KU LEUVEN

Basics of biological chemistry

Assignment

January 2015 Finals

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

Note: reference material for this part mostly come from the recommended class book [1]

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

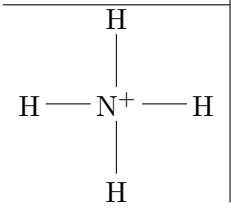
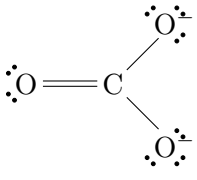
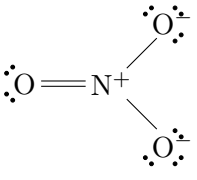
`Q:` Name all reactants and reaction products.
`A:`

- $(NH_4)_2CO_3$: Ammonium Carbonate
- $Zn(NO_3)_2$: Zinc Nitrate
- NH_4NO_3 : Ammonium Nitrate
- $ZnCO_3$: Zinc Carbonate (also known as "Smithsonite")

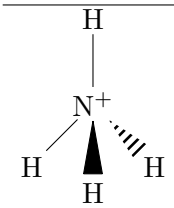
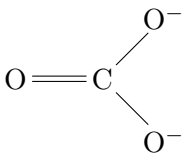
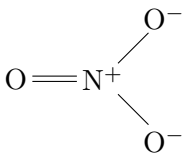
c.) Lewis structure, VESPR

`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
		$\cdot Zn^{2+}\cdot$	

- 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 below:

- $Zn(NO_3)_2$ each O are -2, N is +5, $(NO3^-)_2$ 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 is 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 = 264.87 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:

```
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-Tyr` (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 thus consist of the following general steps:

- 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 it will be captured by a ribosome that will either bind to the ER or not depending on the signal encoded in the mRNA. 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-Tyr`
- TGTATC -> TGTATG : the resulting polypeptide will be `Met-His-Thr-Tyr`

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, its side chain is also significantly larger/bulkier due to the presence of an aromatic ring.

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 by affecting ribosomal activity [3].

- Macrolide : prevents peptidyltransferase from linking the peptide from the tRNA to the growing polypeptide chain.
- Tetracycline : this one functions by preventing proper binding of tRNA to mRNA in the ribosome.

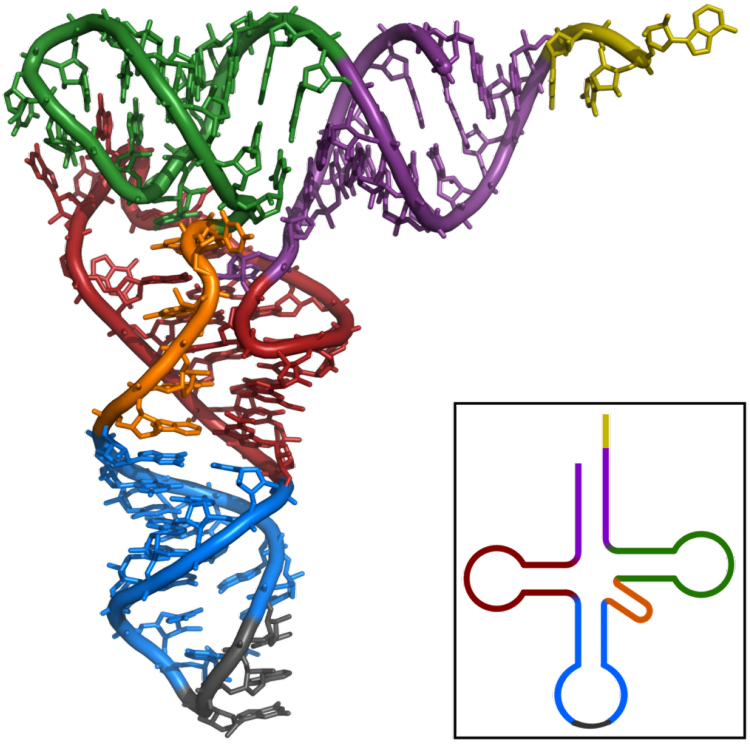
e.) Comparison of error rates

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 through an extensive proof reading system. On the other hand, there is no proof reading for transcription. 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 that will eventually be degraded by the cell.

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 [5]. The structure of the tRNA contains a couple of loops and contains parts with base pairing (hydrogen bonds). This structure is critical for the correct capture, processing, and release of the tRNAs by the ribosomes. A couple of important sections can be identified which are common to tRNAs and critical to their function :

- Anticodon arm (blue): that loop will contain the anticodon (black) which will base pair with the mRNA codon.
- Acceptor stem (purple): which is the attachment site of the amino acids.
- T-Arm (green): that region is a special recognition site for the ribosome. It allows a tRNA-ribosome complex to form and translation to proceed.



2 Questions from Prof. B. Sels

Note: reference material for this part mostly come from the recommended class book [1]

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:` The fours main categories of polypeptide consist of the carbohydrates, the nucleic acids, the proteins (polypeptides), and the lipids. Here is my attempt at reorganizing them based on the following categories:

a.) Energy

- Carbohydrates for short term storage of energy, either for immediate release of energy (glucose, galactose, etc), or for midterm storage of energy (Polysaccharide glycogen).
- Lipids can be used in a triacylglycerols form to store energy for the long term.
- The universal energy conveyor of the cellular life is ATP, which is a triphosphated adenosine (nucleic acid).

b.) Structure

- Glycerophospholipids are the most abundant lipids found in the cell membrane.

- Steroids such as cholesterol are important for the fluidity of the membrane.
- Fibrous proteins are used to form the exoskeletton and the misc filaments inside the cell (Actin, Tubulin, etc). They also play an important part of the movement capabilities for unicellular organism (flagella, cilia)
- Polysaccharides can be used for structure as well, for example as cellulose for the rigidity of the plants, or as chitin for the exosqueleton of the insects.
- Peptidoglycans are a major component of bacterial cell walls (they give it strength)
- Waxes, which are non polar esters of long-chain fatty acids and long chain of monohydroxylic alcoohols are widely distributed in nature as protective, waterproof coatings on leaves, fruits, animal skin, fur, and feathers.

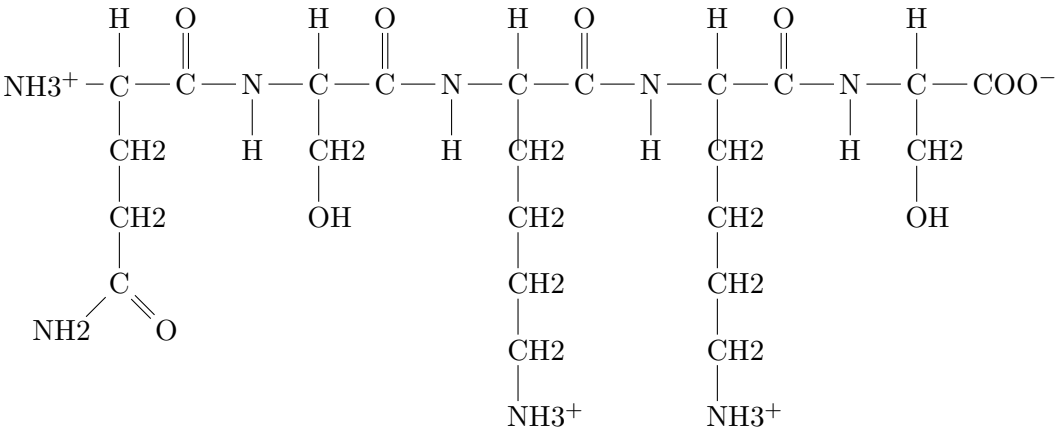
c.) Communication

- DNA is the central repository of information for the organism genetic makeup, which is passed on through the generations.
- RNA is the intermediate messenger for the translation of proteins.
- Modified amino acids are involved in communication too (eg Thyroxine and Melatonin). Important in this category are the cAMP, and cGMP which are often found as secondary messenger units for communication within the cell.
- A host of membrane proteins that help recognizing and process signals are found on most cells. An important family of these membrane proteins are the G-Proteins which help with signal transduction.
- Neurotransmitters that carry signal from one neurons' synapses to another. Many of these neurotransmitters are synthesized from amino acids precursors.

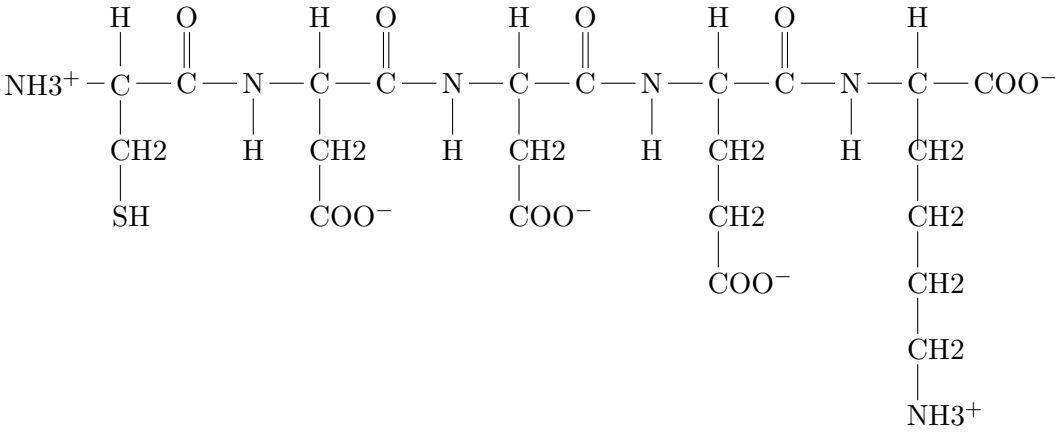
2.2 Chemical structure of proteins and proteins separation

`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

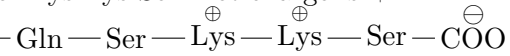


- Cys-Asp-Asp-Glu-Lys

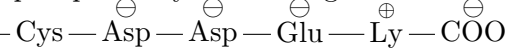


Under physiological conditions (ie, pH around 7.35), these would be the net charge on each polypeptide:

- Gln-Ser-Lys-Lys-Ser: net charge is +2



- Cys-Asp-Asp-Glu-Lys: net charge is -2



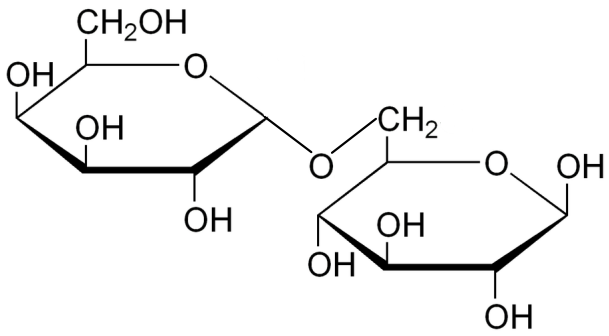
Separation of both proteins can thus be achieved by ion exchange chromatography since they both have quite a distinct charge [2]. For example, we could use anion exchange chromatography, which would capture the negatively charged polypeptide, and let the positively charged one pass through. The former could then be recovered later on by washing away the column.

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:

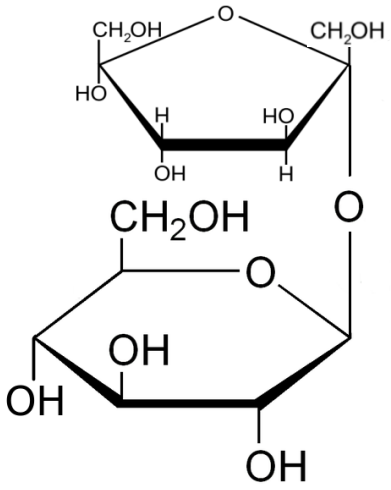
- β-anomer of $\alpha(1\rightarrow6)$galactoglucose

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 monosaccharide 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:



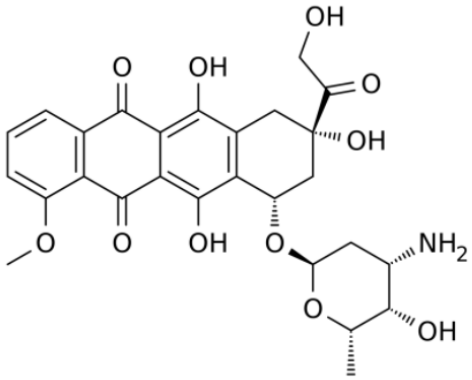
- β,α(1→2)glucofructose

The same principle are applied here for the dissacharide consisting of Glucose and fructose:



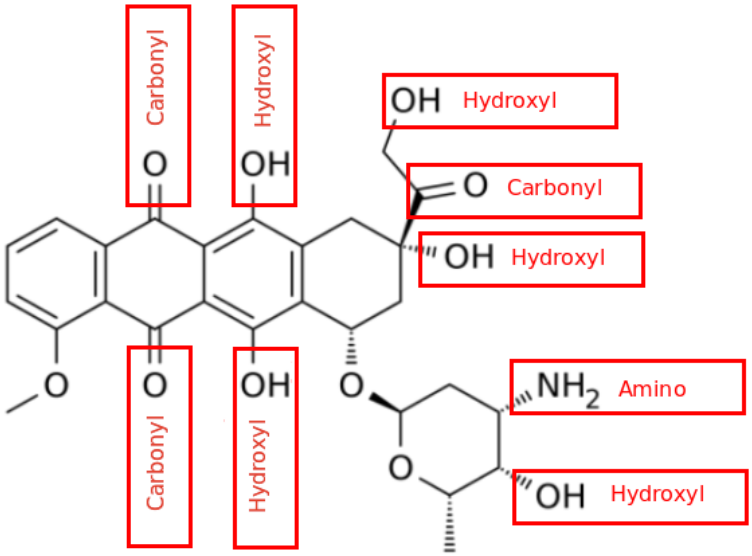
3 Questions from Prof. D. De Vos

Note: reference material for this part mostly come from the recommended class book [1]
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)

We can also observe that the molecule (which is the molecule of Doxorubicin, used among other things for treatment of cancer via chemotherapy [4]) contains interesting linkages, most notably ether bonds, of which the electron pairs on the oxygens can partake in H-Bonds with water and thus make the molecule more hydropholic.

References

[1] George Odian Ira Blei. *General, Organic, and Biochemistry.* W.H. Freeman and Company, 2006.

[2] L. Moran, R. Horton, G. Scrimgeour, and M. Perry. *Principles of Biochemistry 5th.* Pearson International, 2014.

[3] Lambert T. Antibiotics that affect the ribosome. *Rev. sci. tech. Off. int. Epiz*, 2012.

[4] Wikipedia. Doxorubicin — Wikipedia, the free encyclopedia, 2014. Available Online; accessed 30-January-2015: `https://en.wikipedia.org/wiki/Doxorubicin`.

[5] Yikrazuul. Trna-phe yeast 1ehz. Available Online; accessed 30-January-2015: `https://commons.wikimedia.org/wiki/File:TRNA-Phe_yeast_1ehz.png#mediaviewer/File:TRNA-Phe_yeast_1ehz.png`.