

Action Center 6

1. A reaction is known to have a ΔH of 20kJ per mol and a ΔS of 82J per K per mol. Above what temperature (in $^{\circ}\text{C}$) will this reaction be spontaneous?

At $T=T_m$, ΔG is zero: $0 = \Delta H - T \Delta S$

$T = \Delta H/\Delta S = -29^{\circ}\text{C}$

Spontaneous at high temperatures

2. Consider the following reactions:



ΔG° for the first reaction is -4.1kcal/mol and ΔG° for the second reaction is 3.2kcal/mol. Given this information, what is the value of ΔG° (in kcal/mol) for the following net reaction?



$$\Delta G^{\circ}(\text{net}) = \Delta G^{\circ}(\text{rxn1}) + \Delta G^{\circ}(\text{rxn2}) = -0.9 \text{ kcal/mol}$$

3. If the concentration of glucose inside an *E. coli* cell is 4.5 mM, how many glucose molecules are in the cell? Assume *E. coli* cell to be a cylinder 2 μm long and 1 μm in diameter.

Volume of a cylinder = $\pi \cdot h \cdot r^2 = 1.57 \mu\text{m}^3/\text{cell} = 1.57 \cdot 10^{-15} \text{ L/cell}$

$0.0045 \text{ mol/L} \cdot 1.57 \cdot 10^{-15} \text{ L/cell} \cdot 6.022 \cdot 10^{23} \text{ molecules/mol} = 4.26 \cdot 10^6 \text{ molecules/cell}$

4. When DNA forms a double helix the measured ΔG is -54.4 kJ/mol at pH7, 1 M NaCl, and 25 $^{\circ}\text{C}$. The enthalpy change for this process is -251 kJ/mol. What is the entropy change for this system?

$$\Delta S = -(\Delta G - \Delta H)/T = -660 \text{ J/mol}\cdot\text{K}$$

5. The template strand of a segment of double-helical DNA contains the sequence: ATGCAGTACATC. What would be the amino acid sequence of the resulting polypeptide, assuming that translation of the relevant mRNA began with the first codon? Include the start codon into your sequence. Also, assume that if a stop codon is encountered prior to reaching the end of the mRNA, translation stops and does not resume, in which case you should enter the sequence of amino acid(s) incorporated into the peptide prior to encountering the stop codon. Report your answer in the one-letter code

The mRNA sequence is identical to that of the coding (i.e. complementary to the template) strand of DNA.

mRNA 5' -> 3'

GAUGUACUGCAU

Recognized codons: AUG-UAC-UGC

Protein sequence (no stop codons prior to the end of mRNA): MYC

		Second Letter				
		T	C	A	G	
First Letter	T	TTT } Phe TTC } TTA } Leu TTG }	TCT } Ser TCC } TCA } TCG }	TAT } Tyr TAC } TAA } Stop TAG } Stop	TGT } Cys TGC } TGA } Stop TGG } Trp	T C A G
	C	CTT } Leu CTC } CTA } CTG }	CCT } Pro CCC } CCA } CCG }	CAT } His CAC } CAA } Gln CAG }	CGT } Arg CGC } CGA } CGG }	T C A G
	A	ATT } Ile ATC } ATA } ATG } Met	ACT } Thr ACC } ACA } ACG }	AAT } Asn AAC } AAA } Lys AAG }	AGT } Ser AGC } AGA } Arg AGG }	T C A G
	G	GTT } Val GTC } GTA } GTG }	GCT } Ala GCC } GCA } GCG }	GAT } Asp GAC } GAA } Glu GAG }	GGT } Gly GGC } GGA } GGG }	T C A G

6. What is the complementary DNA sequence for CGATGGCATA?

5' -> 3'

TATGCCATCG

7. What is the net charge of the following peptide at pH 4.7: AGLCEK Use the pKa values in the table below:

Group	pKa
N-terminal amino	8.0
C-terminal carboxyl	3.1
Asp, Glu	4.0
Lys	10.4
Arg	12.5
His	6.0
Tyr	10.5
Cys	8.4

As a rule of thumb, we assume that if the pH is 2 or more units above or below the pKa, the functional group will be completely protonated/deprotonated. So at pH 4.7 Lysine and the N-terminal amino group will be completely protonated and carry a positive charge. Cysteine will also be completely protonated and thus carries zero charge. Since glutamate and the C-terminal carboxyl groups are within the 2 pH unit range they will only be partially protonated. We have to use Henderson-Hasselbalch to determine the fraction of each that is in the unprotonated form (i.e. carry a negative charge).

Glu:

$$[\text{COO}^-]/[\text{COOH}] = 10^{(\text{pH}-\text{pKa})} = 5.012$$

$$\text{fraction of } [\text{COO}^-] = 5.012/(5.012+1) = 0.8337$$

C-Terminus:

$$[\text{COO}^-]/[\text{COOH}] = 39.8$$

$$\text{fraction of } [\text{COO}^-] = 0.9775$$

$$\text{Net Charge} = +1(\text{lys}) + 1(\text{N-term}) - 0.8337(\text{Glu}) - 0.9775(\text{C-term}) = 0.19$$

8. Treatment of a decapeptide with Sanger's reagent reveals that the N-terminal residue is glycine. The intact decapeptide is then subjected to partial hydrolysis to give peptides whose amino acid compositions are shown below. Based on these data, what is the sequence of the decapeptide?

- a. A,W
- b. V,P,D
- c. P,V
- d. A,E
- e. W,A,R
- f. R,G
- g. E,A,L
- h. M,P,L,E

GRWAELMPVD

9. A pentapeptide obtained from treatment of a protein with trypsin was shown to contain R,D,L,S, and Y. To determine the amino acid sequence, the peptide was cycled through the Edman degradation procedure three times. The composition of the peptide remaining after each cycling was as follows: After cycle 1: R,D,L,S After cycle 2: R,D,S After cycle 3: R,S. What is the sequence of the pentapeptide?

YLDSR (R has to be the last because the peptide was generated with trypsin)

10. A polypeptide is approximately 312 residues in length. What is the length (in Å) of the polypeptide if it was a true alpha-helix? What would be its length if it were a beta-strand?

$$\text{alpha-helix: } 312 \times 1.5 \text{ Å} = 468 \text{ Å}$$

$$\text{beta-sheet: } 312 \times 3.5 \text{ Å} = 1092 \text{ Å}$$