KU LEUVEN

Basics of biological chemistry

Assignment

January 2015 Finals

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1 Questions from Prof. J. Vanderleyden – dr. H. Steenackers

1.1 Chemical reaction equation

Consider the following reaction: $(NH_4)_2CO_3 + Zn(NO_3)_2 \rightarrow NH_4NO_3 + ZnCO_3$

a.) Balance the equation

$(NH_4)_2CO_3 + Zn(NO_3)_2 \rightarrow 2\ NH_4NO_3 + ZnCO_3$

b.) Reactants and products

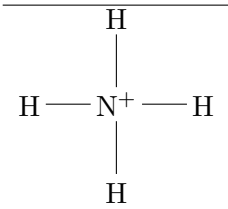
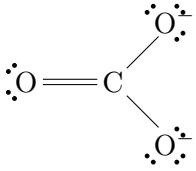
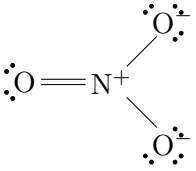
`Q:` Name all reactants and reaction products.
`A:`

- $(NH_4)_2CO_3$: Ammonium carbonate
- $Zn(NO_3)_2$: Zinc nitrate
- NH_4NO_3 : Ammonium nitrate
- $ZnCO_3$: Zinc carbonate

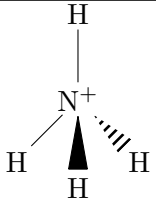
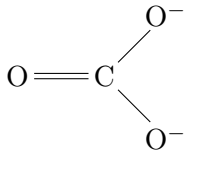
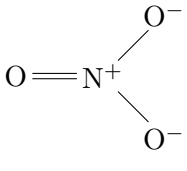
c.) Lewis structure, VESPR

`Q:` Construct the Lewis structures of the polyatomic ions you recognize and predict their molecular structure using the VSEPR theory.
`A:`

- Lewis Structure of the ions:

Ammonium	Carbonate	Zinc	Nitrate
		Zn^{2+}	

- Molecular structure prediction:

Ammonium	Carbonate	Zinc	Nitrate
		Zn^{2+}	

d.) Oxidation states

`Q:` Determine the oxidation state of all the atoms in all the compounds. Is this an oxidation-reduction reaction?
`A:` Ammonium Carbonate and Zinc Nitrate (the reactants) are very soluble in water and will thus move freely as charged ions. The Zinc and Carbonate ions will precipitate. The reaction is not an oxydo-reduction as shown by the details :

- $Zn(NO_3)_2$ each O are -2, N is +5, and $(NO3^-)_2$ is -2 and Zn is +2
- $(NH_4)_2CO_3$ N is -3, each H are +1, and $(NH_4)_2$ is +2. C is +4 and each O is -2, and $(CO_3)^{-2}$ is -2.
- NH_4NO_3 for NH_4, the oxidation state is +1, and for NO_3 it's -1
- $ZnCO_3$ for Zn, the oxidation is +2, and it's -2 for CO_3

e.) Mass

`Q:` How many grams of ZnCO3 can be prepared from 400g Zn(NO3)2 by using sufficient(NH4)2CO3?
`A:` Let's start by computing the molecular weight of the 2 reactants:

Molecular weigth of $Zn(NO_3)_2$ 189.36 g/mol

Molecular weigth of $(NH_4)_2CO_3$ 96.09 g/mol

Given that there are 400g of $Zn(NO_3)_2$, we can calculate the number of moles of reactant (and ignore that of $(NH_4)_2CO_3$ since it is in excess):

Moles of $Zn(NO_3)_2$ 400 g / 189.36 g/mol = 2.11237 moles

From this last figure, we can infer that the number of moles of $ZnCO_3$ will be 2.11237. Given the molecular mass of $ZnCO_3$, we can compute the amount of $ZnCO_3$ produced to be: 2.11237 mol * 125.3889 g/mol = 264.8678 g.

1.2 DNA sequence analysis

The following diagram shows part of a template DNA strand, with sections X,Y and Z being the exons of a gene:

```
5'                        3'
GTA GGT TGT ATC GAT GGT CAT
---     -------         ---
 X         Y             Z
```

a.) DNA Replication

`Q:` What is the corresponding sequence on the new daughter strand made from the given parent strand during replication?
`A:` Given the principle of base pairing, we can determine the daughter sequence to be (here in the 3' to 5' direction):

```
5’                        3’
GTA GGT TGT ATC GAT GGT CAT
CAT CCA ACA TAG CTA CCA GTA
3’                        5’
```

b.) Translated Protein

`Q:` What polypeptide sequence will be synthesized from the given template DNA? Give a short overview of the different processes (and enzymes) involved in the synthesis of polypeptides from template DNA. Where in the cell do these processes take place?
`A:` The synthesized polypeptide will consist of the amino acids `Met-Asp-Thr-STOP` (corresponding mRNA: `5’AUGGAUACAUAC`). Since it is mentioned that exons are present, we can assume the translation will take place with the eukaryotic machinery. It will consist of the following stages:

- Transcription: In the nucleus, the RNA Polymerase II will be recruited and will bind to the promoter of the gene. It will produce, by moving in the 5’ to 3’ direction, a pre messenger RNA which will be identical to the DNA template sequence (with the exception that Uracyl will be used instead of Thymine, and also the addition of a 5’ CAP). That messenger RNA will then be processed by the spliceosome, which will remove the introns, and a Poly-A tail will also be added at the 3’ end of the mRNA. The mRNA is then ready to go outside of the nucleus to be translated.
- Translation: the mRNA leaves the nucleus and passes through the reticulated ER where it will be captured by a ribosome that will either bind to the ER or not. It will then start scanning for a start codon in the mRNA. From that point on, the synthesis of a polypeptide will be accomplished by reading 3 base pairs at a time and pairing these 3 with the correct tRNA. After that, the polypeptide will either be processed further and sent to the golgi apparatus, or will remain in the cytosol.

c.) Mutated exon

`Q:` What polypeptide sequence will be synthesized if the ATC in exon Y is mutated to TTC? What polypeptide sequence will be synthesized if the ATC in exon Y is mutated to ATG? Which of those substitution mutations is likely to be more harmful? Why?
`A:` Here are the new sequences with mutated exons:

- TGTATC -> TGTTTC : the resulting polypeptide will be `Met-Glu-Thr-STOP`
- TGTATC -> TGTATG : the resulting polypeptide will be `Met-His-Thr-STOP`

The second mutation would be the most disruptive. Indeed the original Aspartate would be negatively charged in the physiological condition, and the Glutamate would also be negatively charged, the only difference between the 2 is then an additional CH2 group in the side chain. Histidine on the the other hand is neutral in physiological conditions, and the side chain is significantly larger.

d.) Interactions with antibiotics

`Q:` Which steps in polypeptide synthesis are affected by resp. the macrolide antibiotics and the tetracycline antibiotics?

A: Both substance have the capabilities to inhibit the synthesis of proteins.

- Macrolide : they have an action in that is thought to prevent peptidyltransferase from linking the peptide from the tRNA to the growing polypeptide chain. This is done by binding to the 50s subunit of the ribosomes in prokaryotes.
- Tetracycline : this one function by preventing the binding of tRNA to mRNA. This is done by binding the 30S ribosomal subunit of the prokaryotic bacterias.

e.) Comparison of error rates

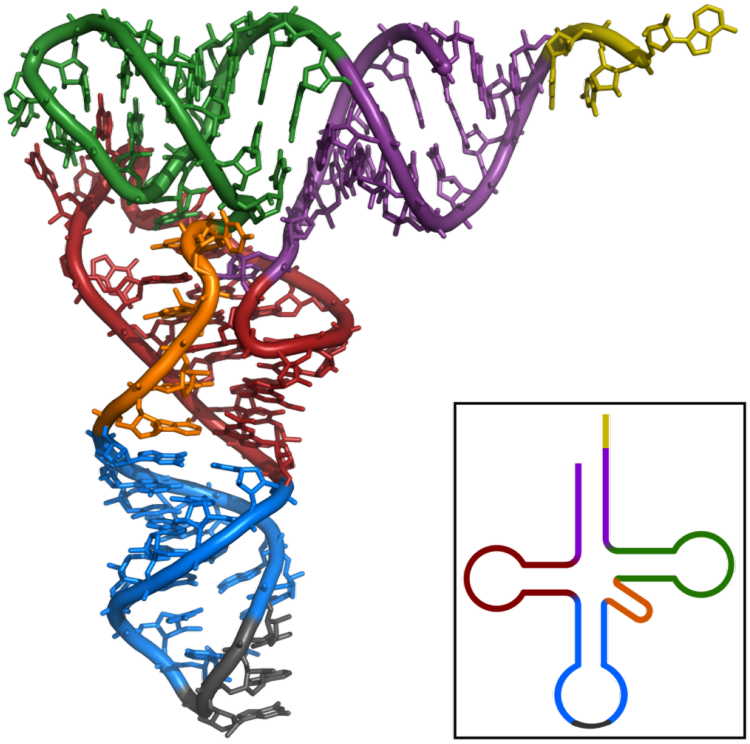
Q: The error rate in RNA synthesis is much higher than the error rate of DNA replication. What is the origin of this difference? Motivate why this is not a serious problem.
A: DNA being the central repository of the genetic information for an organism, the fidelity of the DNA replication is required to ensure the continuity of the species and its viability accross multiple generation. The cell needs thus enforce a high fidelity of the replication process. On the other hand, whenever an incorrect mRNA is transcribed, the effect are very local and temporary, indeed there is no real harm in producing a couple of non-functioning mRNA or proteins.

1.3 tRNA 3D-Structure

Q: All tRNA molecules have a particular 3D-structure. Which functional groups and which chemical bonds/interactions contribute to this particular structure? Why is this particular structure of importance for the biological function?
A: below is a representation of a tRNA structure[1]. The structure of the tRNA contains a couple of loops and is maintained through base pairing (hydrogen bonds). Couple of functional groups can be identified that are common to tRNAs:

- anticodon arm (blue): that loop will contain the anticodon (black) which will base pair with the mRNA codon.
-

[1] info http://commons.wikimedia.org/wiki/File:TRNA-Phe_yeast_1ehz.png#mediaviewer/File:TRNA-Phe_yeast_1ehz.png



2 Questions from Prof. B. Sels

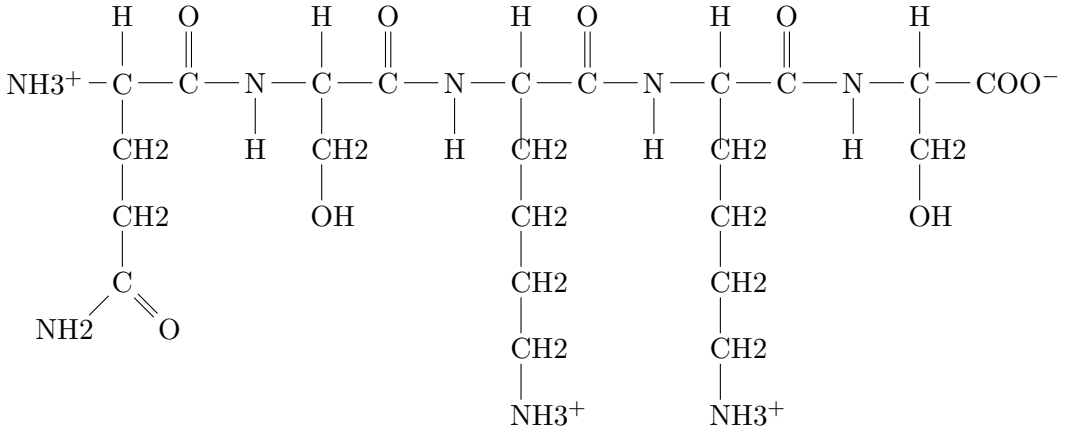
2.1 Biopolymer organisation

`Q:` The course and the textbook systematically organize four important biopolymers mainly according to their chemical structure. Attempt a complete reorganization of the various biopolymer structures (and subfamilies!) according to the following three physiological functions: energy, structure, and communication. Explain the physiological function of each biopolymer type with regard to its chemical structure and/or physical properties.
`A:`

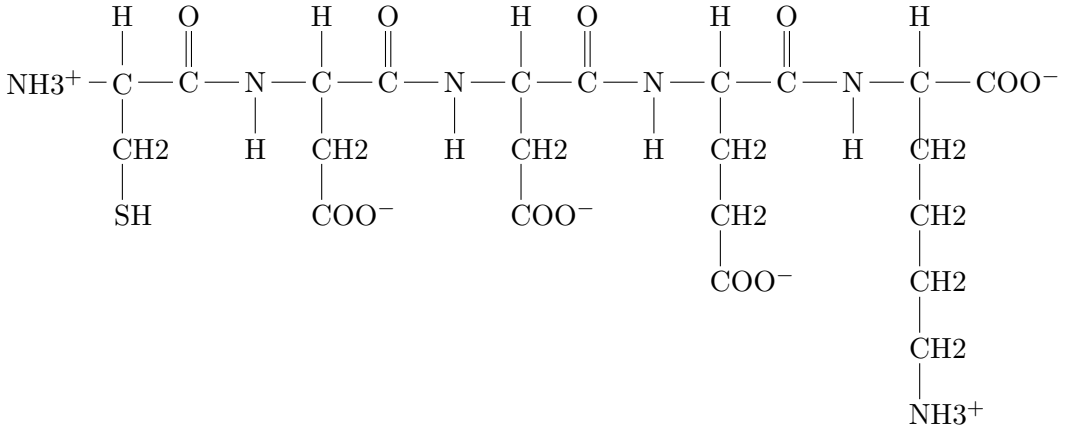
2.2 Chemical structure of proteins and proteins separation

`Q:` Draw the chemical structure of the following two oligopeptide structures, a) Gln-Ser-Lys-Lys-Ser and b) Cys-Asp-Asp-Glu-Lys, determine its net charge in physiological conditions. How would you separate the two peptides ?
`A:` These are the chemical structures of:

- Gln-Ser-Lys-Lys-Ser



- Cys-Asp-Asp-Glu-Lys



Under physiological conditions (ie, pH around 7.35), these would be the net charge on each polypeptide:

- Gln-Ser-Lys-Lys-Ser: net charge is +2
  $\overset{\oplus}{\mathrm{NH3}}-\mathrm{Gln}-\mathrm{Ser}-\overset{\oplus}{\mathrm{Lys}}-\overset{\oplus}{\mathrm{Lys}}-\mathrm{Ser}-\overset{\ominus}{\mathrm{COO}}$
- Cys-Asp-Asp-Glu-Lys: net charge is -2
  $\overset{\oplus}{\mathrm{NH3}}-\mathrm{Cys}-\overset{\ominus}{\mathrm{Asp}}-\overset{\ominus}{\mathrm{Asp}}-\overset{\ominus}{\mathrm{Glu}}-\overset{\oplus}{\mathrm{Ly}}-\overset{\ominus}{\mathrm{COO}}$

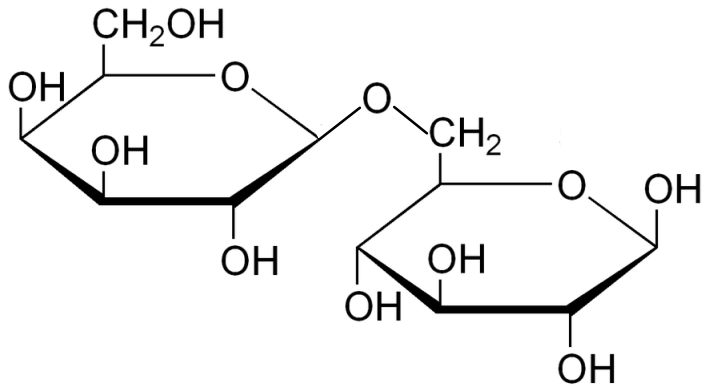
Separation of both proteins can thus be achieved by ion exchange chromatography since they both have a distinct charge.

2.3 Chemical structure of disaccharides

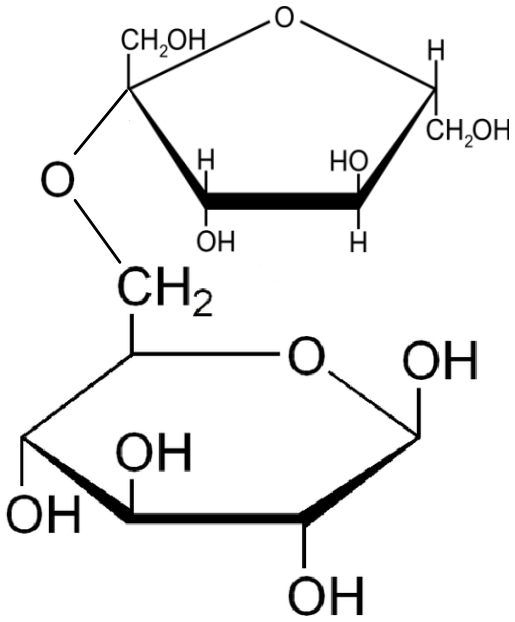
`Q:` Draw the chemical structure of the following disaccharides: a) the β-anomer of $\alpha(1\rightarrow6)$galactoglucose and b) $\beta,\alpha(1\rightarrow2)$glucofructose.
`A:` These are the chemical structure of:

- β-anomer of $\alpha(1\rightarrow6)$galactoglucose

Beta anomers have a cis relationship between the CH_2OH group on the C_1 and the OH group on the C_6. This helps us determine the structure of the monosaccharides galactose and glucose. The polymerisation is achieved through an α binding between the C_6 of the Galactose, and the C_1 of the glucose molecule, giving the following molecular structure:

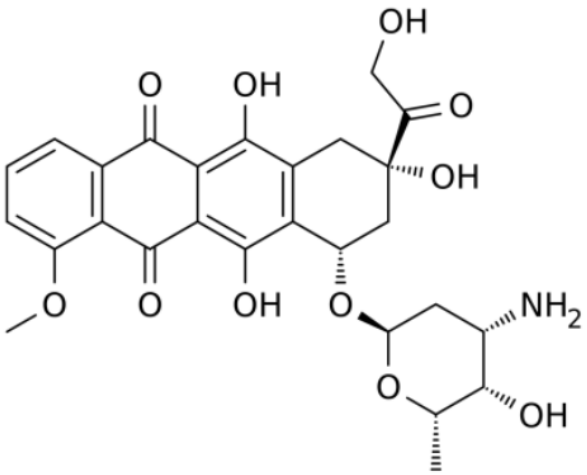


- β,α(1→2)glucofructose



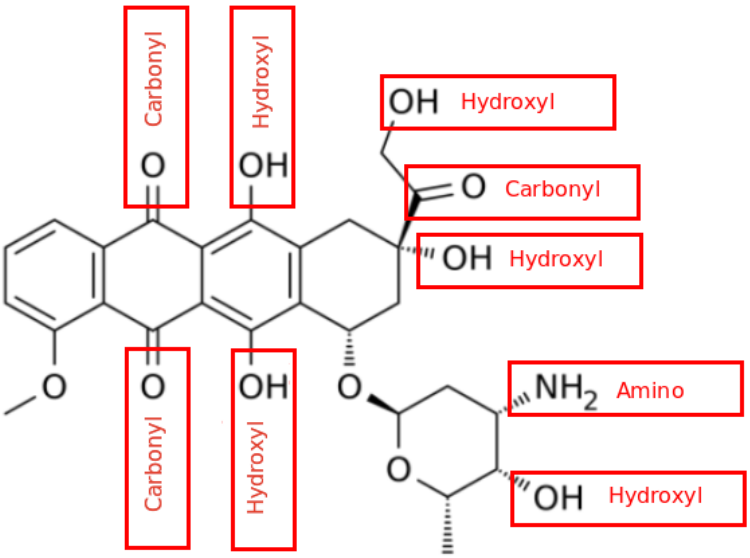
3 Questions from Prof. D. De Vos

Considering the following molecule:



3.1 Functional groups

Q: Name all functional groups
A: See annoted figure below



3.2 Water and oil solubility factors

Q: Indicate which groups make the molecule rather water-soluble than oil-soluble
A: The following groups can partake in hydrogen bonds with water molecules and increase the solubility of the molecule in water :

- Hydroxyl groups (5 of them)
- Carbonyl groups (3 of them)

- Amino group (1 present)