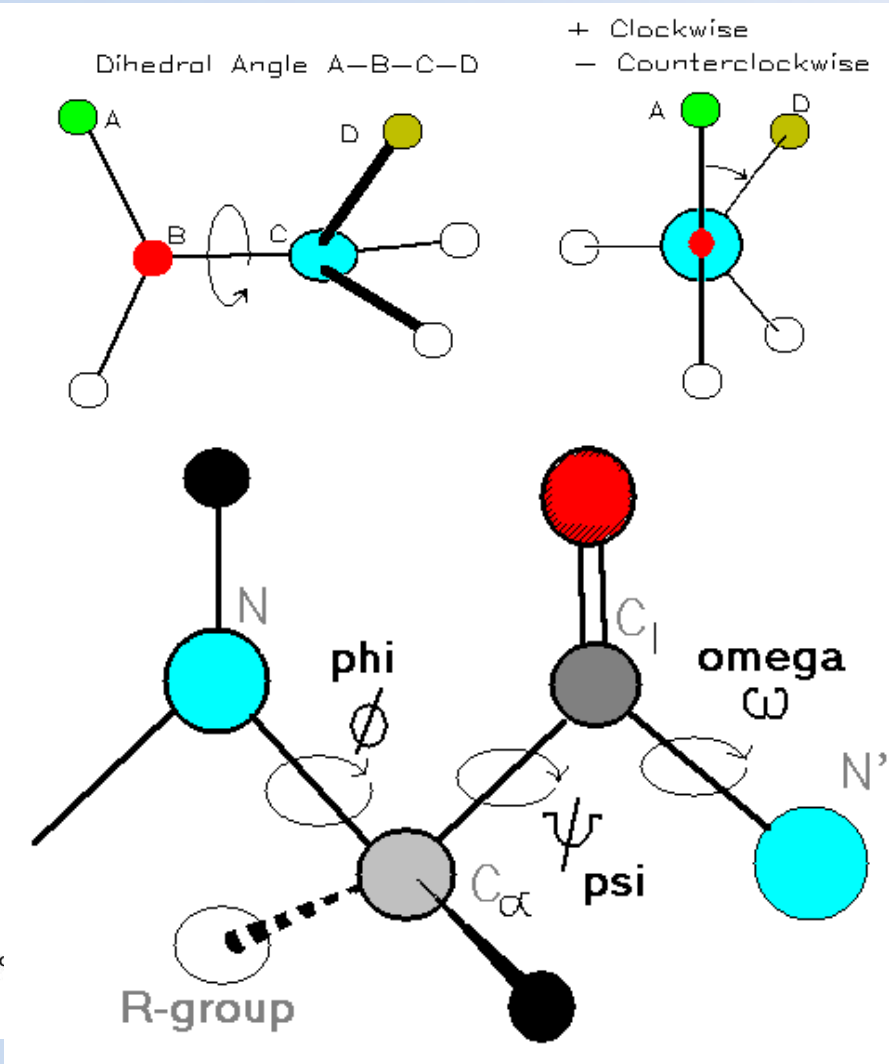
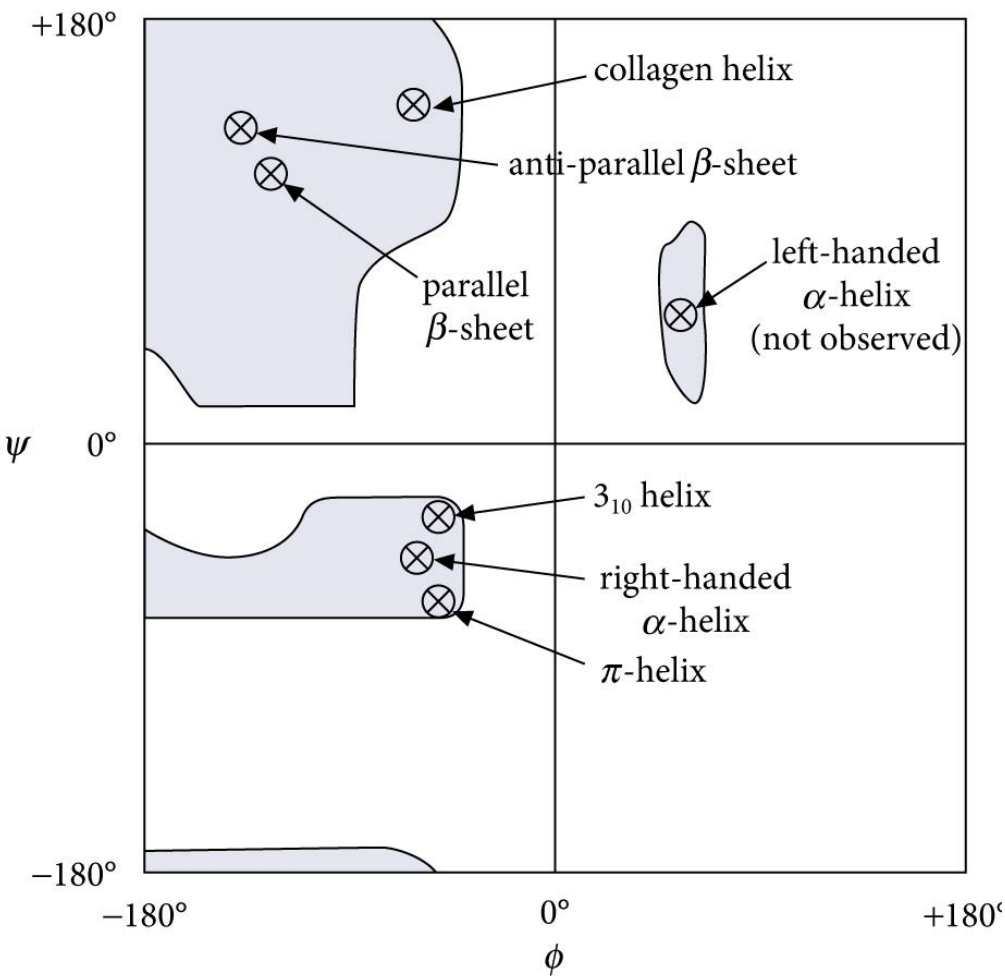
Jozef Hritz, Lubomír Janda, Blanka Pekárová
Radka Dopitová

Tento projekt je spolufinancován Evropským sociálním fondem a státním rozpočtem České republiky.



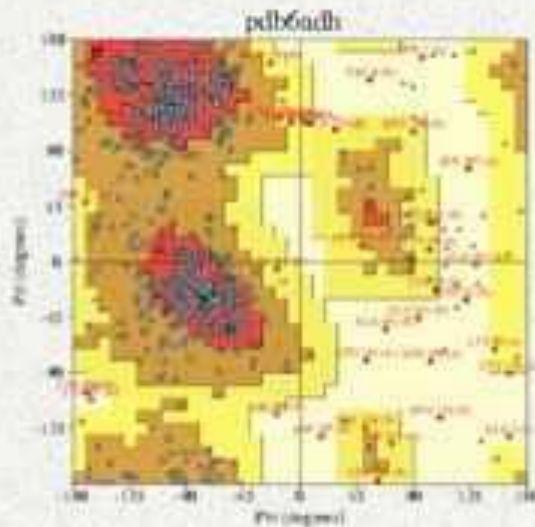
INVESTICE DO ROZVOJE VZDĚLÁVÁNÍ

1.4. The secondary structure of proteins

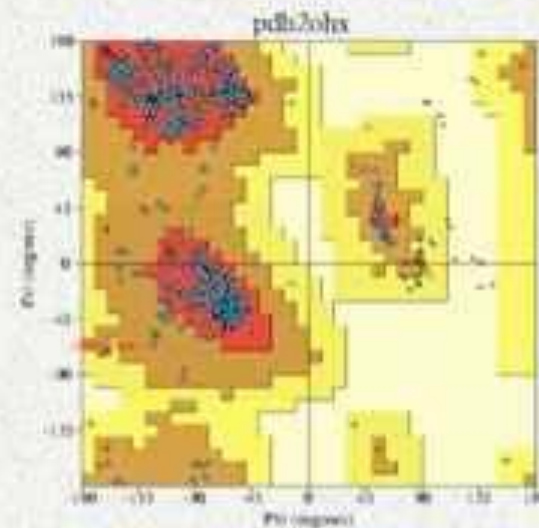


1.4. The secondary structure of proteins

Ramachandran plot for a bad (left) and good (right) quality structure



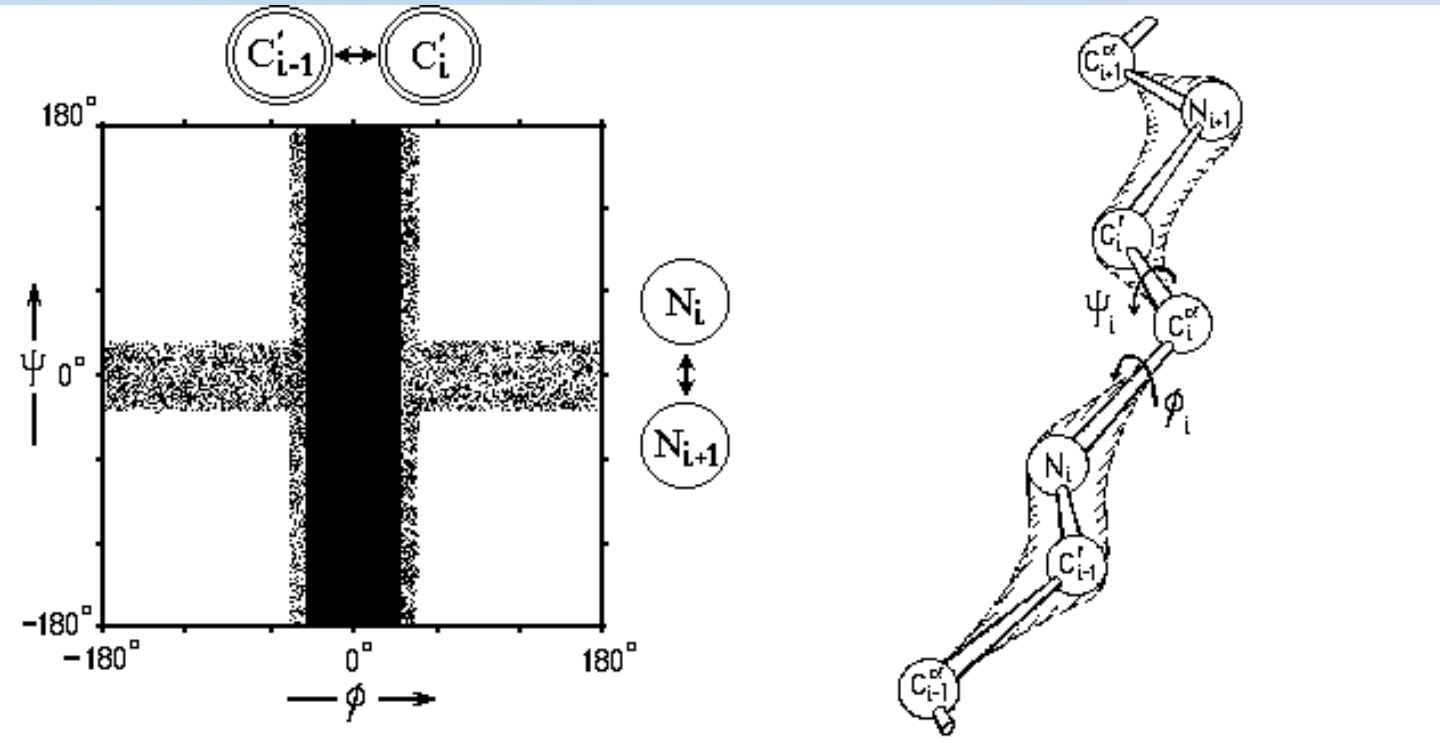
Low resolution (2.9 Å)



High resolution (1.8 Å)

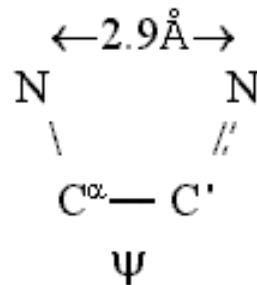
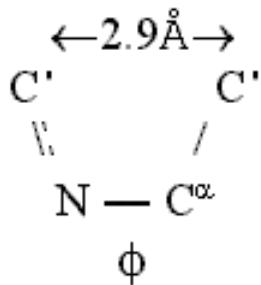
1.4. The secondary structure of proteins

Energetically unfavorable conformational areas



$$2.9\text{\AA} < r_{\min}(C\dots C) = 3.0\text{\AA}$$

$$2.9\text{\AA} > r_{\min}(N\dots N) = 2.7\text{\AA}$$

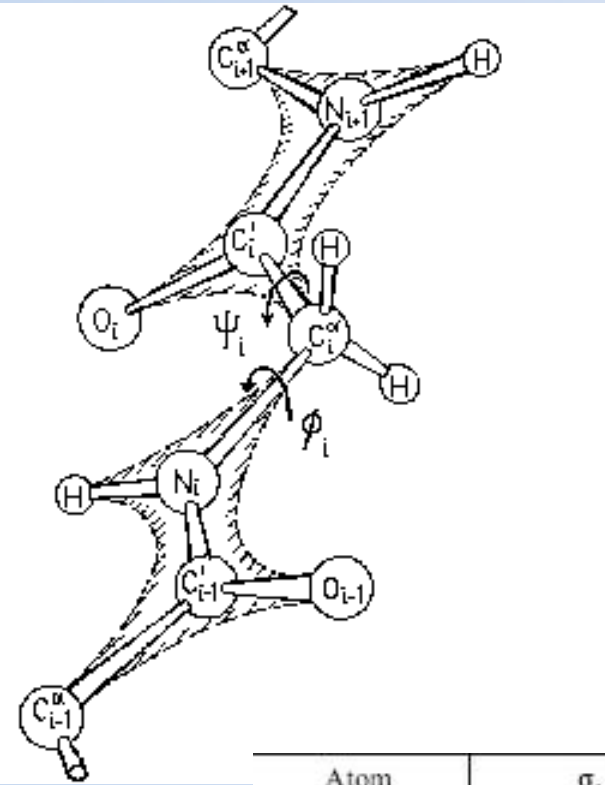
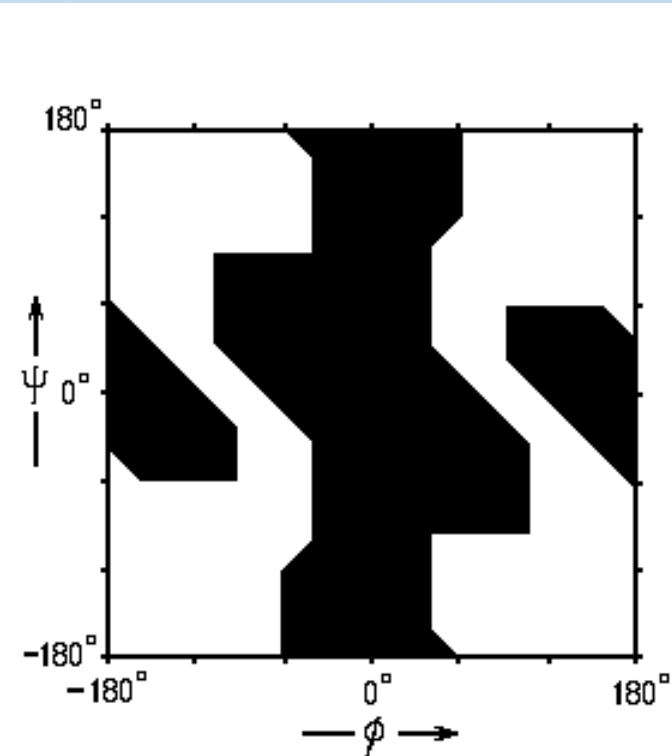


Atom	σ , Å	ϵ , kcal/mol
O	2.96	0.210
N	3.25	0.170
C in C=O	3.75	0.105
Other C	3.50	0.080
H on N	0.00	0.000
H on C	2.50	0.050

1.4. The secondary structure of proteins

Additional energetically unfavorable conformational areas because of the presence of carbonyl oxygen

Glycine – less sterically restricted because of lacking the side-chain

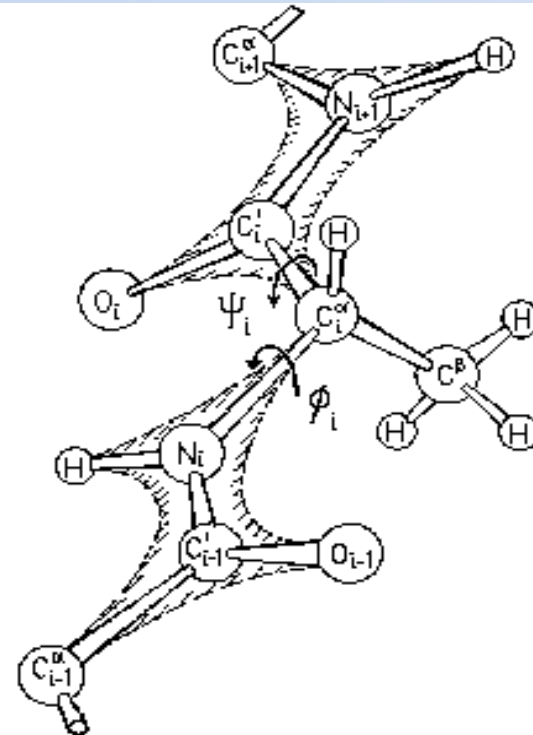
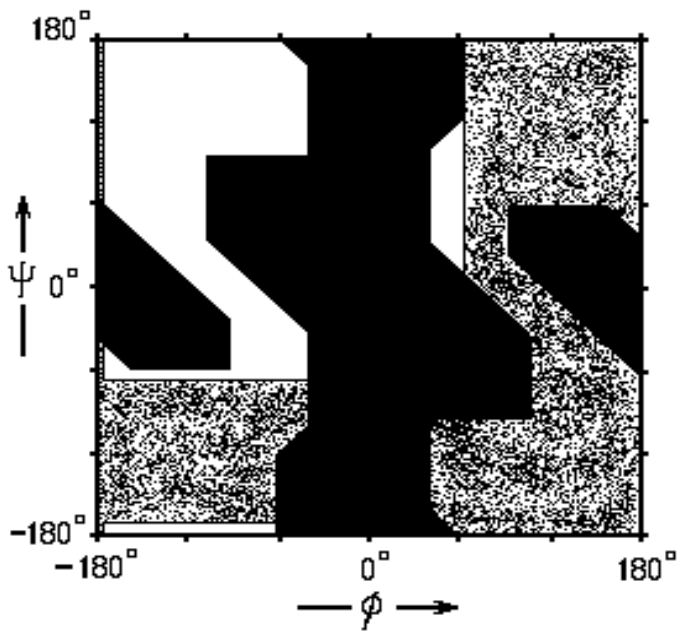


Atom	$\sigma, \text{\AA}$	$\epsilon, \text{kcal/mol}$
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N	3.25	0.170
C in C=O	3.75	0.105
Other C	3.50	0.080
H on N	0.00	0.000
H on C	2.50	0.050

1.4. The secondary structure of proteins

Additional energetically unfavorable conformational areas because of the presence of C^β

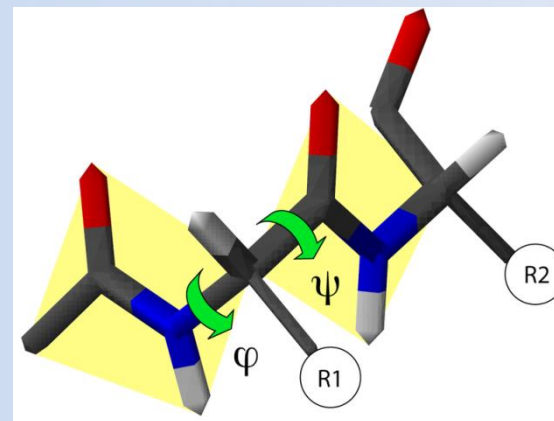
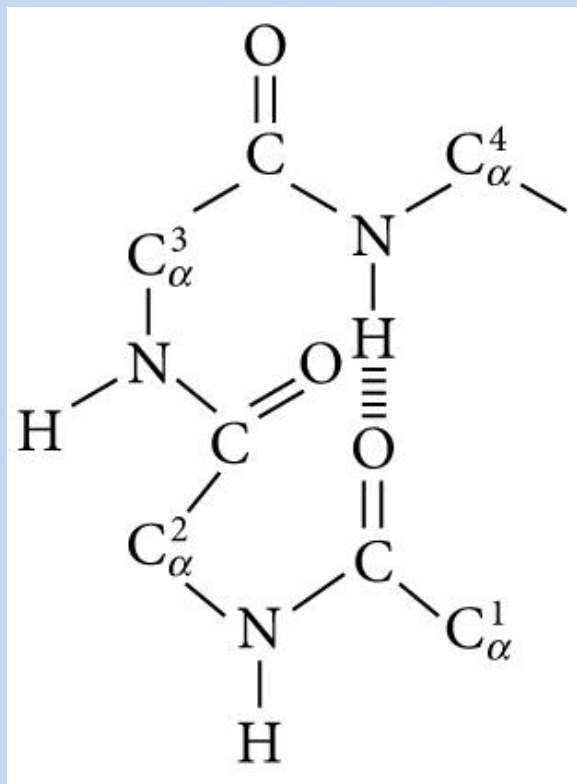
Alanine



Atom	σ , Å	ϵ , kcal/mol
O	2.96	0.210
N	3.25	0.170
C in C=O	3.75	0.105
Other C	3.50	0.080
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H on C	2.50	0.050

1.4. The secondary structure of proteins

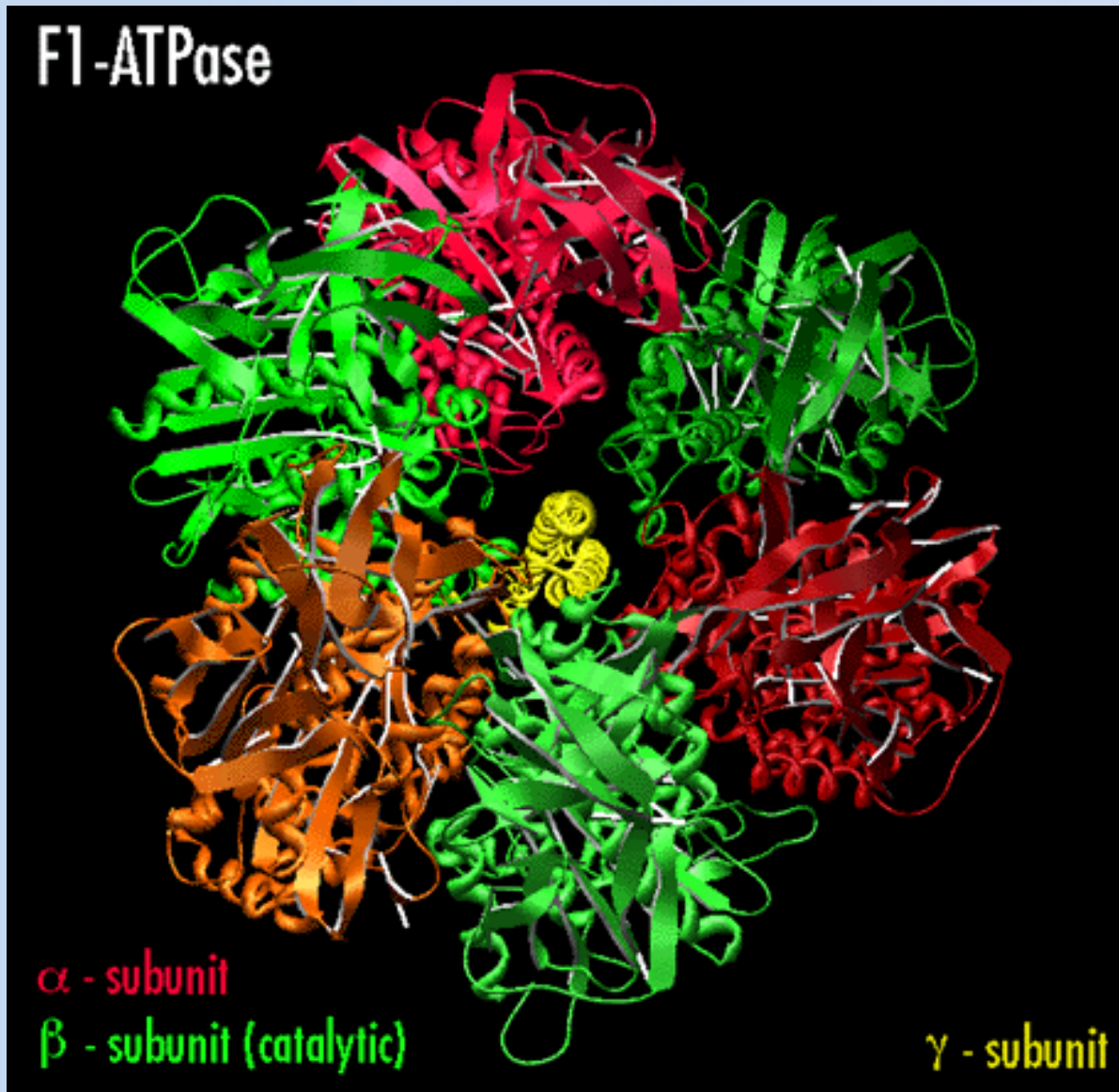
1.4.3. Other structural features in proteins



Structural preferences of the different amino acids

Met, Glu, Leu, Ala	+	alpha - helices
Pro, Gly, Tyr	-	alpha helices
Val, Ile, Phe	+	beta sheets
Pro, Asp	-	beta sheets
Pro, Gly, Asp	+	beta turn
Met, Val, Ile	-	beta turn

1.6. The quaternary structure of proteins



1.3. The primary structure of proteins

1.3.2. Information available from the amino acid sequence of a protein

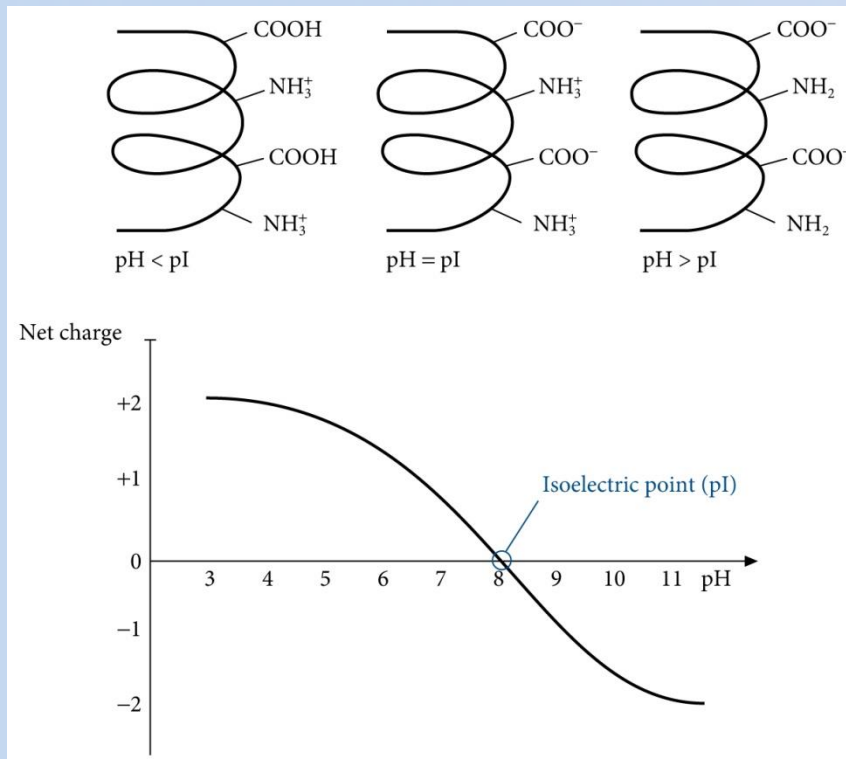
1.3.2.1. Exact molecular mass

1.3.2.2. Isoelectric point

1.3.2.3. Absorption coefficient

1.3.2.4. Hydrofobicity

http://www.expasy.ch/tools/pi_tool.html



Beer–Lambert law $A = \varepsilon * c * l$

A is the absorbance at a particular wavelength (without units; merely a ratio):

$$A = \log (I_0/I_t)$$

I_0 is the intensity of the incident light (light striking the cuvette).

I_t is the intensity of the transmitted light (the light leaving the cuvette).

ε is the absorption coefficient (degree of absorption) ($M^{-1} \text{ cm}^{-1}$).

l is the path length of the cuvette (cm).

c is the concentration of the solution (M).

Linear form of Beer-Lambert law is valid only for lower values of A.

Please solve a problem.

Question 1: How many mg of protein you have in 5 ML of purified protein if its molar extinction coefficient is $15000 \text{ M}^{-1}\text{cm}^{-1}$; molecular weight 20 kDa. Advice – units!

Measured absorption in cuvette with 1 cm optical path-length is 0.3 at 280 nm. 10 points

Mass concentration equals to the molar concentration multiplied by molecular weight of the protein.
points

8

Unit **M** correspond to the **mol.L⁻¹**
points

6

$$\text{g.L}^{-1} = \text{mg.ml}^{-1}$$

4 points

Solution:

$$A = \epsilon cl$$

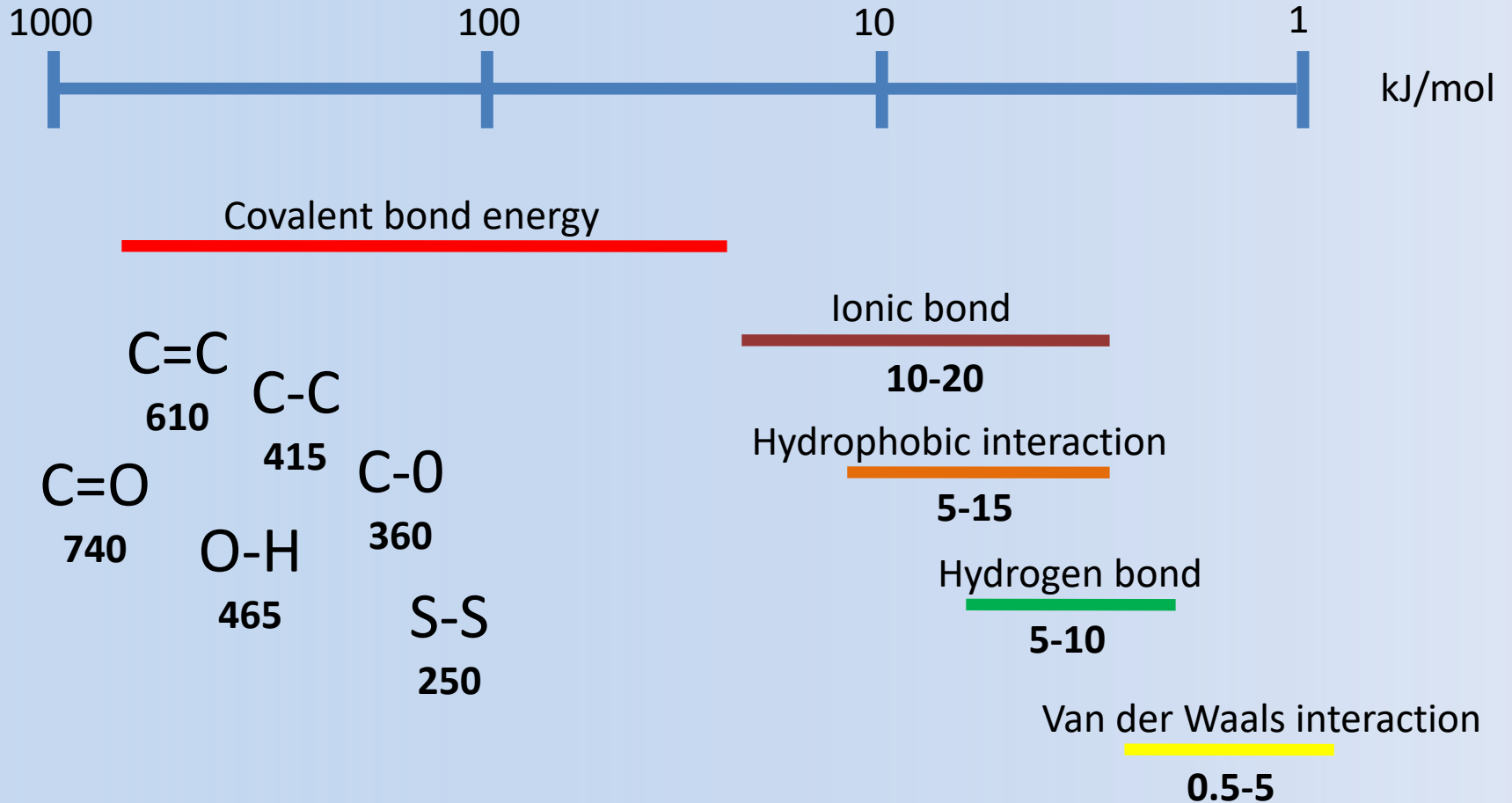
$$c [M] = A/\epsilon l = 0.3 / (15000 \text{ M}^{-1}\text{cm}^{-1} * 1 \text{ cm}) = 0.00002 \text{ M} = 0.02 \text{ mM}$$

$$C [\text{g.L}^{-1}] = 0.00002 \text{ mol.L}^{-1} * 20000 \text{ g.mol}^{-1} = 0.4 \text{ g.L}^{-1} = 0.4 \text{ mg.ml}^{-1}$$

$$m [\text{mg}] = C * V = 0.4 \text{ mg.ml}^{-1} * 5 \text{ ml} = \underline{2 \text{ mg}}$$

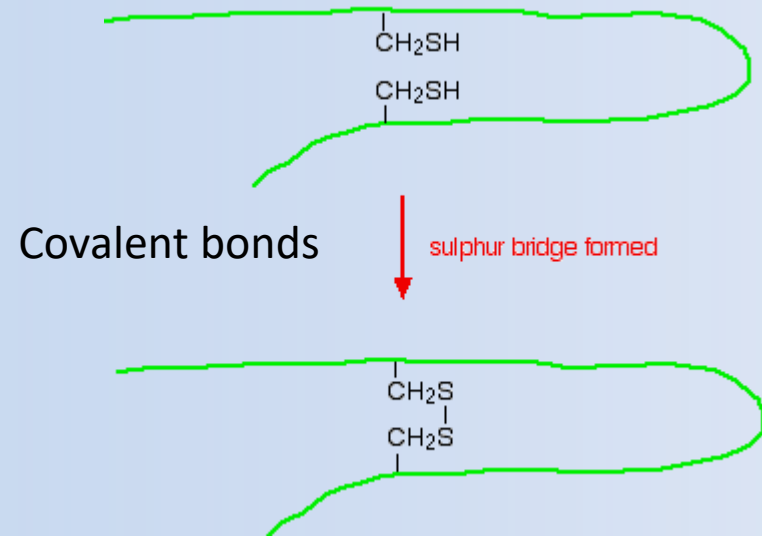
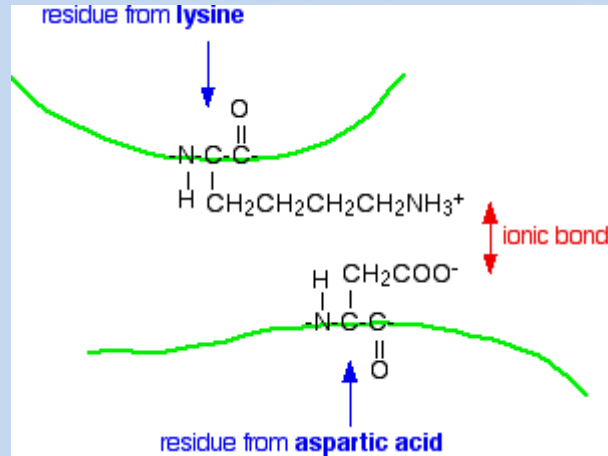
1.7. Forces contributing to the structures and interactions of proteins

Bond strenght

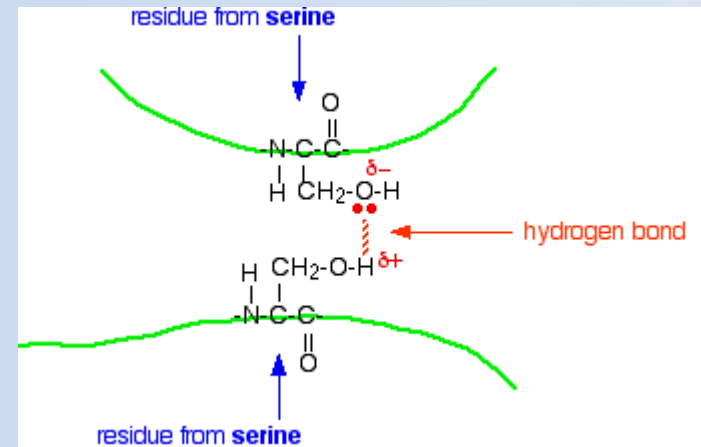
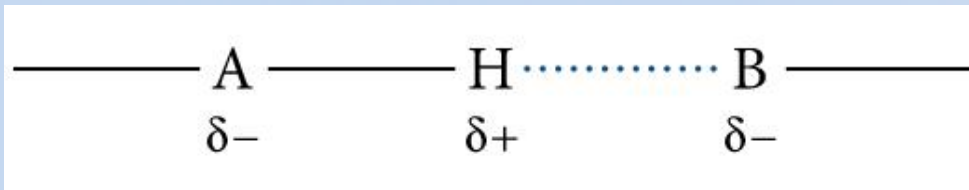


1.7. Forces contributing to the structures and interactions of proteins

1.7.1. Ionic (electrostatic) interactions



1.7.2. Hydrogen bonds



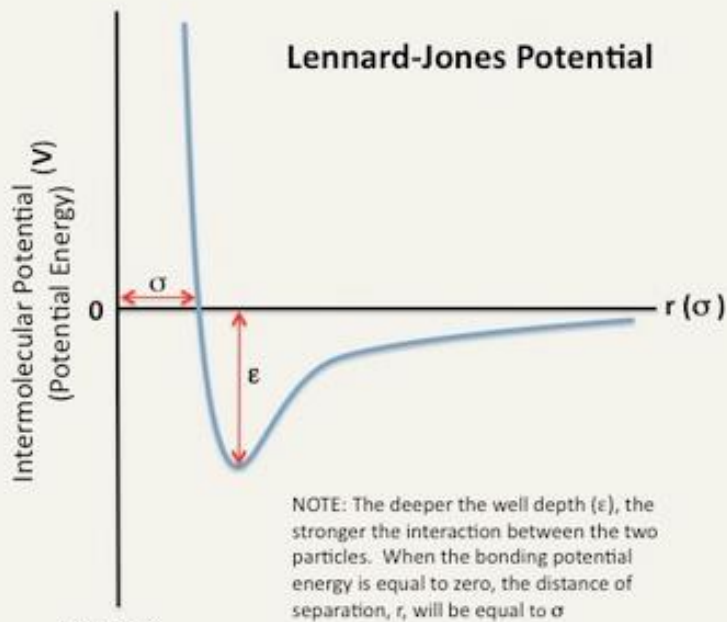


Figure B

Atom	$\sigma, \text{\AA}$	$\epsilon, \text{kcal/mol}$
O	2.96	0.210
N	3.25	0.170
C in C=O	3.75	0.105
Other C	3.50	0.080
H on N	0.00	0.000
H on C	2.50	0.050

Combination rules for Lennard-Jones potential

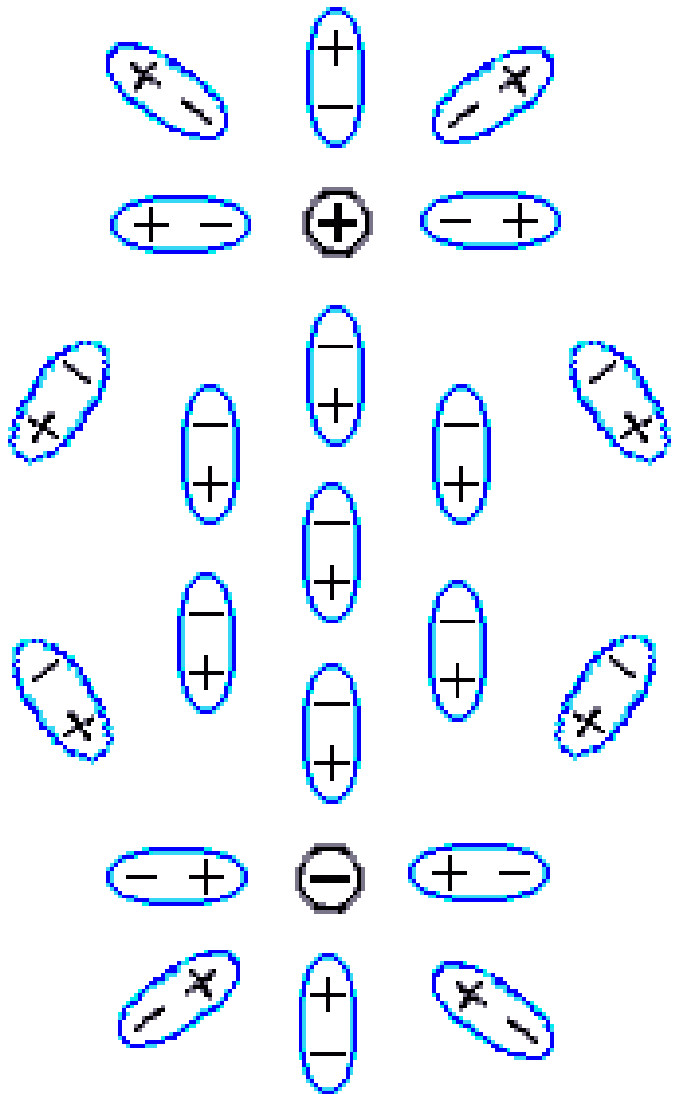
$$S_{ij} = \frac{S_{ii} + S_{jj}}{2}$$

$$e_{ij} = \sqrt{e_{ii}e_{jj}}$$

$$E_{ij}^{LJ} = 4e_{ij} \left[\frac{S_{ij}}{r_{ij}^{12}} - \frac{S_{ij}}{r_{ij}^6} \right]$$

Electrostatic interactions at different media

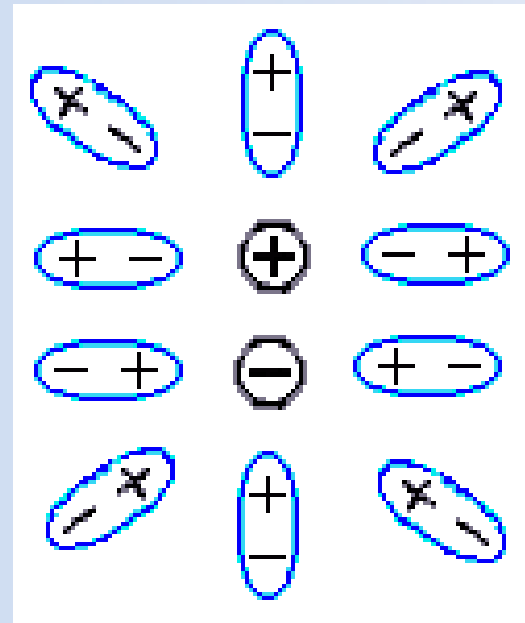
$\epsilon_r = 80$



$$E_{ij}^{el} = \frac{1}{4\pi\epsilon_0\epsilon_r} \frac{q_i q_j}{r_{ij}}$$

$\epsilon = ?$

intermed.
 “vacuum”, $\epsilon \sim 1$?
 but absence
 of intermed.
 dipoles can
 only increase
 interaction...



$\epsilon_0 = 8.85 \cdot 10^{-12} \text{ C} \cdot \text{N}^{-1} \cdot \text{m}^{-2}$, $q = 1.6 \cdot 10^{-19} \text{ C}$

Relative permittivity:

- vacuum: $\epsilon_r = 1$
- water: $\epsilon_r = 80$
- protein $\epsilon_r \sim 4$

$$E_{ij}^{el} = \frac{1}{4\pi\epsilon_0\epsilon_r} \frac{q_i q_j}{r_{ij}}; k_e = \frac{1}{4\pi\epsilon_0}$$

$$E_{ij}^{el} = \frac{k_e}{\epsilon_r} \frac{q_i q_j}{r_{ij}}$$

$$E_p^{total} = \sum_{i,j} E_{ij}^{el} + E_{ij}^{LJ}$$

Useful Physical/Chemical Constants

Constant

Avogadro's Number

Faraday Constant

Molar Gas Constant

Coulomb's Constant

Speed of Light (Vacuum)

Boltzmann Constant

Charge on a Proton/Electron

Standard acceleration of gravity

Planck's Constant

Value

$$N_A = 6.022 \times 10^{23} \text{ mol}^{-1}$$

$$F = 96\,485.33 \text{ C mol}^{-1}$$

$$R = 8.314 \text{ J mol}^{-1} \text{ K}^{-1}$$

$$k_e = 8.987 \times 10^9 \text{ N m}^2 \text{ C}^{-2}$$

$$c = 299\,792\,458 \text{ m s}^{-1}$$

$$k_b = 1.38 \times 10^{-23} \text{ J K}^{-1}$$

$$e = 1.602 \times 10^{-19} \text{ C}$$

$$g = 9.8 \text{ m s}^{-2}$$

$$h = 6.6 \times 10^{-34} \text{ m}^2 \text{ kg / s}$$

Please solve a problem.

Question 2: What is the total potential energy of system consisting of salt ions Na⁺ and Cl⁻ in kJ/mol? For the electrostatic energy contribution consider the permittivity of water environment

	Mw[g/mol]	σ [Å]	ϵ [kJ/mol]
Na ⁺	23	2.3	0.5
Cl ⁻	35	4.3	0.5

Ions are separated by 0.28 nm distance.

20

points

$$S_{ij} = \frac{S_{ii} + S_{jj}}{2}; e_{ij} = \sqrt{e_{ii}e_{jj}}$$

18 points

Coulombic energy term correspond to the energy per particle, not per mol

16 points

N.m = J

12 points

Be careful, which energy term is positive and which negative

8 points

Solution:

$$E_{ij}^{el} = \frac{k_e q_i q_j}{\epsilon_r r_{ij}} N_A = \frac{9 * 10^9 Nm^2 C^{-2} [-(1.6 * 10^{-19} C)(1.6 * 10^{-19} C)]}{80 * 0.28 * 10^{-9} m} 6.022 * 10^{23} mol^{-1} =$$

$$= -6.2 * 10^3 J mol^{-1} = -6.2 kJ mol^{-1}$$

$$E_{ij}^{LJ} = 4\epsilon_{ij} \left[\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6 \right] = 4 * 0.5 kJ.mol^{-1} \left[\left(\frac{3.3A}{2.8A} \right)^{12} - \left(\frac{3.3A}{2.8A} \right)^6 \right] =$$

$$= 2 kJ.mol^{-1} [7.29 - 2.7] = 9.18 kJ.mol^{-1}$$

$$E_p^{total} = E_{ij}^{el} + E_{ij}^{LJ} = -6.2 kJ mol^{-1} + 9.18 kJ mol^{-1} = 3 kJ mol^{-1}$$

According what principle there should be the melting of an ice?

The crude meaning of entropy and free energy

Where is the higher probability to find one particular molecule of air here in our classroom (p_c) or in astronomy observatory at Lomnický štít (p_L)?

$$\begin{aligned} p_c/p_L &= [V_c \exp(-E_c/kT)] / [V_L \exp(-E_L/kT)] \\ &= [\exp(-(E_c - T^*k \ln(V_c))/kT)] / [\exp(-(E_L - T^*k \ln(V_L))/kT)] \end{aligned}$$

where $S = k \ln(V)$ is entropy;

more general: $S = k [\text{logarithm of the number of accessible states of the particle}]$

and $F = E - T^*S$ is (Helmholtz) free energy (for system at constant volume)

$$p_c/p_L = \exp(-F_c/kT) / \exp(-F_L/kT) = \exp(-(F_c - F_L)/kT)$$

Difference between Helmholtz and Gibbs free energy

T=const:

Helmholtz free energy	Gibbs free energy
V=const	P=const
$F=E-TS$	$G=H-TS=F+PV$
E	enthalpy $H=E+PV$
	chemical potential: $\mu=G/N$
probability $\propto \exp(-F/kT) \rightarrow \max$ F $\rightarrow \min$	probability $\propto \exp(-G/kT) \rightarrow \max$ G $\rightarrow \min$

Typical value of PV for liquids at atmospheric pressure is very small in comparison with the thermal energy of the body. Therefore very often the term “

Let's estimate the work against the external atmospheric pressure related to the insertion of 1M of water.

Let's estimate the work against the external atmospheric pressure related to the insertion of 1M of water.

1M of water: $18 \text{ g} \cdot \text{mol}^{-1}$, $18 \text{ cm}^3 \cdot \text{mol}^{-1}$

at atmospheric pressure $pV = 10^5 \text{ Pa} * 18 * 10^{-6} \text{ m}^3 \cdot \text{mol}^{-1} = 1.8 \text{ J} \cdot \text{mol}^{-1}$

It is negligible value in comparison to the thermal energy.

$$G=H-TS; dG=dH-TdS-SdT$$

At $T=\text{const}$ ($dT=0$)

at equilibrium, $G=\text{min}$, $dG=0$, $dH-TdS=0$

It implies:

$$T = dH/dS$$

Definition of heat capacity: $C_p=(dH/dT)_{P=\text{const}}$

$$S=-(dG/dT)_{P=\text{const}}$$

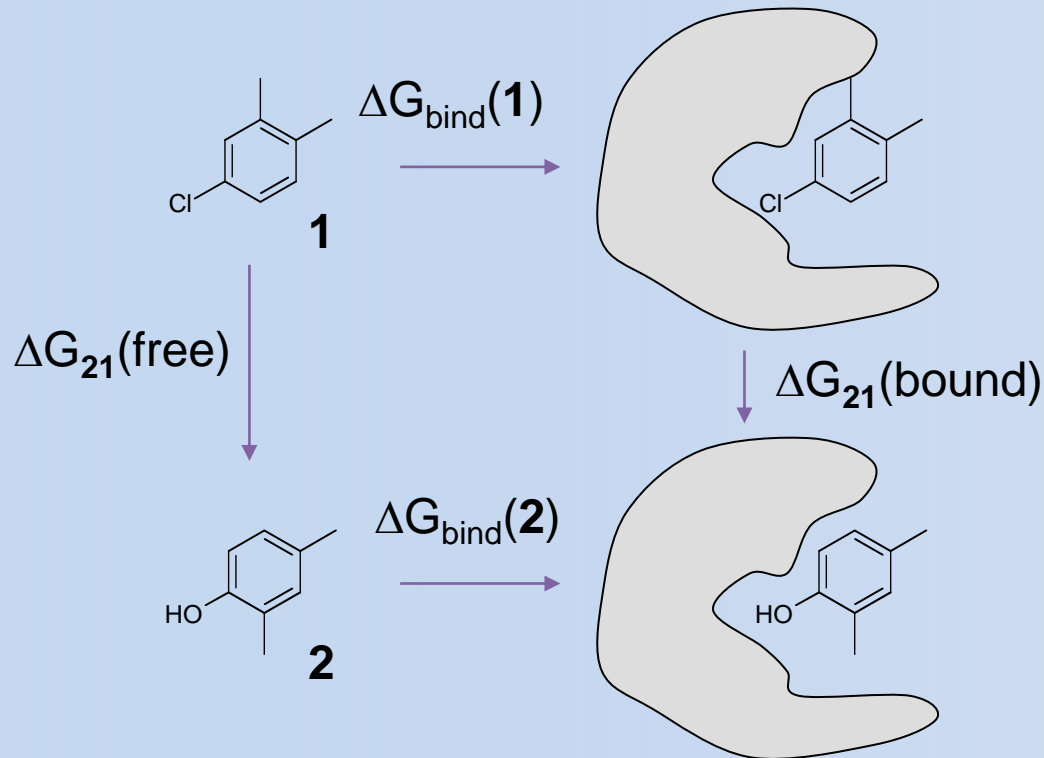
Free energy – driving force

Typical Examples:

- (1) Conformational changes
- (2) Affinity of the ligand binding
- (3) Solubility
- (4) Lipophilicity
- (5) Protein in folded vs unfolded state

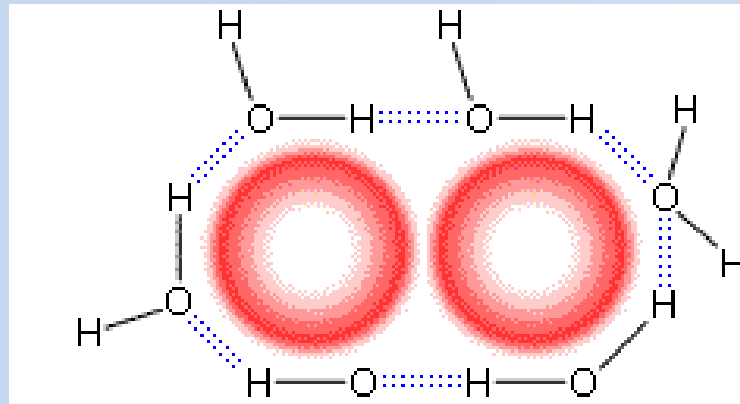
In the computational simulations it is easy to calculate the potential or kinetical energy of the system. However, it is much more challenging to calculate the free energy differences.

Thermodynamic cycle for binding affinities



$$\begin{aligned} \Delta\Delta G_{\text{bind}} &= \Delta G_{\text{bind}}(\mathbf{2}) - \Delta G_{\text{bind}}(\mathbf{1}) \\ &= \Delta G_{21}(\text{free}) - \Delta G_{21}(\text{bound}) \end{aligned}$$

Hydrophobic bond between non-polar particles

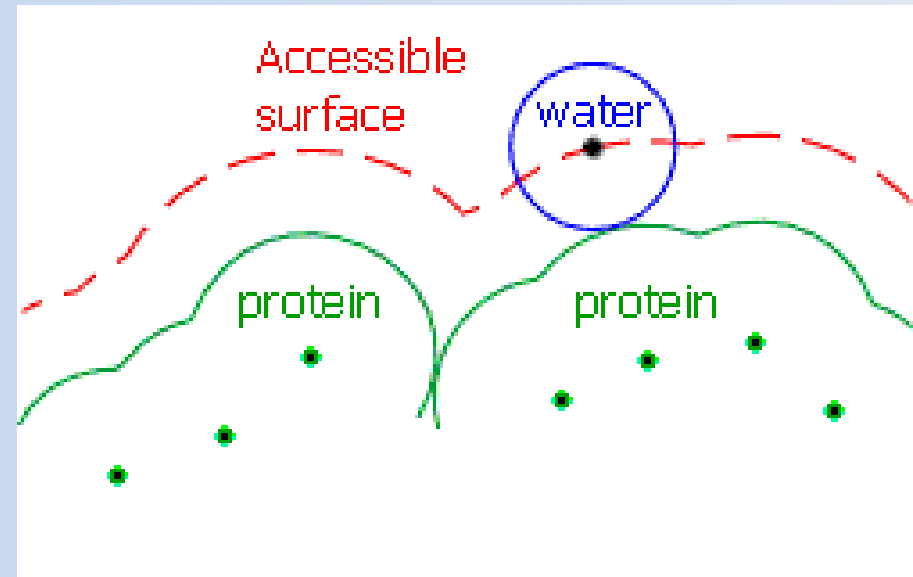
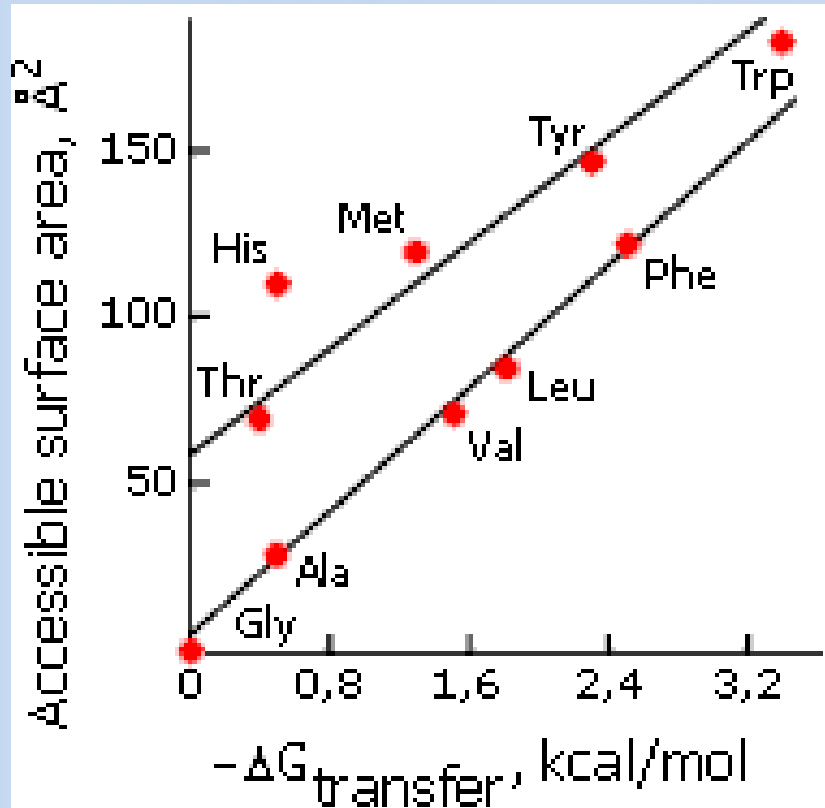


Hydrophobic free energy increases almost proportionally to the accessible surface area of the non-polar molecules.

Its value is $\sim 85-105 \text{ J} \cdot \text{mol}^{-1} \cdot \text{\AA}^{-2}$

The accessible surface area of amino-acid side-chains and their hydrophobicity

~ -50 Å² for each polar atom



Adopted from Schulz G.E., Schirmer R.H. Principles of protein structure. 1979

Hydrophobic effect is the principle component of the protein 3D structure formation/stability.

Second look on the hydrogen bonding

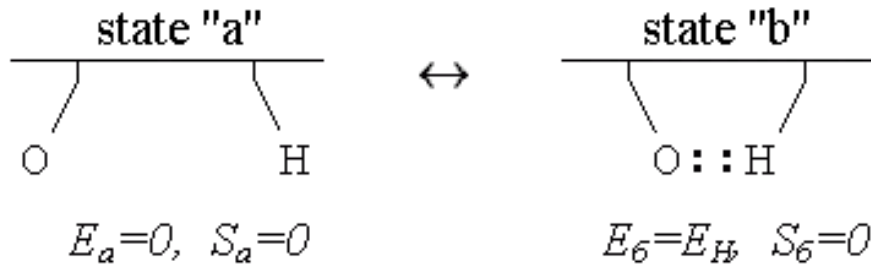
Role of water

H-bond energy is $\sim 5 \text{kcal} \cdot \text{mol}^{-1} = 21 \text{kJ} \cdot \text{mol}^{-1}$

in water H-bond energy is only $\sim 5\text{-}6 \text{kJ} \cdot \text{mol}^{-1}$

Large difference in increase of protein stability by forming of intraprotein H-bond in vacuum vs. water!!!

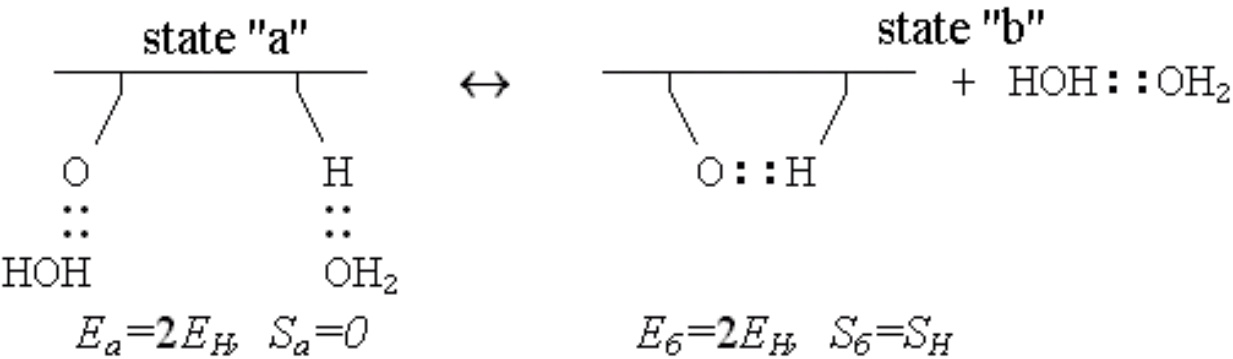
In vacuum:



$$E_b - E_a = E_H \quad S_b - S_a = 0$$

$$F_b - F_a = (E_b - E_a) - T(S_b - S_a) = E_H$$

In water:



$$E_b - E_a = 0, \quad S_b - S_a = S_H$$

$$F_b - F_a = (E_b - E_a) - T(S_b - S_a) = -TS_H$$

Difference in entropy of water molecule.

At the melting temperature 273 K

increase in entropy is compensated by decrease in energy

Melting heat of ice: $334 \text{ J} \cdot \text{g}^{-1}$ ($80 \text{ cal} \cdot \text{g}^{-1}$)

$$334 \text{ J} \cdot \text{g}^{-1} * 18 \text{ g} \cdot \text{mol}^{-1} = 6.012 \text{ kJ} \cdot \text{mol}^{-1} (1.5 \text{ kcal} * \text{mol}^{-1})$$

Conclusions

- Free energy difference is the most important determinant of behavior in solutions
- Free energy has enthalpic and entropic part
- The increasing importance of entropic part with the increasing temperature
- Probability of certain state is given by Boltzmann formula
- Binding affinity depends on both – bound and unbound state in water