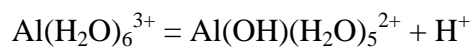


Problem 15. Complexation reactions in the determination of inorganic ions

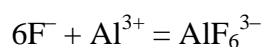
1. After the endpoint, the excessive Al^{3+} ions undergo hydrolysis, which makes the medium acidic, and the indicator turns red:



2. On heating, the hydrolysis equilibrium shifts rightwards.
3. Cryolite Na_3AlF_6 being formed upon the titration is only slightly soluble in water. Hence, NaCl was added to further decrease its solubility and shift the equilibrium of complex formation rightwards.
4. Neutralization of the sample solution before titration is missing. This operation is mandatory if an acid–base indicator is used to observe the endpoint and the sample is suspected to contain acids. Heating makes the endpoint sharper but is not as critical.
5. In this case a reverse titration was applied. Fluoride precipitates calcium:



and the excess of fluoride is titrated with AlCl_3 :



6. 10.25 mL of 0.1000 M AlCl_3 gives 1.025 mmol of Al^{3+} , corresponding to 6.15 mmol of F^- . The initial amount of NaF was 0.500 g, or 11.91 mmol, i.e. 5.76 mmol of F^- was spent for the precipitation of calcium. The amount of calcium is $2.88 \cdot 10^{-3}$ mol.



As can be seen from the equation, HCl is spent in this process, and its excess is titrated with NaOH in the presence of an acid-base indicator. (To be more precise, the excess of HCl reacts with KF yielding a weak acid HF , which is then titrated with NaOH .)

8. The solution of free silicic acid (a weak acid with $\text{p}K_a$ of about 10) will be slightly acidic; hence, the indicator used in the neutralization of the sample should change its color in a weakly acidic medium (methyl red, $\text{p}K_a \approx 5$). In weakly alkaline media (color change range of two other indicators), a considerable part of the silicic acid will be present in the form of a silicate ion, the buffer solution of which will consume a certain amount of the reacting HCl .

9. The amount of NaOH and the excess of HCl are the same and equal to 0.550 mmol. Hence, the amount of HCl spent for the reaction with silicic acid is $0.994 - 0.550 = 0.444$ mmol, and the amount of silicic acid is 0.111 mmol.

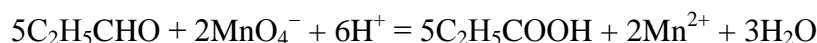
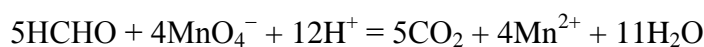
Problem 16. Malaprade reaction

1. With glycerol: $\text{HCOOH} + 2 \text{HCHO}$, with butane-1,2-diol: $\text{C}_2\text{H}_5\text{CHO} + \text{HCHO}$

2. $\text{HCHO} - 2\text{e}^- \rightarrow \text{HCOOH};$ $\text{HCOOH} - 2\text{e}^- \rightarrow \text{CO}_2;$

$\text{C}_2\text{H}_5\text{CHO} - 2\text{e}^- \rightarrow \text{C}_2\text{H}_5\text{COOH};$ $\text{Mn}^{+7} + 5\text{e}^- \rightarrow \text{Mn}^{2+};$

The complete reactions are:



The total mass of the mixture: $m_A = n_{\text{gly}}M_{\text{gly}} + n_{\text{but}}M_{\text{but}}$.

The number of mols of $1/5 \text{KMnO}_4$ spent for the oxidation of aldehyde groups:

$$n_{\text{ald}} = 4 \cdot 2n_{\text{gly}} \text{ (2 moles of } \text{CH}_2\text{O} \text{ from glycerol, } 4\text{e}^- \text{ each)} + 2n_{\text{gly}} \text{ (HCOOH from glycerol, } 2\text{e}^-) + 2n_{\text{but}} \text{ (C}_2\text{H}_5\text{CHO from butylene glycol, } 2\text{e}^-) + 4n_{\text{but}} \text{ (1 mol of } \text{CH}_2\text{O} \text{ from butylene glycol, } 4\text{e}^-) = 10n_{\text{gly}} + 6n_{\text{but}}.$$

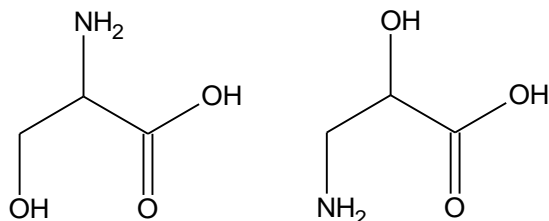
Solving these two simultaneous equations (with $M_{\text{gly}} = 92$ and $M_{\text{but}} = 90$) one gets:

$$n_{\text{but}} = 0.0101 \text{ mol, } n_{\text{gly}} = 0.0079 \text{ mol.}$$

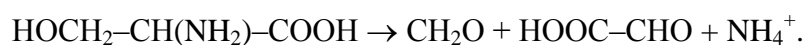
3. The carboxylic group could either exist in the original compound **B** (a) or be formed during the oxidation (b).

(a). Let us suppose a minimum amount of oxygen-containing groups in **B**: 0.001 mol of $-\text{COOH}$ (45 mg) and two hydroxyl groups ($\equiv\text{C}-\text{OH}$ $29 \text{ g/mol} \cdot 0.002 \text{ mol} = 58 \text{ mg}$); then, 0.001 mol of nitrogen should be also present (14 mg); this gives the total mass of 117 mg, which is even higher than the mass of **B** (105 mg). Therefore, part of oxygen originates from the oxidant or water as a result of the substitution of amine nitrogen atom (which has transformed into the ammonium ion) with oxygen (so, amino groups in Malaprade reaction behave as hydroxyl ones). In case **B** contains one oxygen atom less, we will get: 1 mmol of $\equiv\text{C}-\text{OH}$ groups (29 mg) + 1 mmol of CHNH_2 (29 mg) + 1 mmol of COOH (45 mg) = 103 mg. To attain the required 105 mg, the following groups can be suggested: CHOH (30 mg), CH_2NH_2 (30 mg) and COOH (45 mg), which brings us to the empirical formula of **B**: $\text{C}_3\text{H}_7\text{NO}_3$. Remembering that nitrogen must be in the form of an amino group, no ether oxygens are permitted and an acid is formed as the result of

oxidation (this can only be HCOOH, and to obtain that, a $-\text{CH}(\text{OH})-$ or $-\text{CH}(\text{NH}_2)-$ group must be present), we can make up a list of possible structures of **B**. In case the carboxylic group was present in the original compound (a), that will be 2-amino-3-hydroxypropionic acid or 3-amino-2-hydroxypropionic acid:

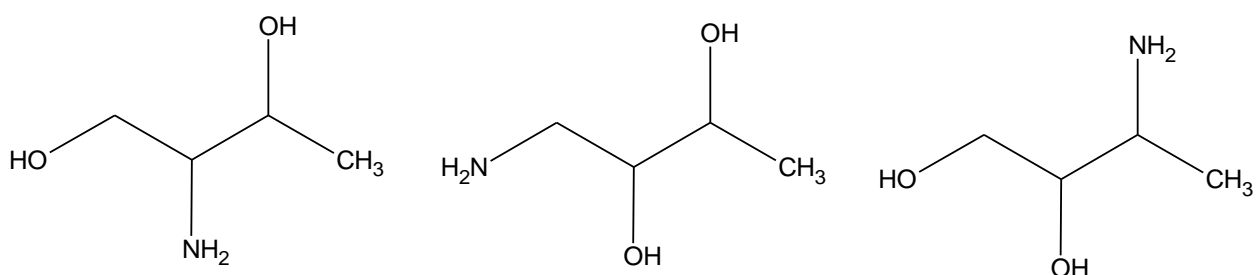


Scheme of their oxidation with periodate:

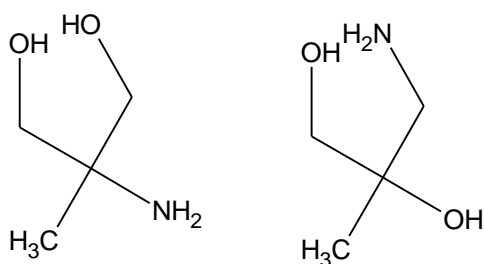


Glyoxylic acid $\text{HOOC}-\text{CHO}$ is oxidized by KMnO_4 to oxalic acid and then to CO_2 (4 mmol equivalents of KMnO_4); together with formaldehyde (4 mmol eq.) it makes up the required 8 mmol eq. to be spent for the titration.

(b). In case compound **B** is originally lacking carboxylic group, the molecular weight of 105 corresponds to compounds containing 1 oxygen atom less and 1 extra carbon atom ($\text{C}_4\text{H}_{11}\text{NO}_2$), i.e. *butane* derivatives containing 1 amino and 2 hydroxyl groups. (*Propanes* with 3 hydroxyl groups and 1 amino group will give molecular weights of 107.) If the butane moiety is unbranched and all three groups (two OH and the NH_2) are vicinal:

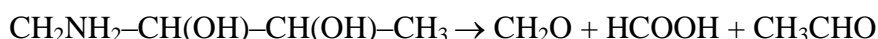


then periodate oxidation yields HCHO , HCOOH and CH_3CHO ; the two isobutane derivatives

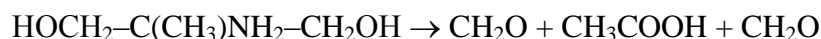


both result in 1 mol of CH_3COOH and 2 moles of HCHO , while all these butanes meet the task requirements, as they require 8 mmol equivalents of KMnO_4 for their oxidation. Compound $\text{HC}(\text{CH}_2\text{OH})_2\text{CH}_2\text{NH}_2$ is not oxidized with periodate. If OH and NH_2 groups are not vicinal, formaldehyde and an aldehyde are formed, but no necessary carboxylic acid is produced. If **B** contains a $\text{C}=\text{O}$ group (for instance, $\text{O}=\text{CH}-\text{CH}(\text{OH})-\text{CH}(\text{NH}_2)-\text{CH}_3$), its formula is $\text{C}_4\text{H}_9\text{NO}_2$ (molecular weight 103), which is not consistent with the problem conditions.

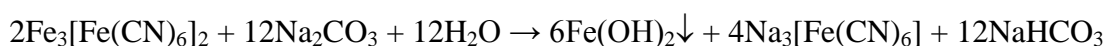
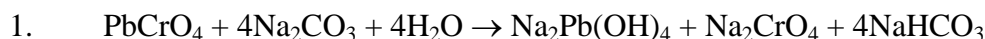
Scheme of periodate oxidation for the linear butane derivatives:



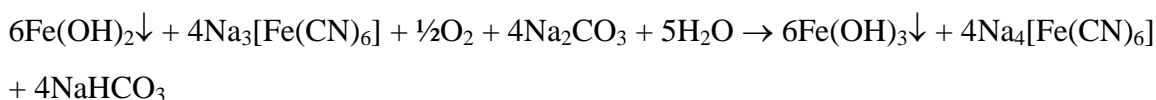
For the branched butanes:



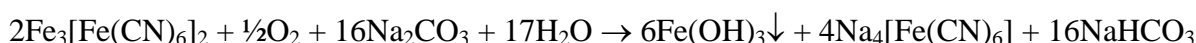
Problem 17. Analysis of Chrome Green



and then

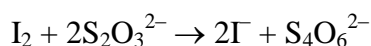
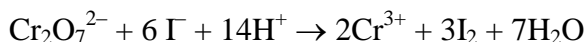


Totally:



Ferric hydroxide is left on the filter.

2. Direct oxidation of thiosulfate with dichromate is not stoichiometric. The reactions normally used are:



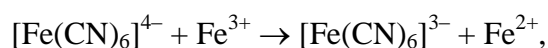
3. If reaction B is induced by reaction A, it implies that reaction A produces some intermediates active with the components of reaction B. In our case, the reduction of Cr(VI) occurs via the formation of intermediate oxidation states of chromium, predominantly Cr(V) species. (At the same time, the oxidation of I^- to I^0 may not require any iodine-containing intermediates.) A reasonable reaction scheme is as follows:



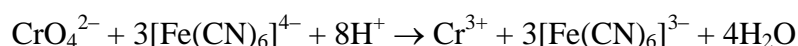
As a result of oxygen involvement, a higher amount of free iodine is obtained, which results in a greater amount of $\text{Na}_2\text{S}_2\text{O}_3$ titrant spent and lower apparent concentration determined.

4. The amount of chromium is found as follows: $3n_{\text{Cr}} = n_{\text{thios}} = 0.0485 \text{ M} \cdot 5.01 \text{ mL} = 0.2430 \text{ mmol}$ ($n_{\text{Cr}} = 0.081 \text{ mmol}$). This corresponds to 26.2 mg of PbCrO_4 ($M = 323.2 \text{ g/mol}$) in the aliquot, or 131 mg totally.

5. Owing to the fast redox equilibrium:



a certain amount of $[\text{Fe}(\text{CN})_6]^{4-}$ will be present in the system. The side reaction



produces an amount of $[\text{Fe}(\text{CN})_6]^{3-}$ equivalent to CrO_4^{2-} reacted. At the titration stage that hexacyanoferrate(III) would also liberate free iodine; hence, the side process can be neglected.

6. Acidification of the sample: $\text{CrO}_4^{2-} + 3[\text{Fe}(\text{CN})_6]^{4-} + 8\text{H}^+ \rightarrow \text{Cr}^{3+} + 3[\text{Fe}(\text{CN})_6]^{3-} + 4\text{H}_2\text{O}$

Titration: $\text{MnO}_4^- + 5[\text{Fe}(\text{CN})_6]^{4-} + 8\text{H}^+ \rightarrow \text{Mn}^{2+} + 5[\text{Fe}(\text{CN})_6]^{3-} + 4\text{H}_2\text{O}$

Hexacyanoferrates may be partially precipitated in the form of Pb^{2+} salts but this does not preclude them from the redox reactions.

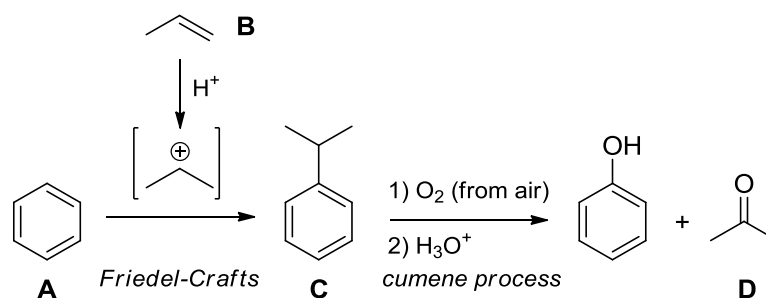
7. On acidification of the 2nd aliquot, chromium is reduced by $[\text{Fe}(\text{CN})_6]^{4-}$ (see i. 5). Then permanganate is spent for the oxidation of $[\text{Fe}(\text{CN})_6]^{4-}$, namely, the amount of $[\text{Fe}(\text{CN})_6]^{4-}$ added plus the amount contained initially in the sample less the amount spent for the reduction of Cr(VI): $5n_{\text{MnO}_4} = n_{\text{Fe added}} + n_{\text{Fe from sample}} - 3n_{\text{Cr}}$. From this equation we can find $n_{\text{Fe from sample}} = 5n_{\text{MnO}_4} - n_{\text{Fe added}} + 3n_{\text{Cr}} = 5 \cdot 0.00500 \cdot 2.85 - 10 \cdot 0.0300 + 0.2430 = 0.07125 - 0.3000 + 0.2430 = 0.0142 \text{ mmol}$ $[\text{Fe}(\text{CN})_6]^{4-}$. One mol of $[\text{Fe}(\text{CN})_6]^{4-}$ results from 0.5 mol of $\text{Fe}_3[\text{Fe}(\text{CN})_6]_2$ (see solution to question 1), therefore, the answer is 4.21 mg of $\text{Fe}_{3/2}[\text{Fe}(\text{CN})_6]$ ($M = 295.6 \text{ g/mol}$) in the aliquot, or the total amount of 21.1 mg.

Problem 18. Chemistry of phenol

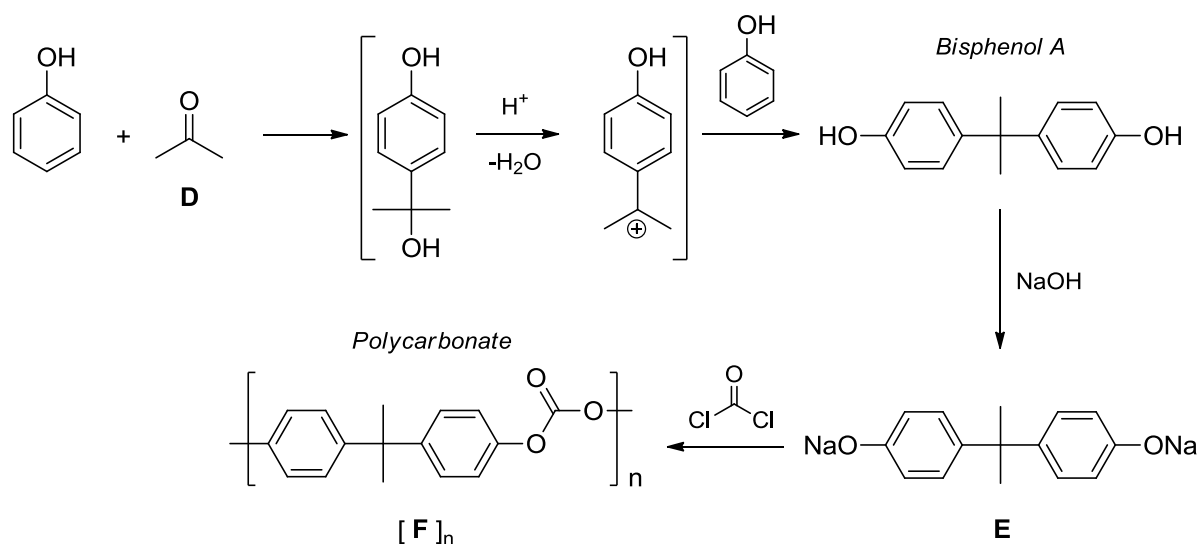
1-2. Structures of benzene **A** and propene **B** are commonly known.

The interaction between **A** and **B** under acidic condition proceeds as Friedel-Crafts alkylation of the aromatic ring with the thermodynamically more stable secondary propyl carbocation as an electrophile. Being a product of the interaction of equal amounts of **A** and **B**, **C** turns out to be

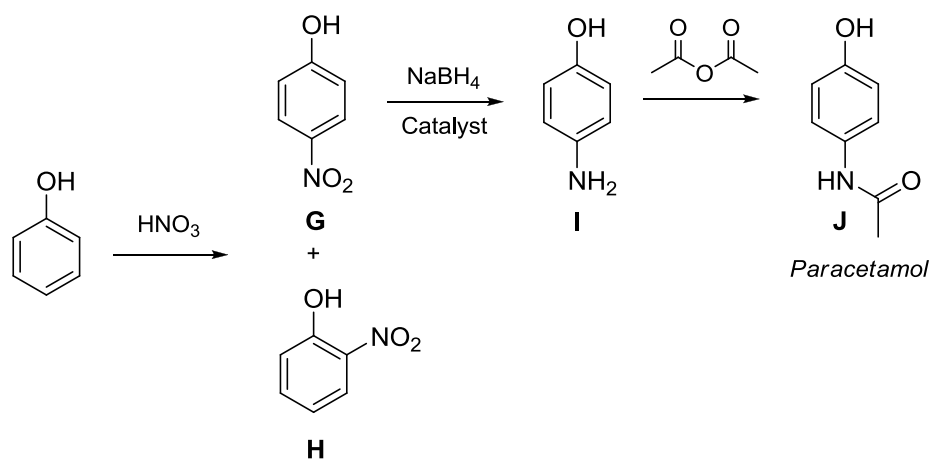
isopropylbenzene, i.e. cumene. Oxidation of **C** with subsequent acidification leads to phenol and acetone **D**. This classical industrial procedure is known as *cumene process*.



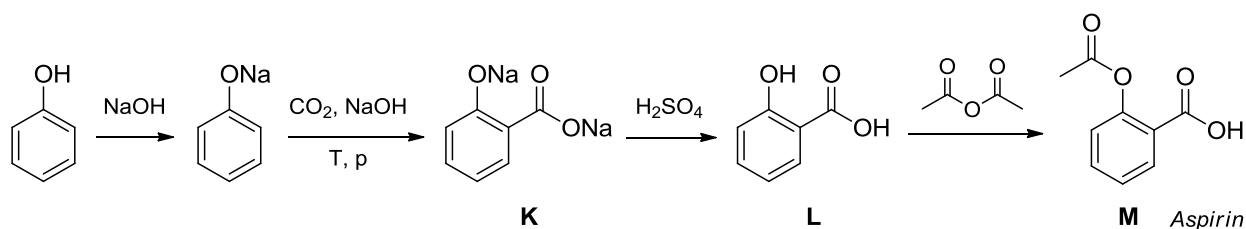
The structure of **D** can also be easily determined from that of *bisphenol A*, which is formed as a result of two consecutive Friedel-Crafts alkylations of phenol. Treatment of *bisphenol A* with NaOH leads to disodium bis-phenolate **E**, which gives *polycarbonate* with the monomeric unit **F** as a result of the reaction with phosgene.



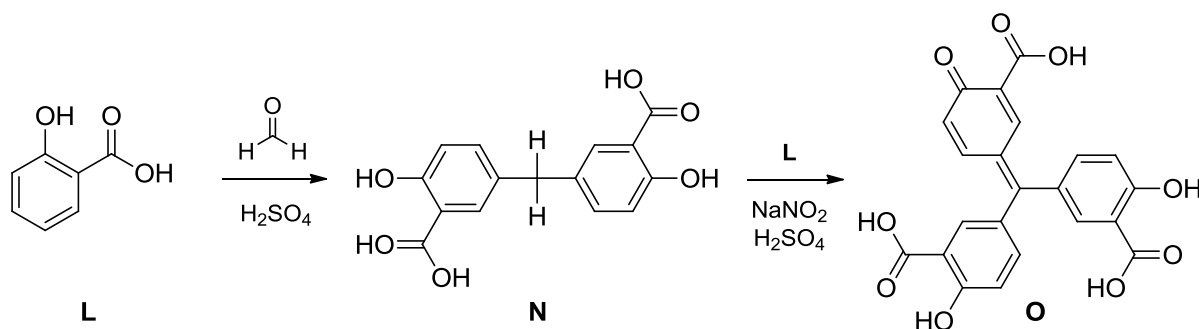
The reaction of phenol with diluted nitric acid proceeds as a mononitration resulting in isomeric nitrophenols **G** and **H**. Due to the activation effect of OH-group in phenol, electrophilic substitution can occur in *ortho*- and *para*-positions of phenol. **G** is *para*-nitrophenol (two planes of symmetry), whereas **H** is *ortho*-nitrophenol (only one plane of symmetry). Further reduction of NO₂-group in *para*-nitrophenol **G** results in *para*-aminophenol **I**. Due to its higher nucleophilicity, NH₂-group (rather than OH-group) in **I** is acetylated with acetic anhydride giving *paracetamol* **J**.



The reaction of phenol with CO_2 in the presence of NaOH proceeds through intermediate formation of sodium phenolate, which interacts with CO_2 under heating and high pressure (Kolbe-Schmitt reaction) to give disodium salicylate **K**. Acidification of **K** with two equivalents of an acid results in salicylic acid **L**, which provides *aspirin* **M** when acetylated with acetic anhydride.



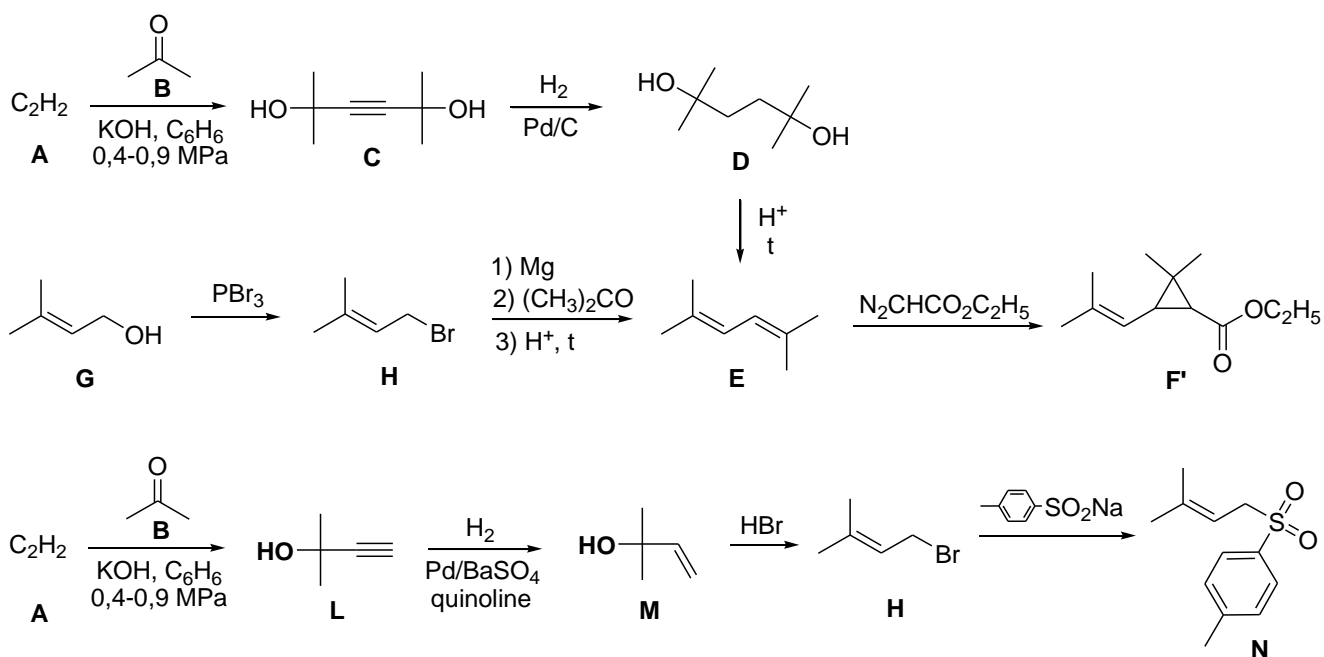
Aluminon synthesis is based on the same approach as previously considered for *bisphenol A*. The reaction of salicylic acid **L** with formaldehyde under acidic conditions affords **N**, which is an analogue of *bisphenol A*. Addition of another equivalent of salicylic acid **L** under oxidative conditions ($\text{NaNO}_2/\text{H}_2\text{SO}_4$) gives the tri-acid **O**, which is a direct precursor of *Aluminon*. Thus, the structure of **O** can be derived from that of *Aluminon*.



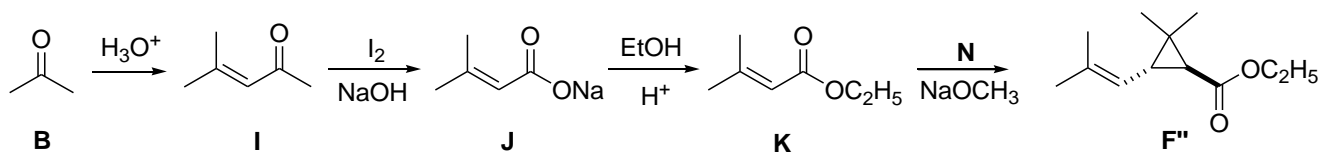
Problem 19. Chrysanthemic acid

1. Chrysanthemic acid is formed as a result of hydrolysis of its ethyl ester, **F**, which, in turn, is obtained by cyclopropanation of **E** with diazoacetic ester. Therefore, **E** is 2,5-dimethylhex-2,4-diene with molecular formula C_8H_{14} . This conclusion is supported by the molecular formula of **D**. Evidently, transformation of **D** to **E** is elimination of two water molecules.

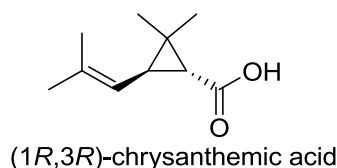
Eight carbon atoms of **D** originate from **A** and **B**. The other reaction between these compounds affords **L** containing 5 carbon atoms (**N** is formed from **H** and $C_7H_7O_2SNa$; the number of carbon atoms in **H** and **L** is the same). The provided information strongly suggests that **A** is acetylene (C_2H_2). Hence, **A** is composed of 2, and **B** should be composed of 3 carbon atoms. Reaction between **A** and **B** was disclosed by Favorskii in 1905 as that between acetylenes and carbonyl compounds. It means that **B** is either propionic aldehyde (C_2H_5CHO) or acetone (CH_3COCH_3). Accounting for the structure of **E**, **B** is acetone. **E** is also formed through the Grignard reaction of acetone with the corresponding $RMgBr$ followed by elimination of water. The structure of **H** can be unambiguously deduced from that of **E** – it is prenyl bromide. So, the natural alcohol is prenyl (3-methylbut-2-en-1-ol). **L** is formed from **A** and **B** under the same reaction conditions but when **A** to **B** ratio is of 1:1. Therefore, **L** is 2-methylbut-3-yn-2-ol. Its hydrogenation in the presence of Lindlar catalyst leads to the corresponding alkene **M**. Subsequent reaction with HBr affords prenyl bromide **H** *via* nucleophilic substitution with double bond migration. The reaction of **H** with sodium 4-toluenesulfinate results in the corresponding sulfone **N**.



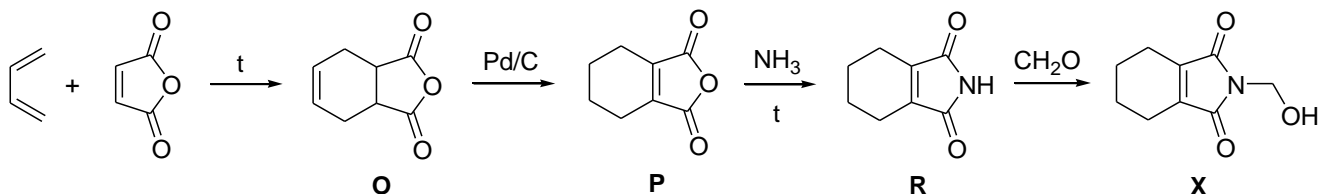
Finally, acid-catalyzed self-condensation of acetone yields 4-methylpent-3-en-2-one (mesityl oxide, **I**). Iodoformic reaction of **I** produces the salt of the corresponding acid **J** which is further transformed into ethyl ester **K**. The reaction of **K** with deprotonated sulfone **N** results in chrysanthemic acid ester **F''**.



2.

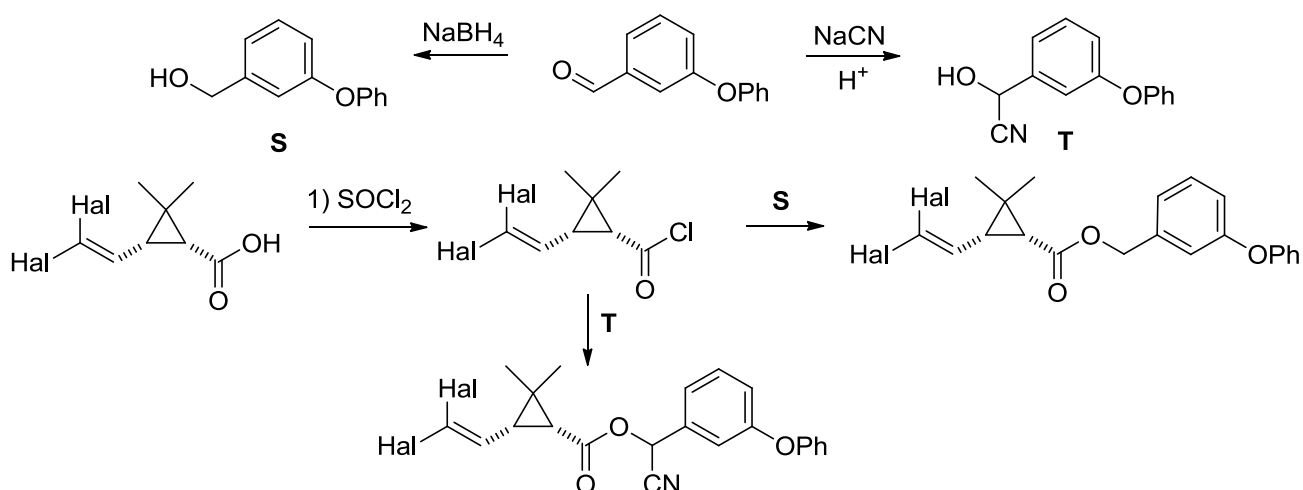


3. The first step is the Diels-Alder reaction. Compound **P** with tetrasubstituted double bond is the most stable isomer of **O** with the same carbocyclic skeleton. Heating of **P** with ammonia leads to imide **R**, which further reacts with CH_2O giving the target alcohol **X**.



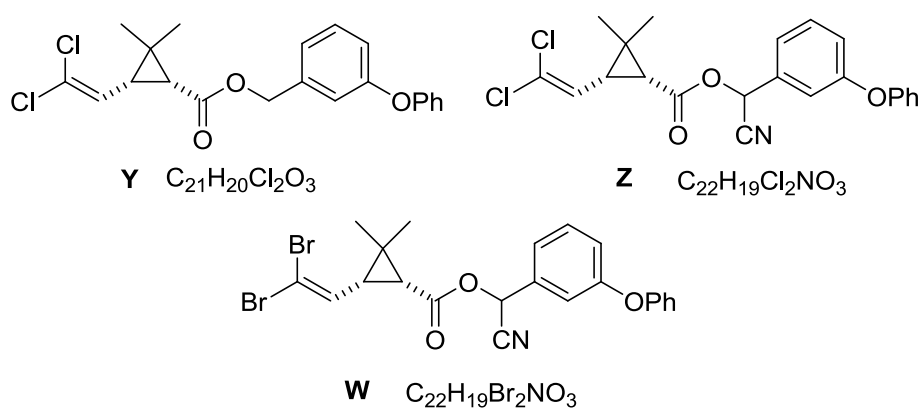
4. Amides and hydrazides do not easily form esters in reaction with alcohols. Oppositely, anhydrides are appropriate reagents for the ester synthesis. Moreover, re-esterification of methyl or ethyl esters with high-boiling alcohols is well-known. These reactions are efficient due to methanol (ethanol) removal from the reaction mixture via distillation (Le Chatelier's principle).

5. Reduction of 3-phenoxybenzaldehyde yields the corresponding benzyl alcohol **S**, while its reaction with NaCN produces cyanohydrin **T**. Reaction of **S** or **T** with 2,2-(dihalovinyl)-3,3-dimethylcyclopropane-1-carbonyl chloride affords the target pyrethroids.



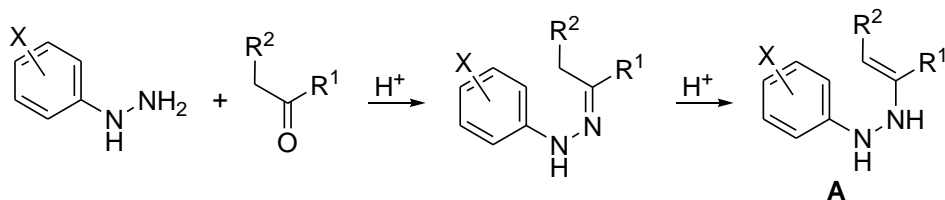
Molecular formulae of the esters formed from alcohol **S** and **T** are $\text{C}_{21}\text{H}_{20}\text{Hal}_2\text{O}_3$ and $\text{C}_{22}\text{H}_{19}\text{Hal}_2\text{NO}_3$, respectively. Halide content in the esters is $2M_{\text{Hal}}/(2M_{\text{Hal}} + 320)$ and $2M_{\text{Hal}}/(2M_{\text{Hal}} + 345)$, respectively. Calculation of halide content in these compounds allows unambiguously deciding on the structures of the pyrethroids.

Content of Hal, %	Using exact atomic mass				Using approximate atomic mass			
	F	Cl	Br	I	F	Cl	Br	I
Ester of S	10.60	18.12	33.28	44.20	10.61	18.16	33.33	44.25
Ester of T	9.91	17.03	31.63	42.36	9.92	17.07	31.68	42.40



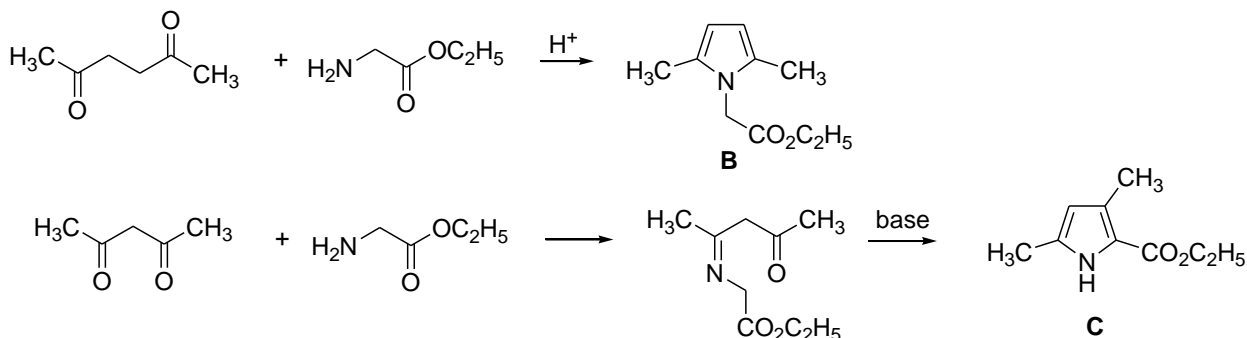
Problem 20. Heterocycles

1. Interaction of ketone with arylhydrazine affords hydrazone, which isomerizes into enhydrazone under acidic conditions.

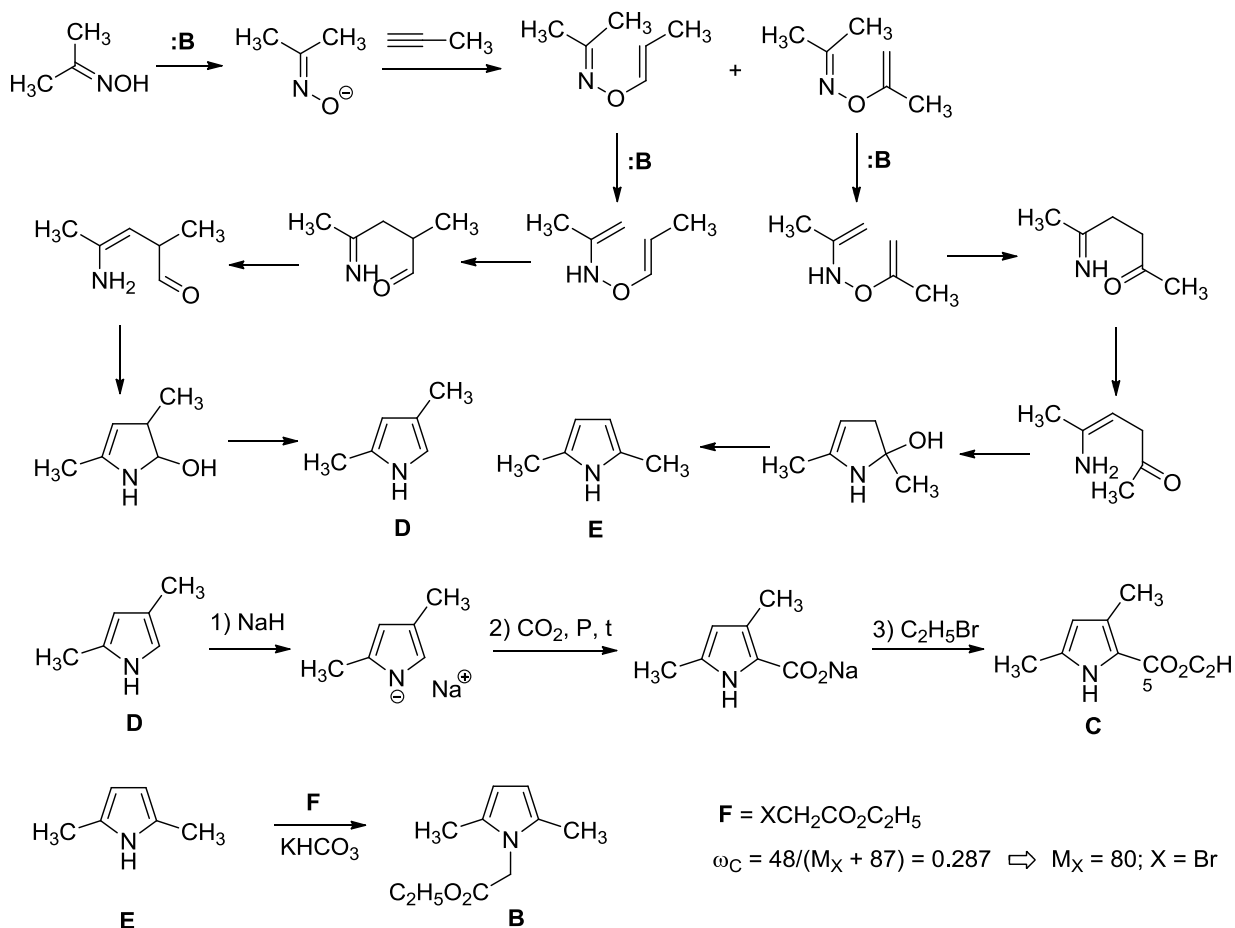


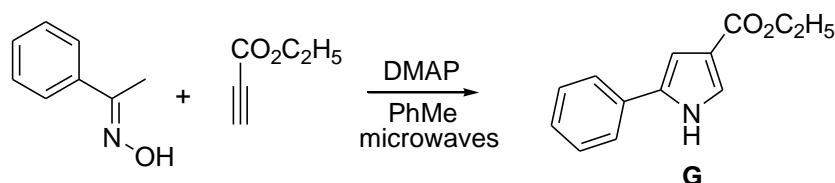
2. Mechanism *a* includes the electrophilic attack of aminoalkyl cation at the aromatic moiety. This attack is very susceptible to electron properties of the aryl group (attack on the electron-enriched aryl ring is much more efficient than that on the electron-depleted arene). The same is expected for mechanism *c*. Only the sigmatropic shift has no significant dependence on substituents in both arenes. Therefore, I. Grandberg proved that the Fischer indole synthesis proceeds via mechanism *b*.

3. Reactions are started by interaction of amine with the carbonyl group furnishing imine. To complete pyrrole moiety formation, monoimine of hexane-2,5-dione should isomerize into the enamine followed by an attack of the amine group on the second C=O group. Formally, imine of pentane-2,4-dione can form the pyrrole ring in two ways. First, it is the interaction of the nitrogen atom with the methyl group. However, the methyl group itself is unreactive towards nucleophiles. Keto-enol equilibrium with involvement of the methyl group in this compound is less probable than that with CH₂-fragment. Even if the equilibrium was true, enol is a nucleophile and cannot react with nucleophilic nitrogen atom. Therefore, the second possibility should be considered, namely, the reaction of the second carbonyl with CH₂ bound to N atom. This reaction is quite probable as CH₂-group is also connected with the electron-withdrawing ester group and can be deprotonated by a base as shown below.

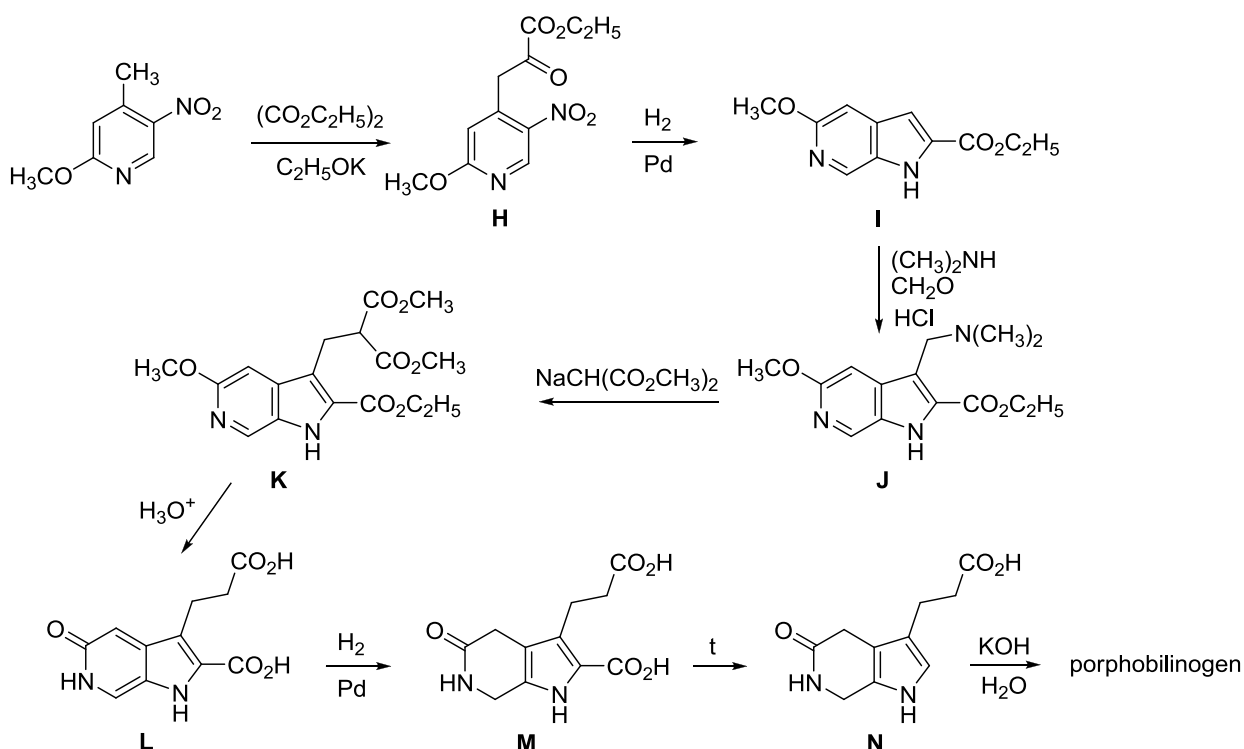


4-5. Two products are formed in the reaction of propyne, and only one product in the case of the alkyne bearing an electron-withdrawing ester group. This allows supposing a nucleophilic attack of a certain intermediate on the alkyne moiety. A base generates a nucleophilic agent from acetone oxime. Again, two ways of deprotonation are possible: *O*-deprotonation and *C*-deprotonation. However, oxime enolate, if formed, should add to alkyne with the formation of hex-4-en-2-one oxime. There is no possibility for the transformation of this oxime into pyrrole ring. The alternative possibility is *O*-deprotonation and nucleophilic addition of the oximate ion to alkyne furnishing *O*-alkenyl acetone oxime. Formation of the C-C bond between the methyl group of acetone and the β -carbon atom of the alkenyl group is needed to complete the pyrrole ring synthesis. At the first glance, such transformation is impossible. However, this system is very similar to the *N*-aryl-*N'*-alkenyl moiety which undergoes the 3,3-sigmatropic rearrangement in the Fischer indole synthesis. Indeed, isomerization of *O*-alkenyl acetone oxime into *O*-alkenyl-*N*-alkenyl derivative creates the fragment required for the 3,3-sigmatropic shift. So, formation of the pyrrole ring giving 2,4-dimethylpyrrole and 2,5-dimethylpyrrole is analogous to that of indole in the Fischer synthesis. The former compound is transformed into **C** via *N*-deprotonation followed by the Kolbe-Schmitt carboxylation and ester formation. To provide **B**, **E** should be *N*-alkylated with ethyl haloacetate. Halogen can be determined from the carbon content in the alkylation reagent.



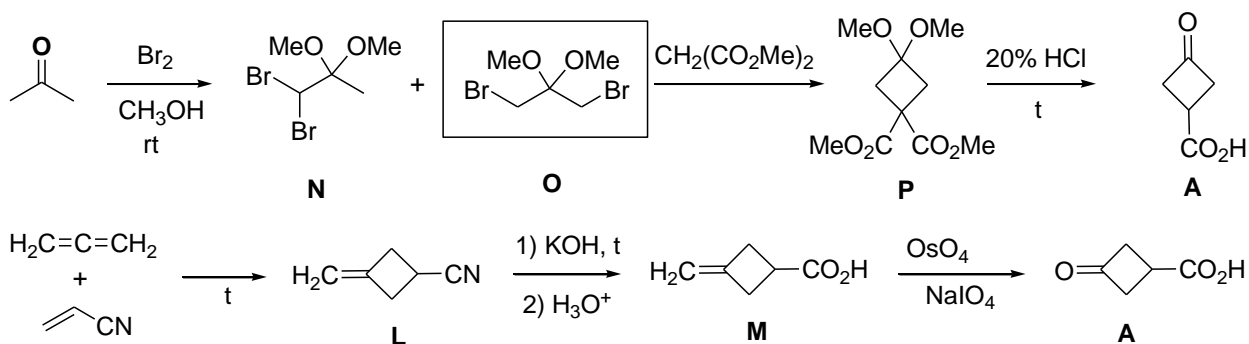


6. Methyl group in the starting compound is very acidic due to activation by both *ortho*-nitro group and *para*-nitrogen atom of pyridine. So, it can be easily deprotonated to further react with diethyl oxalate providing the corresponding ketoester **H**. Reduction of the nitro group gives aniline. Condensation of the amino group with the appropriately located ketone moiety affords the 6-azaindole derivative **I** ($C_{11}H_{12}N_2O_3$). Aminomethylation of this indole furnishes the gramine derivative **J** which undergoes nucleophilic substitution with sodium dimethylmalonate producing **K**. Its hydrolysis results in a compound with the molecular formula of $C_{11}H_{10}N_2O_5$. It means that: a) hydrolysis of the malonate fragment is accompanied by decarboxylation; b) the ester moiety at the C2 position of the indole is hydrolyzed too. However, even if so, the molecular formula should be $C_{12}H_{14}N_2O_5$. The difference equals to CH_2 . Hydrolysis of OCH_3 -group in *ortho*-position to pyridine nitrogen is the only possibility. Indeed, hydrogenation of this pyrrolopyridone yields **M**. Its decarboxylation and hydrolysis of the amide function finally leads to porphobilinogen.



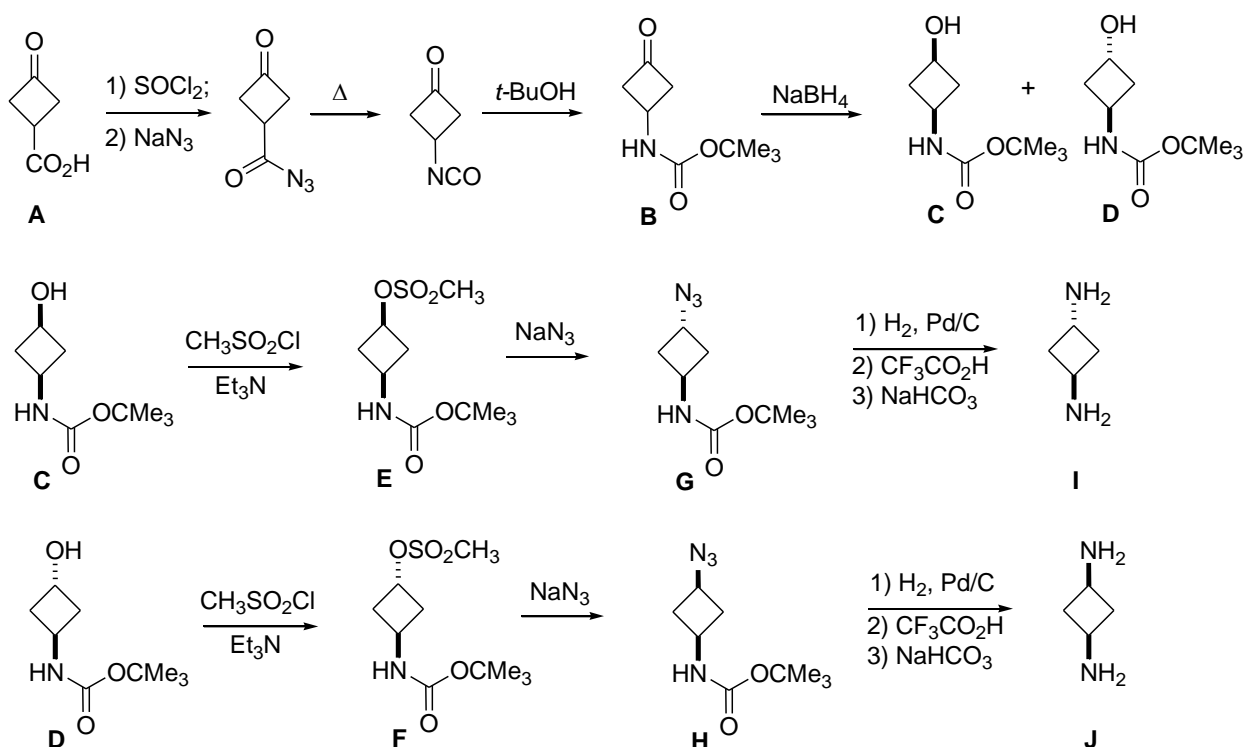
Problem 21. Cyclobutanes

1. Hydrocarbon **K** consists of 90% C and 10% H. Its simplest formula is $(C_3H_4)_n$, and it has a single type of H atoms. So, it is allene, $H_2C=C=CH_2$. **A** has 5 carbon atoms. Therefore, allene reacted with $CH_2=CHCN in a ratio of 1:1 and lost one carbon atom during the following steps. Various products can be supposed for this reaction, however, it is known that allene is prone to undergo cycloaddition as 2π -component. Acrylonitrile undergoes cycloaddition as 2π -component too. So, the product should be a cyclobutane derivative, which is consistent with the next scheme. The C and H content in **N** and **O** provides for their molecular formula ($C_5H_{10}Br_2O_2$). In this respect, two sub-processes should proceed: a) acetone is doubly brominated; b) ketone is transformed into ketal in the reaction with methanol catalyzed by HBr evolved in the bromination step. Two dibromoacetones (1,1- and 1,3-) can be formed. Reaction of the latter with dimethyl malonate affords the corresponding cyclobutane derivative. Its treatment with hydrochloric acid leads to the hydrolysis of ketal into ketone and esters into an acid. So, the product should be 3-oxocyclobutane-1,1-dicarboxylic acid. However, its formula is $C_6H_6O_5$. Therefore, hydrolysis is also accompanied by decarboxylation of the malonic acid moiety. So, **A** is 3-oxocyclobutanecarboxylic acid. Accounting for it, **L** is the product of [2+2] cycloaddition, *i.e.*, 1-cyano-3-methylenecyclobutane. Its hydrolysis followed by oxidation of C=C double bond produces **A**. Finally, the schemes for preparation of **A** are as follows:$

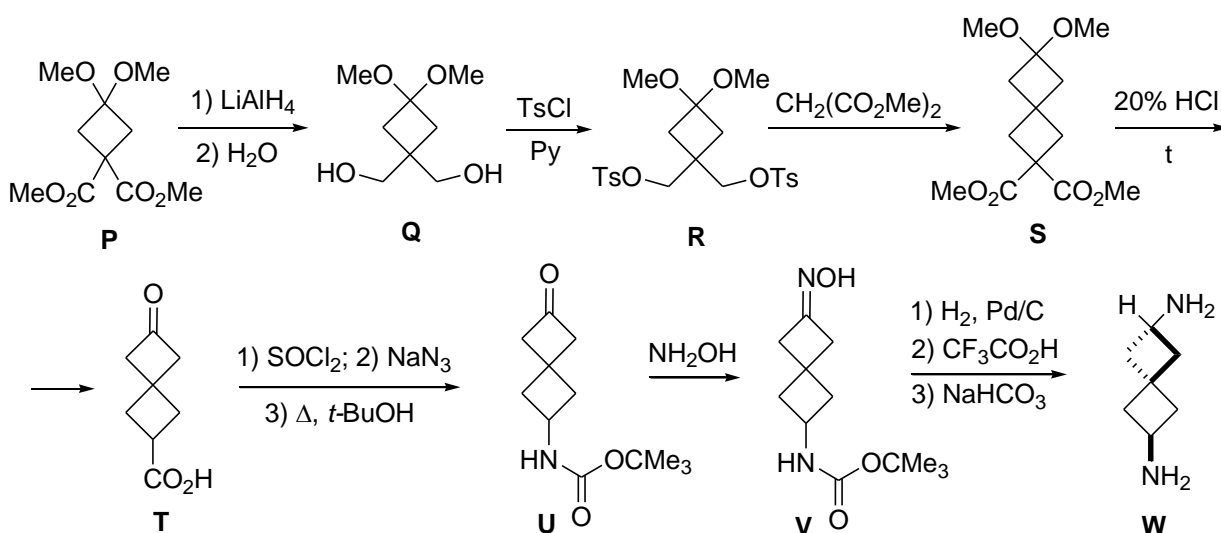


Reaction of **A** with $SOCl_2$ furnishes acyl chloride, which reacts with NaN_3 affording acyl azide. Heating of $RCON_3$ produces isocyanate $R-N=C=O$, which immediately reacts with *t*-BuOH giving rise to *N*-Boc-protected 3-aminocyclobutanone **B**. Reduction of keto group with $NaBH_4$ leads to *cis*- and *trans*-isomers of the corresponding aminocyclobutanol. Further reaction with CH_3SO_2Cl produces mesylates, which undergo S_N2 displacement with NaN_3 affording aminoazides. Reduction of azido group and deprotection of amine furnishes *cis*- and *trans*-isomers of 1,3-diaminocyclobutane. Therefore, **J** is *cis*-1,3-diaminocyclobutane (two planes of symmetry), and **I** is *trans*-isomer (one plane of symmetry). Similarly, **G** is *trans*-, and **H** is *cis*-

isomer. As the S_N2 reaction proceeds with inversion of the configuration, compound **E** (leading to **G**) is *cis*-, and **F** is *trans*-isomer.

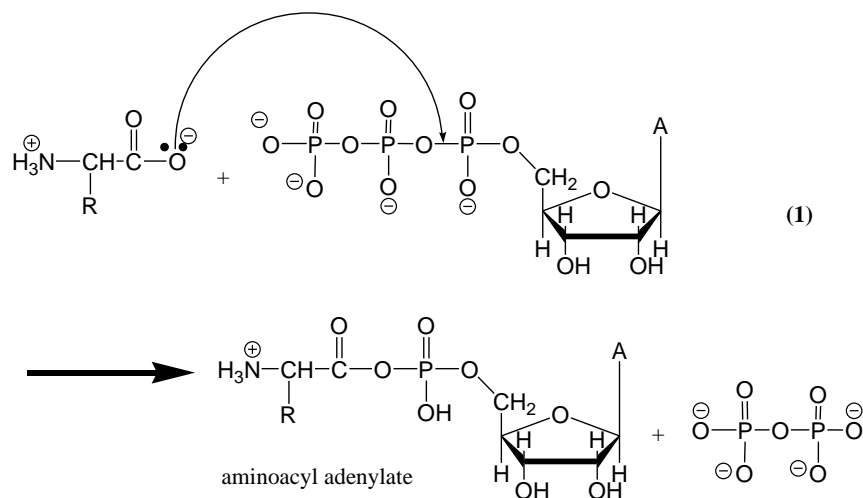
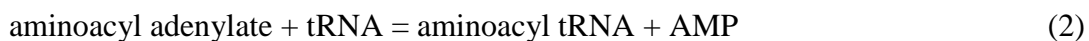
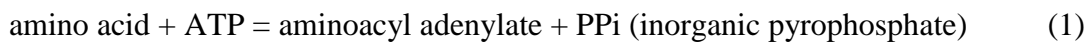


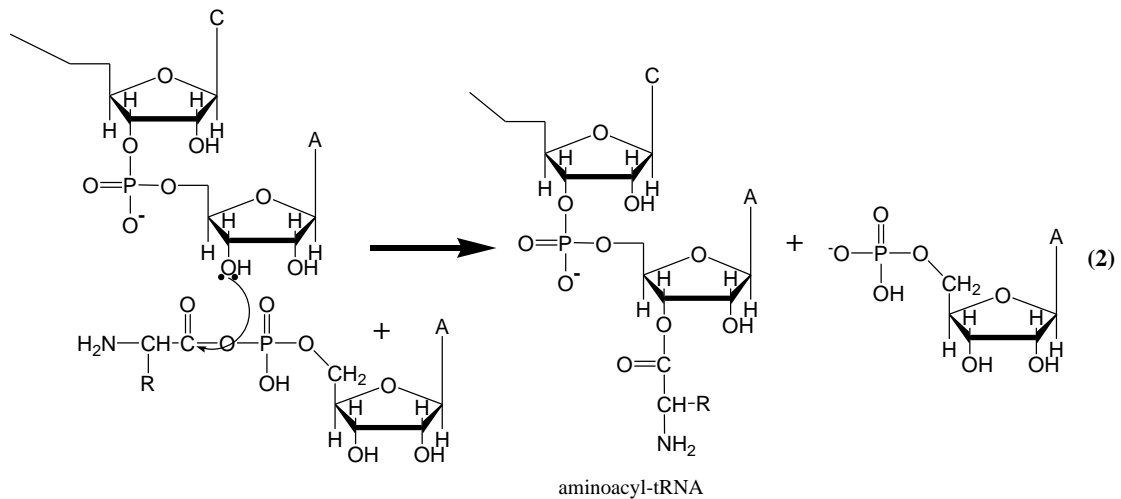
2-3. Reduction of **P** with LiAlH_4 gives the corresponding diol **Q**, which is transformed into ditosylate **R**. Reaction of **R** with dimethyl malonate leads to formation of the second cyclobutane ring (**S**). Hydrolysis of **S** proceeds similarly to that of **P**, *i.e.*, it produces ketoacid **T**. Further transformations are also similar to those in the first scheme and produce spiro[3.3]heptane-2,6-diamine **W**. This compound has no plane or center of symmetry. It is chiral due to axial chirality (similarly to 1,3-disubstituted allenes), thus, it can be resolved into two enantiomers.



Problem 22. Introduction to translation

1. There are $4^3=64$ different three-nucleotide combinations of 4 nucleotides. Only 61 codons encode amino acids added to the growing polypeptide chain. 3 remaining combinations are STOP codons determining termination of the translation process.
2. No, because of redundancy of the genetic code: most amino acids are encoded by several codons.
3. Leucine is encoded by 6 different codons, thus it is delivered to a ribosome by 6 different tRNAs. Being encoded by only 1 codon, methionine is transported by a sole tRNA. In some organisms the latter codon is also responsible for the translation start, encoding the N-terminal amino acid N-formylmethionine. Still, methionine and N-formylmethionine are transported by different tRNAs.
4. The equations of consecutive reactions are:





Thus, the carboxylic group of the amino acid reacts with 3'-OH group of its tRNA.

5. a) Met-Asp-His-Ala-Ile-Asn-Val-Val-Gly-Trp-Ser-Val-Asp-Thr-Leu-Asp-Asp-Gly-Thr-Glu-Ala or fMet-Asp-His-Ala-Ile-Asn-Val-Val-Gly-Trp-Ser-Val-Asp-Thr-Leu-Asp-Asp-Gly-Thr-Glu-Ala, depending on the biosynthesizing species (Eukaryotes, Prokaryotes, or Archaea).
- b) The third amino acid is tyrosine, and the last one is valine. All the rest positions are the same.
- c) The N-terminal amino acid is leucine. All the rest positions are the same. It should be noted that the translation in bacteria would not start without the START codon.
- d) The last but one codon is changed into STOP codon, which will result in the oligopeptide shorter by 2 amino acid residues than that in i. 5a.

6. AUG-GAU/C-GUN-AAU/C-CAU/C-CCN-GAA/G-UAU/C-GGN-AAA/G

7. The protein consists of 51000/110 \approx 464 amino acid residues.

Hence, it is encoded by the mRNA containing 464*3+3=1395 nucleotide residues including the STOP codon.

The length of mRNA is 1395*0.34=474.3 \approx 474 nm.

The time needed for biosynthesis of the protein is:

1395/20=69.7 \approx 70 s, that is a bit more than one minute.

8. Taking into account that the A:C ratio is 1:5, the probability of finding A and C at any position is 1/6 and 5/6, respectively. Thus, the probability of finding certain codons is:

$$AAA = (1/6)^3 = 1/216$$

$$CCC = (5/6)^3 = 125/216$$

$$AAC = (1/6)^2 * 5/6 = 5/216$$

$$CCA = (5/6)^2 * 1/6 = 25/216$$

$$ACA = 1/6 * 5/6 * 1/6 = 5/216$$

$$CAC = 5/6 * 1/6 * 5/6 = 25/216$$

$$ACC = 1/6 * (5/6)^2 = 25/216$$

$$CAA = 5/6 * (1/6)^2 = 5/216$$

Using the table of genetic code one gets: Lys:Asn:Thr:Pro:His:Gln=1:5:30:150:25:5

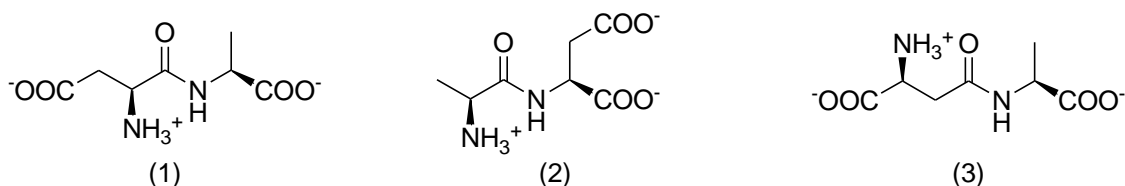
9. Anticodon has no influence on the CCA3' terminus. Thus, the mutant tRNA will add tyrosine to the positions where serine was initially expected with respect to mRNA sequence. This may lead to improper folding of the protein and total or partial loss of its functional activity.
10. Glu is encoded by GAA and GAG, and His by CAU and CAC. Two substitutions (of the 1st and 3rd residues) are needed to make this mutation true, which is quite improbable. Single residue mutations occur much more frequently, and Glu to Gln mutation can serve as an example (together with many other mutations of this type).

Problem 23. Intriguing translation

1. If **X** is an acyclic dipeptide, **A** and **B** should be composed of 28 atoms in total (25+3 for H₂O). In the case of an acyclic tripeptide similar calculations lead to 31 atoms in total (25+6 for 2H₂O), this being true for any of two combinations of residues in the tripeptide (**A+2B** or **2A+B**). Analysis of the structures of all proteinogenic amino acids given in Wikipedia suggests glycine as one with the minimal number of atoms (10) followed by alanine formed by 13 atoms. Thus, the tripeptide with the minimal number of atoms is composed of 2 glycines and 1 alanine. The total number of atoms (33) in the amino acids forming this tripeptide exceeds 31, which makes any tripeptide as well as large peptides impossible. Therefore, **X** is a dipeptide.
2. Both α -carboxylic and α -amino groups exist mostly in the ionic forms at pH 4.7. Ionization state of the side groups at the given pH value should be determined individually based on their pK_a values as reported in Wikipedia. One should leave into consideration only amino acids with the number of atoms less than 19 (28-10=18; this is maximal possible value in case one of two amino acids is glycine). Surprisingly, the data found on different Wikipedia pages lead to contradictory results. According to the former weblink (http://en.wikipedia.org/wiki/Proteinogenic_amino_acid), only ten amino acids can be further considered. These are:

Amino acid	Prevailing form at pH 4.7 (according to Wikipedia)	Number of atoms	Amino acid	Prevailing form at pH 4.7 (according to Wikipedia)	Number of atoms
Gly		10	Asp		15
Ala		13	Pro		17
Cys		14	Thr		17
Sec		14	Asn		18
Ser		14	Glu		18

The listed amino acids provide for the following dipeptides (without regard to N- and C-termini): Ser-Cys, Ser-Sec, Cys-Sec, Gly-Asn, Gly-Glu и Asp-Ala. Taking into account the residue positioning (N- or C-terminal), one gets two different dipeptides for each of 4 former pairs, and 3 dipeptides for each 2 latter pairs (note that β -carboxyl group of Asp and γ -carboxyl group of Glu can be also involved in peptide bond formation; see an example below).



Thus, the total number of dipeptides equals to 14. However, serious caution is needed when using Wikipedia, since it is a collection of the user-generated content. Note that pKa values of some groups are absolutely incorrect (section “Side Chain Properties”). In particular, the side group of Asn is absolutely non-protonated at pH 4.7. Finally, the correct number of individual peptides is 12 (excluding Gly-Asn and Asn-Gly).

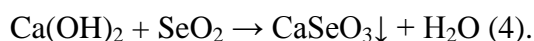
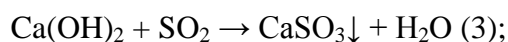
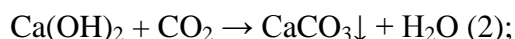
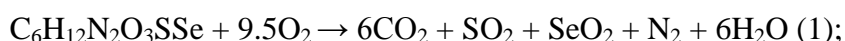
Screenshot of the webpage http://en.wikipedia.org/wiki/Proteinogenic_amino_acid dated 20.10.2012 is given below. Being irresponsible of these mistakes, authors of the problem promise to correct the data after publishing the Solutions to Preparatory problems.

Amino Acid	Short	Abbrev.	Side chain	Hydrophobic	pKa	Polar	pH	Small	Tiny	Aromatic or Aliphatic	van der Waals volume
Alanine	A	Ala	-CH ₃	X	-	-	-	X	X	-	67
Cysteine	C	Cys	-CH ₂ SH	-	8.18	-	acidic	X	X	-	86
Aspartic acid	D	Asp	-CH ₂ COOH	-	3.90	X	acidic	X	-	-	91
Glutamic acid	E	Glu	-CH ₂ CH ₂ COOH	-	4.07	X	acidic	-	-	-	109
Phenylalanine	F	Phe	-CH ₂ C ₆ H ₅	X	-	-	-	-	-	Aromatic	135
Glycine	G	Gly	-H	X	-	-	-	X	X	-	48
Histidine	H	His	-CH ₂ -C ₃ H ₃ N ₂	-	6.04	X	weak basic	-	-	Aromatic	118
Isoleucine	I	Ile	-CH(CH ₃)CH ₂ CH ₃	X	-	-	-	-	-	Aliphatic	124
Lysine	K	Lys	-(CH ₂) ₄ NH ₂	-	10.54	X	basic	-	-	-	135
Leucine	L	Leu	-CH ₂ CH(CH ₃) ₂	X	-	-	-	-	-	Aliphatic	124
Methionine	M	Met	-CH ₂ CH ₂ SCH ₃	X	-	-	-	-	-	-	124
Asparagine	N	Asn	-CH ₂ CONH ₂	-	5.41	X	weak basic	X	-	-	96
Pyrolysine	O	Pyl	-(CH ₂) ₄ NHCOC ₄ H ₉ NH ₂	-	-	X	weak basic	-	-	-	
Proline	P	Pro	-CH ₂ CH ₂ CH ₂ -	X	-	-	-	X	-	-	90
Glutamine	Q	Gln	-CH ₂ CH ₂ CONH ₂	-	-	X	weak basic	-	-	-	114
Arginine	R	Arg	-(CH ₂) ₃ NH-C(NH) ₂ NH ₂	-	12.48	X	strongly basic	-	-	-	148
Serine	S	Ser	-CH ₂ OH	-	5.68	X	weak acidic	X	X	-	73
Threonine	T	Thr	-CH(OH)CH ₃	-	5.53	-	weak acidic	X	-	-	93
Selenocysteine	U	Sec	-CH ₂ SeH	-	5.73	-	acidic	X	X	-	
Valine	V	Val	-CH(CH ₃) ₂	X	-	-	-	X	-	Aliphatic	105
Tryptophan	W	Trp	-CH ₂ C ₈ H ₆ N	-	5.885	-	weak basic	-	-	Aromatic	163
Tyrosine	Y	Tyr	-CH ₂ -C ₆ H ₄ OH	-	10.46	X	weak acidic	-	-	Aromatic	141

Note: The pKa values of amino acids are typically slightly different when the amino acid is inside a protein. Protein pKa calculations are sometimes used to calculate the change in the pKa value of an

At the same time, the pK_a values found at the other webpage (http://en.wikipedia.org/wiki/Amino_acid) are correct.

3. One should analyze all five variants of dipeptides (with no regard to N- and C-termini) from i. 2 by calculating masses of corresponding precipitates. Typical procedure is given below for the correct answer (Cys-Sec):



Number of moles of dipeptide: $1.000 \text{ g} / 271.19 \text{ g/mol} = 3.687 \cdot 10^{-3} \text{ mol}$. Thus, the mass of precipitate is:

$$m(\text{precipitate}) = 3.687 \cdot 10^{-3} \text{ mol} * (6 * 100.09 + 120.14 + 167.04) \text{ g/mol} = 3.273 \text{ g}$$

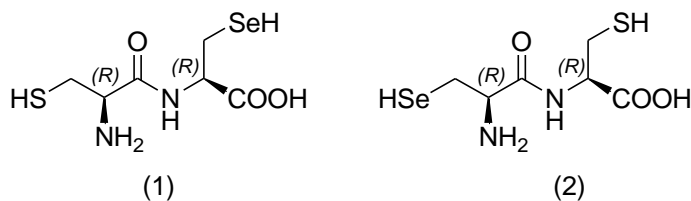
However, further calculations according to the equations of chemical reactions of precipitate dissolution in hydrochloric acid



provide for contradictory results. Gas volume given in the task is by approx. 15% less than that obtained from the calculations. The only reason behind the difference is the deficiency of

hydrochloric acid with respect to the precipitate amount (Note that by contrast to the rest of the task, there is no indication of an excess or deficiency in the case of hydrochloric acid!).

Since the available data is insufficient to decide on the sequence of amino acid residues, both Cys-Sec and Sec-Cys are accepted as correct answers for **X**.

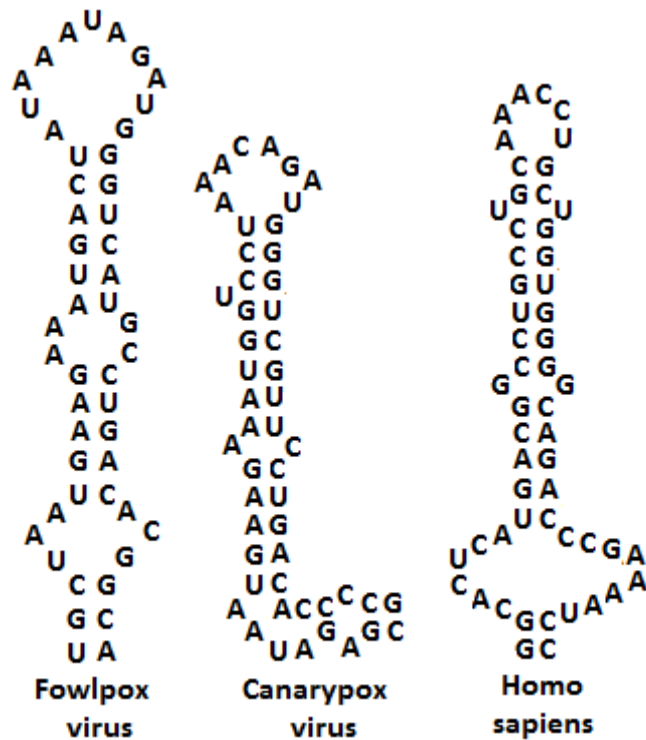


4. The $-SeH$ group is a much stronger reducing agent than the $-SH$ group. Thus, Sec is very readily oxidized, which makes its presence as free selenocysteine inside a cell impossible.

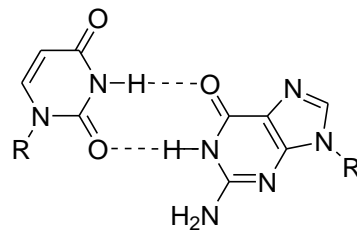
5. Searching for a correlation between the given images and sequences is much easier than can be expected. There could be many ways to reach the correct answer. A sample strategy is given below. First, one should decide which of the fragments refers to human RNA. Genomes of the viruses belonging to the same family should be phylogenetically close, with a slight divergence from the common ancestor. Indeed, sequences 1 and 3 reveal high similarity, both dramatically differing from sequence 2, the latter thus being attributed to human cell. Next step is the search for nucleotides corresponding to the black boxes in the image of human RNA. Note that there are colorless and grey boxes to the ends from black ones. These include 9 nucleotides at the 5'- and 11 nucleotides at the 3'-end. These forbidden areas are highlighted red in the hereunder sequence. Nucleotides corresponding to the black boxes are located between the red fragments, and should be twice two consecutive purine nucleotides AG, AA or GG (all options highlighted yellow). Furthermore, there should be exactly 30 nucleotides between the yellow fragments, which allows the final assignment (highlighted yellow and underlined).

AGGCACUCAUGACGGCCUGCCUGCAACCUGCUGGUGGGGCAGACCCGAAAAUCCAC

Thus, the encircled codon is UGA, which can be also found in fragments 1 and 3. Using the above strategy, one can fill in the rest two images and find the correlation between the images and fragments (fragments 1, 2, and 3 refer to the images of the fowlpox virus, homo sapiens, and canarypox virus, respectively).



6. Guanine-uracil is the so-called Wobble Base Pair.



7. UGA, according to the table of genetic code, is known as the STOP codon terminating translation. However, it is stated in the problem that the chain elongation proceeds after UGA (variants 2 and 3 invalid). UGA is similarly located in sequences of very dissimilar organisms (a mammal and viruses), which underlines its importance for translation and makes variant 5 hardly possible. Variant 4 can be also discriminated, since translation is an uninteruptible process.

Thus, variant 1 is the correct answer. Indeed, UGA in a certain motive (referred to as **SECIS element**, **Selenocysteine Insertion Sequence**) is read as the codon determining selenocysteine inclusion into polypeptides. In viruses, SECIS element is located in the translated region of RNA. In eukaryotes, this hairpin-like structure is found in the unreadable part of mRNA (in 3'-untranslated region, 3'-UTR), and Sec is not found in human proteins.

8. Knowledge of the UGA position allows setting the reading frame. In principle, there could be various mutations meeting the requirements. Examples are given below.

Choosing a mutation, one should keep in mind that the wild type and mutant codons must encode the same amino acid. Also, nucleotides of this codon should not be involved in maintaining the secondary structure of SECIS element (no hydrogen bonding to opposite nucleotides). Thus, one can suggest U-23→C-23 mutation for the fowlpox virus (both are tyrosine codons), and A-28→G-28 mutation for the canarypox virus (both are lysine codons).

Problem 24. Unusual amino acids: search for new properties

1. Calculation of molar ratios of carbon, hydrogen and oxygen in **A-C** allows determining their minimal molecular weights corresponding to the net formulae (note that isotopic ratios of C, H, N and O are native):

Compound	Calculation of ratios	Calculation of minimal molecular weights, g/mole
A	$n(\text{C}) : n(\text{H}) : n(\text{O}) = \frac{31.09}{12.01} : \frac{5.74}{1.008} : \frac{16.57}{16.00} = 5 : 11 : 2$	$M = \frac{60.05 \cdot 100}{31.09} = 193.1$
B	$n(\text{C}) : n(\text{H}) : n(\text{O}) = \frac{26.67}{12.01} : \frac{5.04}{1.008} : \frac{17.77}{16.00} = 4 : 9 : 2$	$M = \frac{48.04 \cdot 100}{26.67} = 180.1$
C	$n(\text{C}) : n(\text{H}) = \frac{9.24}{12.01} : \frac{3.10}{1.008} = 1 : 2.25 = 1 : 4$	$M = \frac{12.01 \cdot 100}{9.24} = 130.0$

With provision of the upper bound ($M < 250$ g/mole), true and minimal molecular weights coincide. The residual molecular weights available for the other two elements (besides C, H, and O) in **A** and **B** are of 90.0 and 91.0 g/mole, respectively. There are two possible reasons behind the difference in the residual molecular weights for **A** and **B** ($91.0 - 90.0 = 1$ g/mole). These are dissimilarity of atomic weights of the fifth elements in **A** and **B** and/or different number of nitrogen atoms in these compounds. All possible variants of the number of nitrogen atoms (cannot exceed 6) in **A** are considered in the hereunder table:

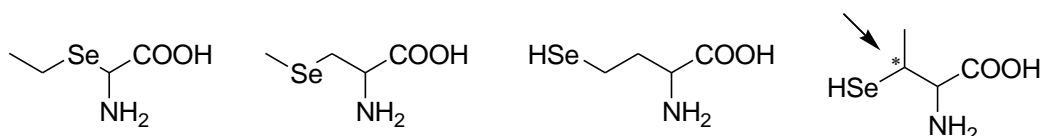
Number of N atoms in A	Residual molecular weight left for the 5th element in A	Variants of the 5 th element	Biochemical sense
1	76	-	-
2	62	2P	To be considered
3	48	1 Ti?	Impossible
		2 Mg?	Impossible
		3 O?	Impossible
		4 C?	Impossible
4	34	-	-
5	20	1 Ne?	Impossible
6	6	6 H?	Impossible

With provision of the inequality given in the problem text, the variant of 2 nitrogen atoms in **A** corresponds to 1 or 2 nitrogen atoms in **B**, and 75 or 63 g/mole left for the 5th element in the latter compound, respectively. No reasonable variants are in agreement with the above values. Therefore, we seem to have come up against a brick wall.

2. Difference by 1 g/mole in the molecular weights of the 5th element in **A** and **B** is left as the only reason. This can be true in case of isotopes (note that native isotope ratios are mentioned only for four elements!). If so, isotopes should be stable (stability of all initial compounds) and most likely of one and the same element (**A**, **B**, and **C** are precursors of the same compound **X**). With account of the equal number of nitrogen atoms in **A** and **B**, the following set of isotope combinations is available: 20-21, 34-35, 48-49, 62-63, 76-77. Furthermore, the difference of 1 g/mole unambiguously suggests only one atom of the 5th element in each of **A** and **B**.

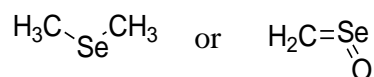
Two sets of stable isotopes (⁴⁸Ti-⁴⁹Ti and ⁷⁶Se-⁷⁷Se) formally fit well. Since there are no native titanium-containing amino acids, the elemental composition of **A** and **B** is finally found as: C, H, N, O, and Se.

3. As determined above, the molecular formula of **B** is C₄H₉SeNO₂. Four structures can be proposed for this α-amino acid. The rightmost structure contains two chiral atoms, thus being invalid, whereas the leftmost one is unstable. So, two central structures are left as the correct answer.



4. Both *R*- and *S*-amino acids are found in nature. Since it is not mentioned in the problem text which exactly of **A** and **B** is found in proteins, it is impossible to unambiguously assign configurations of α-carbon atoms without additional information.

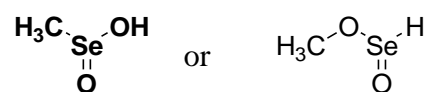
5. Gases **A1**, **B1**, and **C1** have molecular weights of 106, 107 and 112 g/mole, respectively. It is seen that the difference in the molecular weights of **A** and **B** (1 g/mole) is retained for their metabolites. Thus, **A1** and **B1** are likely to be isotopologues. Besides selenium, **A1** and **B1** contain elements with a total residual molecular weight of $106 - 76 = 30$ g/mole. Since gaseous metabolites contain hydrogen, there are two possible variants of their molecular formula: C₂H₆Se or CH₂SeO. With provision of identity of hydrogen atoms in **A1**, the following structures are possible:



Of these two, only dimethylselenide does not contain π -bonds. Finally, **A1** is $(\text{CH}_3)_2^{76}\text{Se}$, and **B1** is $(\text{CH}_3)_2^{77}\text{Se}$.

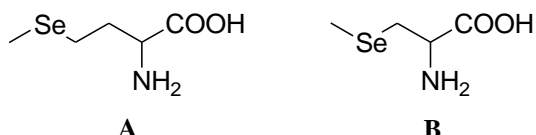
6. The atomic weight of selenium isotope in **C1** is $76 + (112-106) = 82$ a.u. (Note that the final metabolite is the same for all three initial original compounds!). Residual molecular weight left for the 4th element in **C** (it consists of only four elements) is $130 - 16 - 82 = 32$ g/mole, which corresponds to two atoms of oxygen. Thus, the molecular formula of **C** is $\text{CH}_4\text{O}_2^{82}\text{Se}$.

Presence of methyl groups in **C1** as well as lack of C–O bonds in the structure allow the final ascertainment of the structural formula of **C** (the leftmost of the hereunder ones with ^{82}Se):



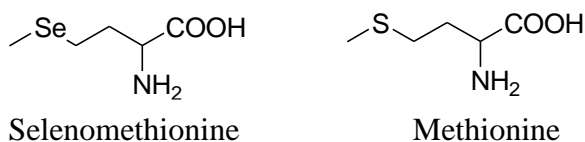
Then, **X** is methyleselenide CH_3SeH , and **C1** is $(\text{CH}_3)_2\text{Se}$ produced as result of **X** methylation (transferase reaction).

7. As determined in i. 6, methylation is the second step of the processes under consideration. With respect to extremely high specificity of enzymes, all substrates subjected to methylation should be very similar. Thus, the isotopologues of **X** ($\text{CH}_3^{76}\text{SeH}$ and $\text{CH}_3^{77}\text{SeH}$) are the only reasonable intermediates on the way from **A** and **B** to **A1** and **B1**, respectively. These intermediates can directly originate only from compounds containing $\text{CH}_3\text{-Se-}$ residue. Thus, selenomethionine and methylselenocysteine can be attributed to **A** and **B**:



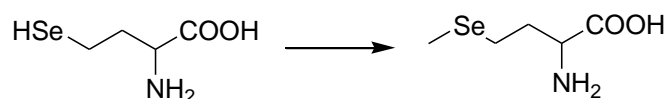
8. Since the experiment under discussion is aimed at revealing pathways of selenium metabolism, it is reasonable to check masses of selenium in each of the administered compounds. Calculations involving the molecular weights of **A**, **B**, and **C** and masses of these compounds in the mixture provide for a wonderful result: the mixture contains 25 μg of each of selenium isotopes.

9. Variant 2 is the correct choice. Selenomethionine is structurally similar to methionine (compare the structures hereunder), which sometimes leads to mistakes in translation and false insertion of selenium-containing amino acid instead of sulfur-containing one.



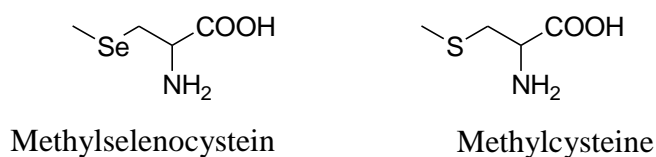
Isotope ^{76}Se is found in nature (~1% of the total selenium pool), so the residue of selenomethionine with ^{76}Se can be found (though rarely) in proteins.

Variant 1 is impossible, since posttranslational modification leading to **A** should involve methylation of selenohomocysteine residue, the latter amino acid also lacking its own tRNA:



Variants 3 and 5 are impossible, since protein biosynthesis admits the only way of polypeptide chain elongation, which involves an amino acid residue transfer from aminoacyl-tRNA.

Variant 4 is impossible for the same reasons as Variant 2. Methylselenocysteine is structurally similar to S-methylcysteine (compare the hereunder structures), which is not a canonical amino acid, thus lacking its own tRNA:



Problem 25. Specific features of *Clostridium* metabolism

1. Glucose consists of carbon, oxygen and hydrogen. As a result of its fermentation in H_2O the following gaseous (at STP) products could be theoretically formed:

- 1) Molecular hydrogen,
- 2) Various hydrocarbons,
- 3) Formaldehyde,
- 4) CO and CO_2 .

Absence of C-H bonds in **C** and **D** allows excluding variants 2 and 3 from further consideration.

Molecular mass of the gas mixture is $10.55 \cdot 2 \text{ g/mol} = 21.1 \text{ g/mol}$. It is obvious that hydrogen is one of the two gases, whereas either CO or CO_2 is the other one. CO seems to be an improbable variant; still all the options should be checked by applying the hereunder formula for n :

$$M(\mathbf{C}) \cdot \frac{n}{n+10} + M(\mathbf{D}) \cdot \frac{10}{n+10} = 21.1$$

$$n = \frac{211 - 10 \cdot m(\mathbf{D})}{M(\mathbf{C}) - 21.1}$$

C	D	Coefficient n
H ₂	CO ₂	12.0
CO ₂	H ₂	8.3
H ₂	CO	9.6
CO	H ₂	27.7

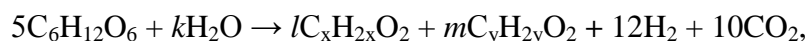
Since n is integer in only one case, **C** and **D** are attributed to H₂ and CO₂, respectively.

Note that bacterial cultures exist in specific, sometimes solid, nutritious media. Thus, conventional data of gases (in particular, of CO₂) solubility in water may be inapplicable.

2. With respect to the results in i. 1, the updated reaction (1) is rewritten as:



a) In the case when each of **A** and **B** is a saturated monocarboxylic acids, the equation transforms into:



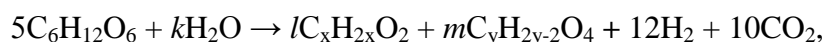
where x and y are the numbers of carbon and hydrogen atoms in **C** and **D**, respectively.

With account of the balance of the elements numbers, one gets the hereunder system of equations:

Element	Balance equation
C	$l \cdot x + m \cdot y = 20$
H	$18 + k = l \cdot x + m \cdot y$
O	$k = 2l + 2m - 10$

It is seen from the first two equations that $k = 2$. Thus, the equation for oxygen can be rewritten as $l + m = 6$

b) In the case when **A** is a saturated monocarboxylic and **B** a saturated dicarboxylic acids (reverse variant is equivalent), the equation transforms into:



where x and y are the numbers of carbon and hydrogen atoms in **C** and **D**, respectively.

Further analysis provides an analogous system of equations:

Element	Balance equation
C	$l \cdot x + m \cdot y = 20$
H	$18 + k = l \cdot x + m \cdot y - m$
O	$k = 2l + 4m - 10$

There is only one set of integer values corresponding to $m = k = 1$. Still, then $l=3.5$, which is in contradiction with the conditions of the problem.

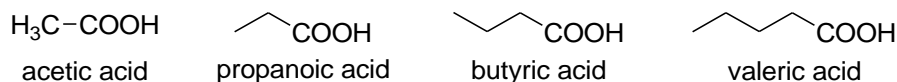
A and **B** with higher number of carboxylic groups (for example, two dicarboxylic acids) are impossible, as this results in negative k , l , or m .

3. l and m are integers, and $l + m = 6$. This suggests the following possible ratios: 1:1 (3:3), 1:2 (2:4) and 1:5. Still, $l \cdot x + m \cdot y = 20$, which makes the ratio of 1:1 impossible (both x and y non-integer, $20/3 = 6.67$). Ratios of 2:1 and 5:1 are theoretically possible. Thus, the correct variants are b, e and f.

4. The next step is a search for integer solutions of the equation $l \cdot x + m \cdot y = 20$ for the ratios established in i. 3.

$l = 2; m = 4$		$l = 1; m = 5$	
x	y	x	y
8	1	15	1
6	2	10	2
<u>4</u>	<u>3</u>	<u>5</u>	<u>3</u>
<u>2</u>	<u>4</u>		

Since the number of carbon atoms decreases as a result of fermentation ($x < 6$ and $y < 6$), only the variants underlined in the above table are left for consideration. These correspond to four unbranched monocarboxylic acids:



Further discrimination of the variants based on the available data is impossible.

For your information: **A** and **B** are acetic and butyric acids, respectively.

5. Since $\mathbf{Z}_{\text{start}}$ and $\mathbf{Z}_{\text{finish}}$ contain the same number of nitrogen atoms, a system of equations (2) and (3) can be set up:

$$\frac{a}{b} = 0.12727 \quad (2); \quad \frac{a}{b+n} = 0.12069 \quad (3)$$

$$b = 18.34 \cdot n$$

where a is the number of N atoms, whereas b and $b+n$ are the total numbers of atoms in $\mathbf{Z}_{\text{finish}}$ and $\mathbf{Z}_{\text{start}}$, respectively.

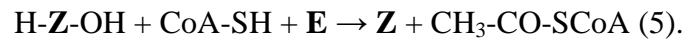
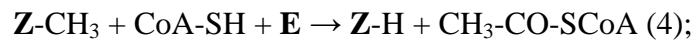
The given limitation of less than 100 atoms in each of $\mathbf{Z}_{\text{start}}$ and $\mathbf{Z}_{\text{finish}}$ can be written as $n < 6$. Variable b is necessarily integer, thus leading to the solely possible combination of $b=55$ and $n=3$. So, $\mathbf{Z}_{\text{start}}$ and $\mathbf{Z}_{\text{finish}}$ are composed of 58 and 55 atoms, respectively. This means that $\mathbf{Z}_{\text{start}}$ loses 3 atoms in acetyl-CoA formation.

6. The difference in the number of hydrogen atoms in $\mathbf{Z}_{\text{start}}$ and $\mathbf{Z}_{\text{finish}}$ is:

$$\Delta N_H = N_H(\mathbf{Z}_{\text{start}}) - N_H(\mathbf{Z}_{\text{finish}}) = 58 \cdot 0.43103 - 55 \cdot 0.41818 = 2$$

Thereby, two of three atoms appearing in acetyl-CoA from $\mathbf{Z}_{\text{start}}$ are hydrogen atoms. Oxygen or carbon can be the third atom lost by $\mathbf{Z}_{\text{start}}$. In the former case, $\mathbf{Z}_{\text{start}}$ loses H_2O , and in the latter case CH_2 -group, which is formally equivalent to substituting a CH_3 -group with 1 hydrogen atom.

Both variants can be rewritten in a form of equations (4) and (5):



Equation (5) is invalid with any \mathbf{E} , whereas equation (4) is correct, if \mathbf{E} is carbon monoxide CO formed via enzymatic reduction of CO_2 .

Since bacteria cultivation proceeds in the presence of isotope-labeled CO_2 , the number and isotope distribution of nitrogen atoms in acetyl CoA are not influenced. Thus, the molecular mass of acetyl-CoA isotopologues is:

$$M(\text{labeled AcCoA}) = \frac{100 \cdot 14.01 \cdot 7}{12.08} = 811.8 \text{ g/mol}$$

Molecular mass of unlabeled acetyl-CoA is 809.5. With account of rounding of nitrogen mass fractions, the difference is of 2 g/mol. Two hereunder variants are possible:

- 1) CO_2 labeled with ^{13}C enters the reaction, thus giving acetyl residue with two ^{13}C atoms;
- 2) CO_2 labeled with two ^{18}O enters the reaction, thus giving acetyl residue with ^{18}O atom.

It is impossible to distinguish between **D1** and **D2** basing on the available data:



The above considered acetyl-CoA biosynthesis is referred to as the Wood-Ljungdahl pathway.

For your information. Exact attributing of **D1** and **D2** is possible using physico-chemical methods of analysis. Both isotopes are stable, which makes the radioactivity based methods useless. The suitable methods include mass-spectrometry (different patterns are formed for molecular fragments) and ^{13}C -NMR spectroscopy (^{18}O isotope is not used in NMR spectroscopy).

7. The initial nucleotide ratio is 1:1, thus the probability of finding G or C at any position equals $\frac{1}{2}$. Hence, the probability of any of eight possible codons is of $\frac{1}{2} \cdot \frac{1}{2} \cdot \frac{1}{2} = \frac{1}{8}$. Four amino acids are each encoded by two codons composed of only G and/or C. Thus, the ratio

between Pro, Arg, Gly, and Ala is 1:1:1:1. However, with account of the limited length of the oligopeptide (about 33 amino acid residues), there could be significant deviations from the above ratio. So, variant 6 is the most correct choice.

8. Using the table of genetic code, one can write down the nucleotide sequences of the initial and mutant mRNA fragments (see designations of N and N1/N2 in Problem 22, i. 6):

UGG-CAU/C-AUG-GAA/G-UAU/C (initial);

UGG-ACN-UAU/C-GGN-GUN (mutant).

Comparison of two sequences suggests that the mutation (insertion of A) occurred right after the first codon. Mutations influencing polypeptide biosynthesis are classified into two groups: the substitution of base pairs and the frameshift. The latter happens upon deletion or insertion of nucleotides in a number not multiple of three. Then, the initial sequence can be rewritten as:

UGGCAUAUGGAGUAU/C

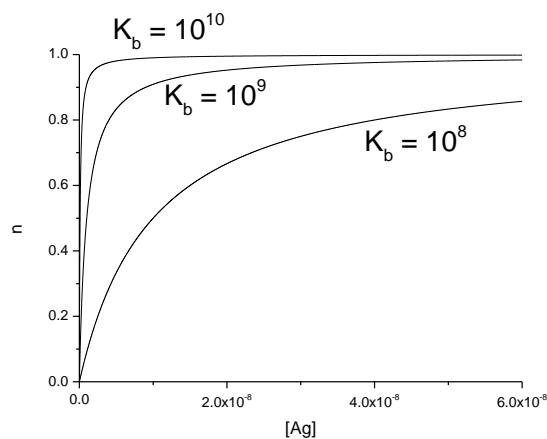
If the mutant protein ends up with the 234th amino acid residue, the biosynthesis is terminated by a STOP codon present next. Since STOP codons always start with U, the completely deciphered sequence of nucleotides is:

UGGCAUAUGGAGUAU

Problem 26. Analysis of complex formation

$$1. \quad K_b = \frac{[Ab*Ag]}{[Ab] \cdot [Ag]}$$

$$2. \quad \bar{n} = \frac{[Ab*Ag]}{[Ab*Ag] + [Ab]} = \frac{K_b [Ab] \cdot [Ag]}{K_b [Ab] \cdot [Ag] + [Ab]} = \frac{K_b [Ag]}{K_b [Ag] + 1}$$

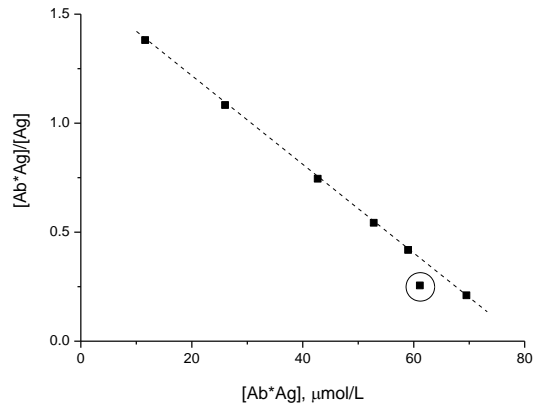


As seen, the titration curves are strongly non-linear, which makes their analysis complicated.

$$3. \quad K_b = \frac{[\mathbf{Ab} * \mathbf{Ag}]}{[\mathbf{Ab}] \cdot [\mathbf{Ag}]} \Rightarrow \frac{[\mathbf{Ab} * \mathbf{Ag}]}{[\mathbf{Ag}]} = K_b (C_{\mathbf{Ab}} - [\mathbf{Ab} * \mathbf{Ag}])$$

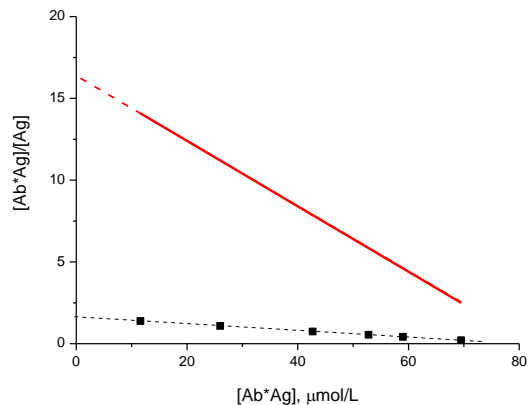
Thus, a plot in such coordinates (referred to as the Scatchard ones) should be a straight line with the slope of $-K_b$ and the intercept of $C_{\mathbf{Ab}} K_b$ ($C_{\mathbf{Ab}}$ is the total \mathbf{Ab} concentration).

This is proved by plotting Set A data, point #6 is seemingly an outlier:



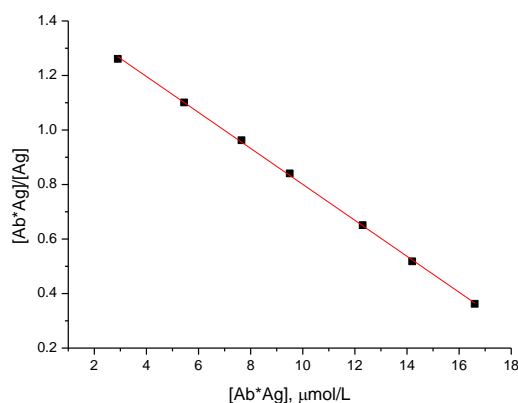
From the experimental data, $K_b = 2 \cdot 10^4$ L/mol.

According to the above equation, with a 10 times higher K_b , values for both the intercept (1.64 from the original data) and the slope should be 10 times higher:



4. If all the binding sites are independent, and K_b does not depend on the fraction of occupied binding sites, mathematically there is no difference between x molecules of antibody with valence N and $N \cdot x$ molecules of antibody with valence 1. Thus, the above mentioned Scatchard equation is only slightly modified to account for several binding sites per antibody:

$$\frac{[\mathbf{Ab} * \mathbf{Ag}]}{[\mathbf{Ag}]} = K_b (N \cdot C_{\mathbf{Ab}} - [\mathbf{Ab} * \mathbf{Ag}]).$$



The experimental data fit a straight line with a slope of -0.0660 (corresponding to $K_b = 6.6 \cdot 10^4$ L/mol) and an intercept of 1.46 . Thus, $1.46 = K_b \cdot N \cdot C_{Ab} = 6.6 \cdot 10^4 \cdot N \cdot 1.1 \cdot 10^{-5} \Rightarrow N = 2$.

5. A clear way to determine C_{Ab} follows from the fact that the K_b value influences both the slope and the intercept of the plot in Scatchard coordinates. As soon as K_b is determined from the slope of the curve, C_{Ab} can be immediately calculated, provided the antibody valence N is known. For instance, for the set A, $N=1$, $K_b = 2 \cdot 10^4$ L/mol; $C_{Ab} = 1.64 / 2 \cdot 10^4 \approx 82$ $\mu\text{mol/L}$, which reasonably corresponds to the given value of 80 μM . It can be concluded, thus, that the ADP protein does not contain any functionally inactive antibodies or other impurities.

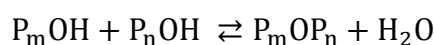
The same analysis for the set B is impossible, because the real enzyme valence is not known *a priori*. (Value $N = 2$ determined above has been obtained under assumption of 100% enzyme purity.)

Problem 27. Inorganic polymers: polyphosphates and polysilicones

1. Well known examples are: C (acetylenic carbon), S (various forms of polymeric sulfur), Se (grey selenium), P (red phosphorus), As (black arsenic), Sb (black antimony). Not all of these substances consist of perfectly linear chain molecules, but for sure these elements are capable of forming quite long polymers.

2. $2\text{HPO}_4^{2-} \rightleftharpoons \text{P}_2\text{O}_7^{4-} + \text{H}_2\text{O}$ (ionization state of the phosphate precursor depends on pH).

3. With P_i standing for a polyphosphate with the degree of polymerization of i , for the reaction

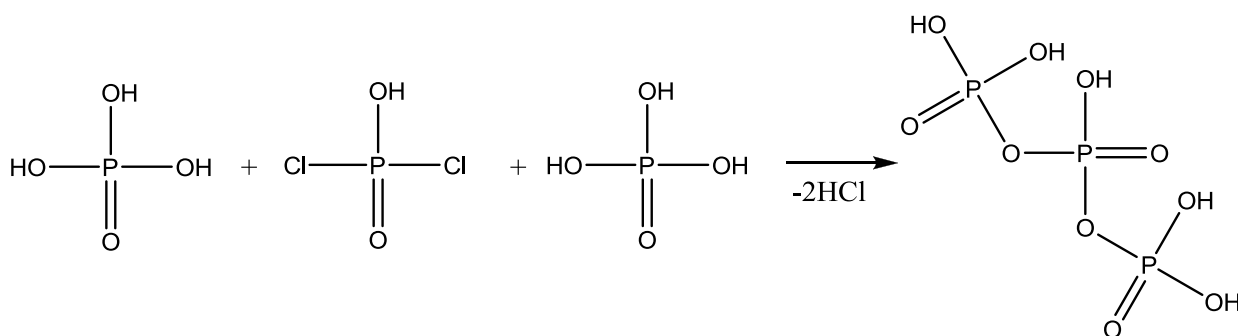


$$K = \frac{[P_{m+n}][H_2O]}{[P_mOH][P_nOH]}$$

As polyphosphates of various degrees of polymerization are not distinguishable, each of concentrations $[P_m]$, $[P_n]$, $[P_{m+n}]$ can be substituted with the total concentration of all phosphate species, thus,

$$K = \frac{[P_{m+n}][H_2O]}{[P_mOH][P_nOH]} = \frac{[H_2O]}{[P_i]}$$

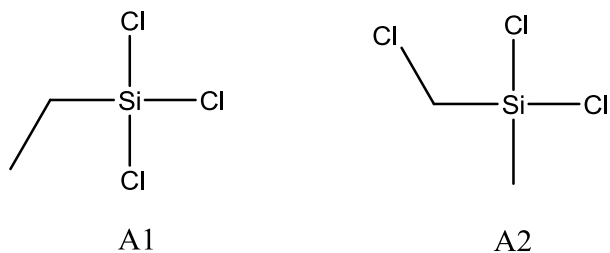
4. The following reasons should be taken into account. First, the free energy of hydrolysis is strongly negative, which means that the free energy of condensation (the reverse reaction) is positive. Thus, the equilibrium constant of an elementary condensation stage is low (less than 1), which is not consistent with the high-polymeric phosphate species. In general, lower equilibrium concentration of (poly)phosphate molecules means that more individual condensations have taken place, which is equivalent to the higher average degree of polymerization of the product. This is true for process ii): lower water concentration (at a certain equilibrium constant value) corresponds to lower equilibrium concentration of phosphate molecules (from the expression derived in i. 3). Thus, process ii) is more favorable than i). However, process iii) is the most favorable. According to the equation



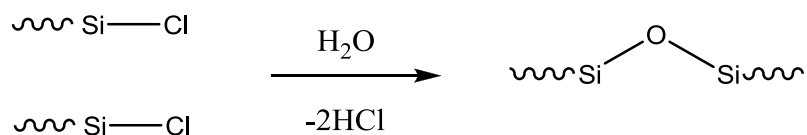
a highly volatile HCl is formed, which is efficiently removed from the reaction mixture by heating. As a result, the equilibrium is shifted rightwards.

Indeed, only route iii) can be applied in practice for the preparation of polyphosphoric acids. Condensation in concentrated solutions (process ii)) is quite slow, and yields significant amounts of polyphosphoric acids only upon heating (molten H_3PO_4 , 230-250°C). Direct condensation in dilute solution (process i)) is so unfavorable that may come true only when coupled with a certain exoergic reaction (for instance, substrate phosphorylation in various biochemical processes) with the actual mechanism much more complicated than direct condensation.

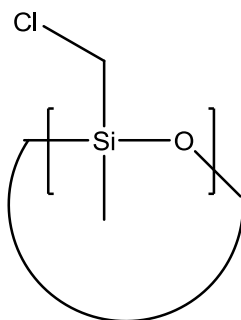
5.



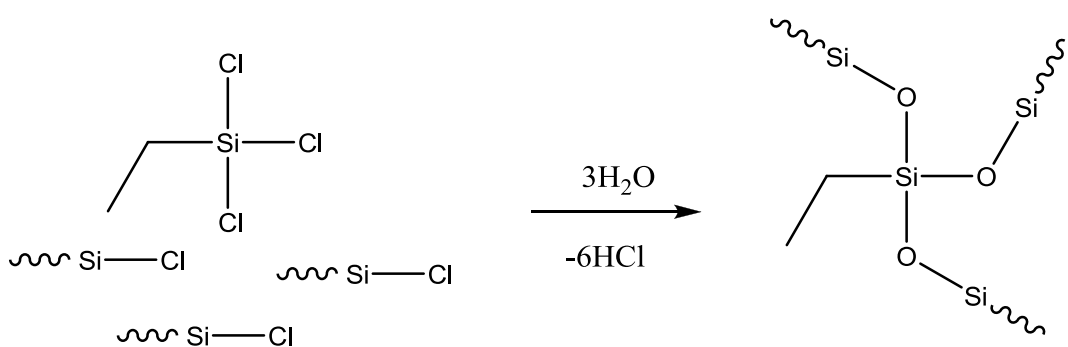
The main chain of the polymer molecule is composed of Si and O atoms:



6, 7. The Si-Cl bond is much more reactive than the C-Cl one in hydrolysis and condensation reactions. Thus, **A2** can be considered bifunctional in polycondensation reaction, giving a non-branched polymer with the cyclic giant macromolecule of poly(chlorodimethylsiloxane) as the final product when absolutely all Si-Cl bonds are reacted:

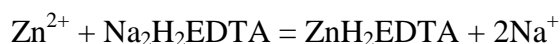
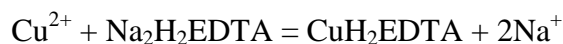
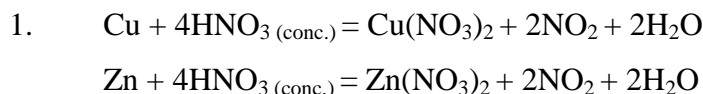


A1 is trifunctional, thus giving rise to a branched polymer:



If hydrolysis of Si-Cl bonds is incomplete, some Cl residues are present in the polymeric product. Incomplete condensation retains a number of OH-groups in the product.

Problem 28. Determination of copper and zinc by complexometric titration



2. Cu^{2+} ions present in the aqueous solution are reduced to Cu^+ by thiosulfate. Moreover, the latter forms with Cu^+ a soluble complex $[\text{Cu}(\text{S}_2\text{O}_3)_3]^{5-}$, which is more stable than $\text{Cu}_2\text{H}_2\text{EDTA}$:



3. Metal ions can be titrated with EDTA if the conditional stability constants β' of the metal – EDTA complexes are not less than 10^8 – 10^9 . The β' values are connected with the real constants β as

$$\beta' = \alpha_{\text{EDTA}} \alpha_{\text{M}} \beta,$$

where α_{EDTA} and α_{M} are molar fractions of $\text{H}_2\text{EDTA}^{2-}$ and free metal ion, respectively. As the values of α_{EDTA} and α_{M} significantly depend on pH of the solution, there is an optimal pH range for the titration of metals. In the case of Cu^{2+} and Zn^{2+} , the pH value within 5 to 6 is optimal. In such slightly acidic medium both metals do not form hydroxy complexes (α_{M} is high), whilst $\text{H}_2\text{EDTA}^{2-}$ is not further protonated (α_{EDTA} is high).

$$4. \quad \alpha(\text{H}_2\text{EDTA}^{2-}) = \frac{K_1 K_2 [\text{H}^+]^2}{(K_1 K_2 K_3 K_4 + K_1 K_2 K_3 [\text{H}^+] + K_1 K_2 [\text{H}^+]^2 + K_1 [\text{H}^+]^3 + [\text{H}^+]^4)}$$

$$[\text{H}^+] = 10^{-6} \text{ M}, K_1 = 1.0 \cdot 10^{-2}, K_2 = 2.1 \cdot 10^{-3}, K_3 = 6.9 \cdot 10^{-7}, K_4 = 5.5 \cdot 10^{-11}$$

$$\alpha(\text{H}_2\text{EDTA}^{2-}) = 0,59$$

5. The first titration (**B**) gives the volume of titrant $V_{\text{Cu+Zn}}$, whilst the second one (**C**) gives V_{Zn} . Zn^{2+} concentration is calculated as follows:

$$c(\text{Zn}^{2+}) = (V_{\text{Zn}} \text{ mL} / 1000 \text{ mL L}^{-1}) \cdot c_{\text{EDTA}} \text{ mol L}^{-1} \cdot 100 \text{ mL} / 10.00 \text{ mL} \cdot 65.39 \text{ g mol}^{-1} / 0.1000 \text{ L}$$

$$c(\text{Zn}^{2+}) \text{ g L}^{-1} = V_{\text{Zn}} \text{ mL} \cdot c_{\text{EDTA}} \text{ mol L}^{-1} \cdot 65.39 \text{ g mol}^{-1} \cdot 0.1 \text{ mL}^{-1}$$

$$c(\text{Cu}^{2+}) = ((V_{\text{Cu+Zn}} - V_{\text{Zn}}) \text{ mL} / 1000 \text{ mL L}^{-1}) \cdot c_{\text{EDTA}} \text{ mol L}^{-1} \cdot 100 \text{ mL} / 10.00 \text{ mL} \cdot 63.55 \text{ g mol}^{-1} / 0.1000 \text{ L}$$

$$c(\text{Cu}^{2+}) \text{ g L}^{-1} = (V_{\text{Cu+Zn}} - V_{\text{Zn}}) \text{ mL} \cdot c_{\text{EDTA}} \text{ mol L}^{-1} \cdot 63.55 \text{ g mol}^{-1} \cdot 0.1 \text{ mL}^{-1}$$

The mass ratio of the metals in alloy is calculated from $c(\text{Cu}^{2+})$ and $c(\text{Zn}^{2+})$ values in g L^{-1} :

$$m(\text{Cu})/m(\text{Zn}) = c(\text{Cu}^{2+})/c(\text{Zn}^{2+})$$

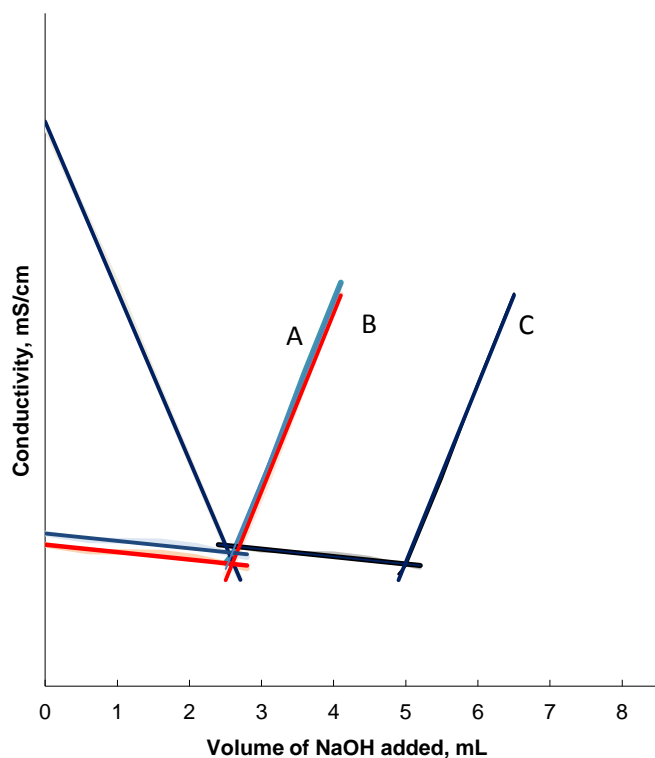
Problem 29. Conductometric determination of ammonium nitrate and nitric acid

1. Equilibria in the system can be described by the following equations:

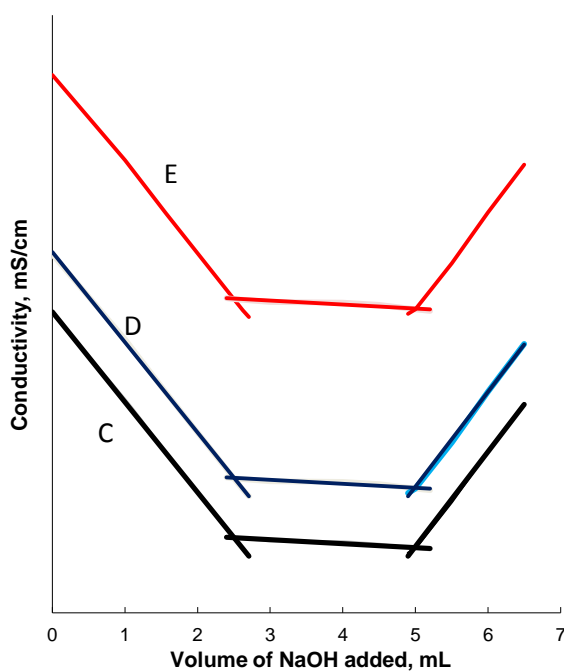


2, 3. Conductivity of a solution is primarily dependent on the concentration of H^+ and OH^- ions (species with the highest mobility) as well as on that of salts. Solutions **A** and **B** contain the same amount of NH_4NO_3 (solution **A** with an excess of ammonia reveals a bit higher conductivity). On the titration curves, there are monotonously descending portions reflecting the displacement of the weak base (NH_3) from its salt (reaction 2). Minimum conductivity is reached when the concentration of protons appearing from NH_4^+ hydrolysis is minimal (reaction 2 completed). This is further changed by a sharp rise corresponding to the increasing excess of alkali.

In the case of solution **C**, the first descending portion is steeper (than those for **A** and **B**) and is associated with diminishing concentration of free protons coming from HNO_3 . The first equivalence point causes a sharp break of the curve (reaction 1 completed). The second descending portion characterized by a lower slope reflects the displacement of the weak base from its salt (reaction 2). Minimum conductivity is also reached when reaction 2 is completed, which is followed by a sharp rise of conductivity due to the alkali excess.



Titration of NH_4NO_3 (**A**), of NH_4NO_3 in the presence of an excess of NH_3 (**B**), and of HNO_3 followed by that of NH_4NO_3 (**C**).



Titration of solutions of HNO_3 and NH_4NO_3 diluted with deionized water (**C**), distilled water (**D**), and deionized water containing NaCl (**E**).

The difference between cases **C**, **D**, and **E** is due to various levels of conductivity caused by the salts that are not titrated with NaOH .

4. Calculations can be done in the same way as for a regular acid-base titration, using titrant volumes in inflection points $V_{\text{NaOH}(1)}$, $V_{\text{NaOH}(2)}$:

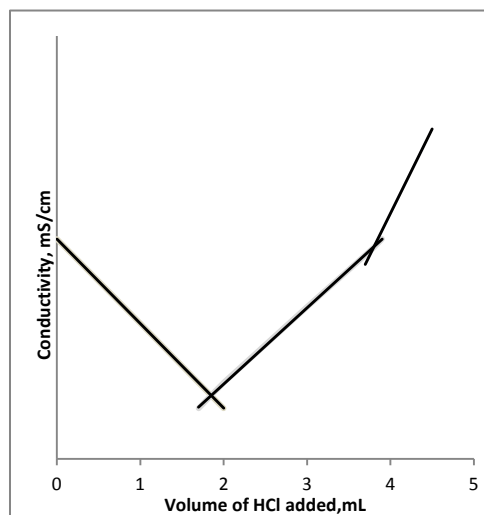
$$c_{\text{H}^+} V_{\text{sample}} = c_{\text{NaOH}} V_{\text{NaOH}(1)}, \quad c_{\text{NH}_4^+} V_{\text{sample}} = c_{\text{NaOH}} (V_{\text{NaOH}(2)} - V_{\text{NaOH}(1)})$$

Examples.

A and B: if 2.45 mL of 0.9987 M NaOH spent until the inflection point, then $c_{\text{NH}_4^+}$ is: $0.9987 \times 2.45 = c_{\text{NH}_4^+} \times 25$; $c_{\text{NH}_4^+} = 0.0979$ M.

C - E: if 2.40 mL of 0.9987 M NaOH spent until the first inflection point (neutralization of HNO_3) in a 25.0 mL sample aliquot, then $c_{\text{HNO}_3} = 0.0895$ M. If the second inflection point reached at 4.85 mL, then $c_{\text{NH}_4^+}$ is: $0.9987 \times (4.85 - 2.40) = c_{\text{NH}_4^+} \times 25$; $c_{\text{NH}_4^+} = 0.0979$ M.

5. HCl first neutralizes the strong base, is followed by neutralization of the weak one. titration curve of a mixture of two bases reveals breaks. NaOH neutralization is accompanied by linear decrease of conductivity due to lowering concentration of highly mobile hydroxyl ions. the first equivalence point, conductivity starts increasing due to the formation of a well dissociating salt (a strong electrolyte) as a result ammonia (a weak electrolyte) neutralization.



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the second equivalence point, conductivity of the solution sharply increases due to the excess of hydrogen ions.

Problem 30. Analysis of fire retardants by potentiometric titration

1. Titration curves for a polyprotic acid (such as phosphoric acid) or a mixture of acids are characterized by more than one endpoint if $K_{a1}:K_{a2} \geq 10^4$ and the equilibrium constant of acidity of the weak acid is more than $n \times 10^{-9}$. The equilibrium constants of acidity of phosphoric acid are: $K_{a1} = 7.1 \times 10^{-3}$, $K_{a2} = 6.2 \times 10^{-8}$, $K_{a3} = 5.0 \times 10^{-13}$. Thus, there are two breaks on the titration curve of phosphoric acid (Fig. 1). The third break is not observed due to very low value of K_{a3} .

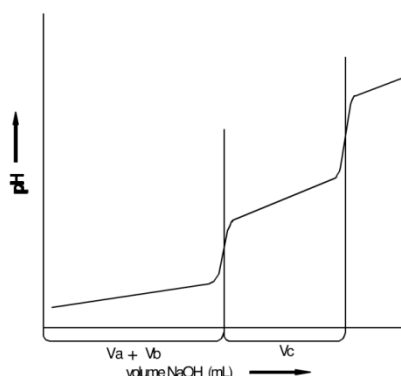
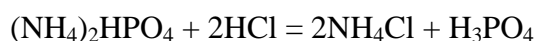


Fig. 1. Titration of a mixture of hydrochloric and phosphoric acids with sodium hydroxide.

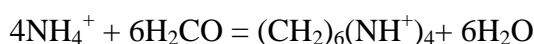
During titration of a *mixture* of hydrochloric and phosphoric acids, the proton of hydrochloric acid and the first proton of phosphoric acid react with sodium hydroxide simultaneously. By the second endpoint H_2PO_4^- is converted into HPO_4^{2-} .

2. The first and second equivalence points of H_3PO_4 are observed at pH of about 4.7 and 9.6, respectively. For determination of hydrochloric and phosphoric acids in their mixture, one can use indicators with color change around these pH values (for example, bromocresol green and thymol phthalein for the first and second titrations, respectively).

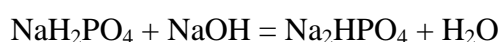
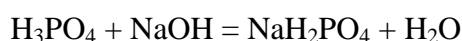
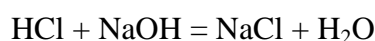
3. The following reaction takes place on addition of HCl to the sample:



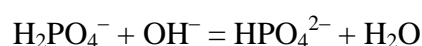
Formaldehyde reacts with ammonium salts to form hexamethylene tetrammonium cation:



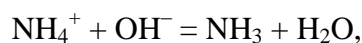
The equations describing the titration of hexamethylene tetrammonium salt, hydrochloric and phosphoric acids with sodium hydroxide:



4. A typical analysis of potentiometric titration data is shown in Fig. 2. The most steeply rising portion on the curve (a) corresponds to the endpoint, which can be found more precisely by studying dependences of the first (maximum on curve (b)) or second (zero value on curve (c)) derivatives. In the presence of ammonium salts, the reaction corresponding to the second endpoint in H_3PO_4 titration



is overlaid by the process



which makes the potential rise gradually rather than sharply (ammonium buffer).

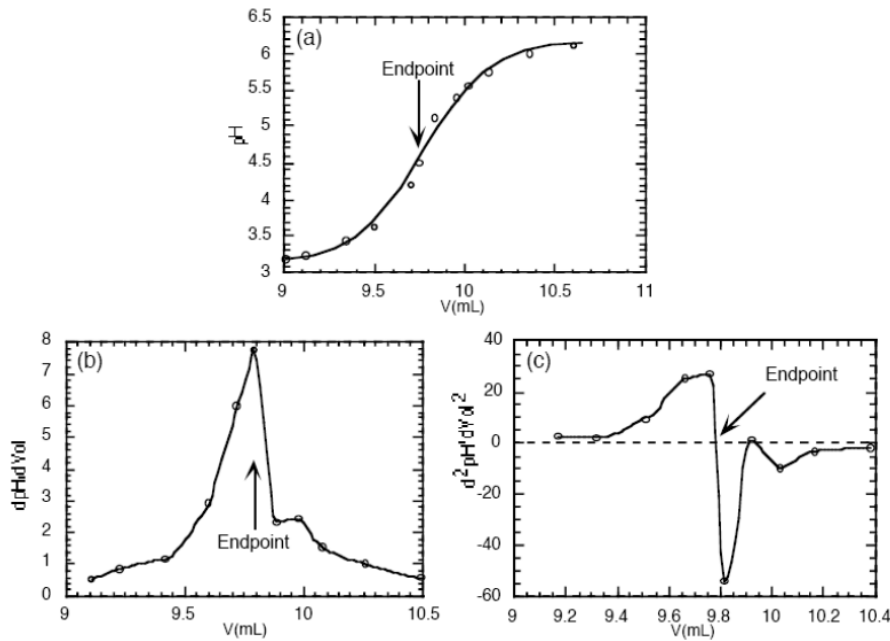


Fig. 2. Typical plots of potentiometric titration: (a) titration curve of an acid with a base; (b) curve of the first derivative; (c) curve of the second derivative.

5. (a) Calculation of phosphate amount

With $V_{\text{NaOH},1}$ designating the volume of sodium hydroxide used in titration **A**, the amount needed to neutralize hydrochloric acid and the first proton of phosphoric acid is:

$$n_{\text{PO}_4} + n_{\text{HCl}} (\text{titrated}) = c_{\text{NaOH}} \times V_{\text{NaOH},1}$$

At the same time,

$$c_{\text{HCl}} \times V_{\text{HCl}} (\text{added}) = n_{\text{HCl}} (\text{titrated}) + 2n_{\text{PO}_4} (\text{HCl spent for the reaction with } (\text{NH}_4)_2\text{HPO}_4)$$

Then,

$$n_{\text{PO}_4} = c_{\text{HCl}} \times V_{\text{HCl}} (\text{added}) - c_{\text{NaOH}} \times V_{\text{NaOH},1}$$

Since $n_{(\text{NH}_4)_2\text{HPO}_4} = n_{\text{PO}_4}$, one finally gets:

$$\omega_{(\text{NH}_4)_2\text{HPO}_4} = 10 \times n_{\text{PO}_4} \times M_{(\text{NH}_4)_2\text{HPO}_4} / m_{\text{mixture}}$$

(b) Calculation of the total amount of diammonium hydrophosphate and ammonium chloride

With $V_{\text{NaOH},2}$ designating the volume of sodium hydroxide used in titration **B** (that is, spent for the neutralization of hexamethylene tetrammonium cation $(\text{CH}_2)_6(\text{NH}^+)_4$ obtained from the ammonium salts), one gets:

$$n_{\text{NH}_4\text{Cl}} + 2n_{\text{PO}_4} = c_{\text{NaOH}} \times V_{\text{NaOH},2}$$

The amount of phosphate $n_{(\text{NH}_4)_2\text{H}_3\text{PO}_4}$ was determined in experiment **A**, which allows calculating the amount of NH_4Cl

$$n_{\text{NH}_4\text{Cl}} = c_{\text{NaOH}} \times V_{\text{NaOH},2} - 2 \cdot (c_{\text{HCl}} \times V_{\text{HCl}} - c_{\text{NaOH}} \times V_{\text{NaOH},1})$$

and its content in the mixture:

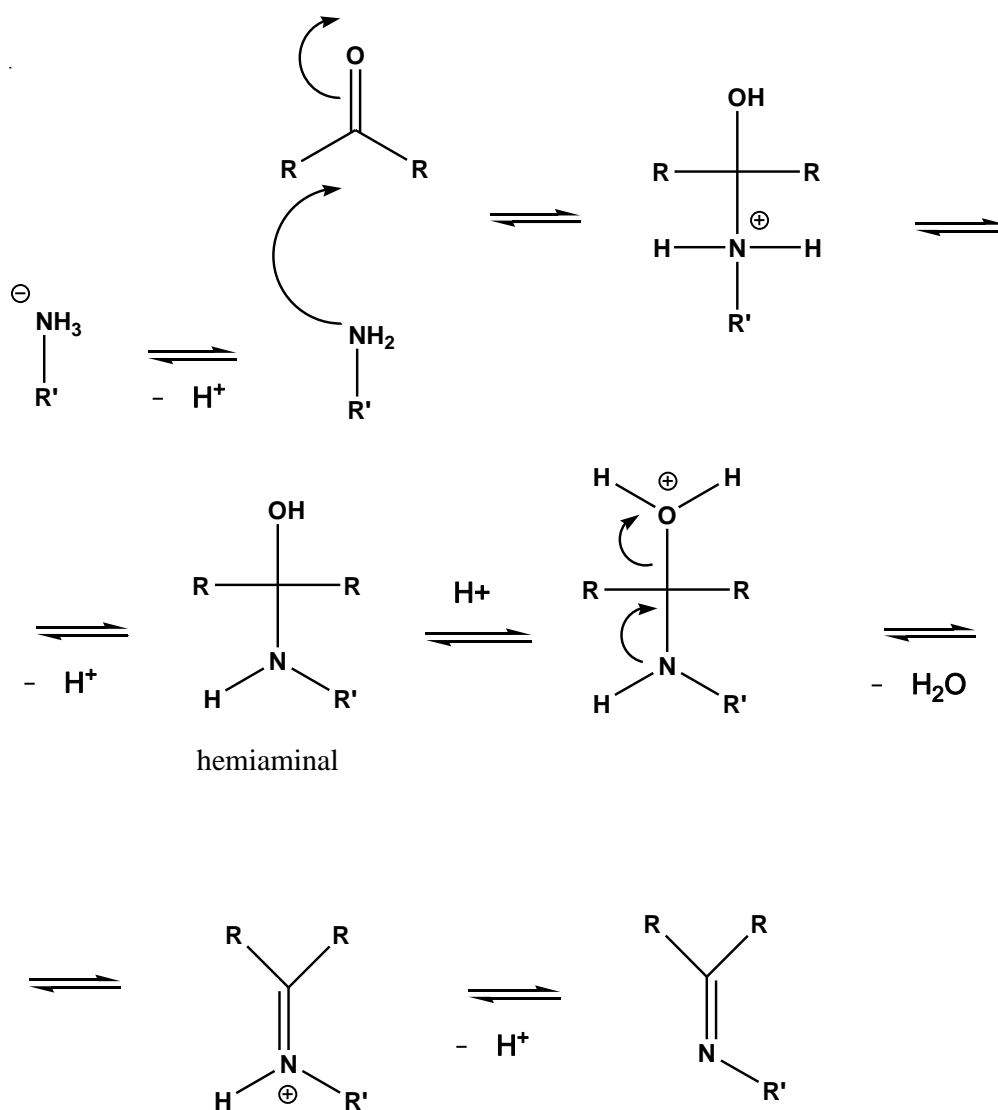
$$\omega_{\text{NH}_4\text{Cl}} = 10 \times n_{\text{NH}_4\text{Cl}} \times M_{\text{NH}_4\text{Cl}} / m_{\text{mixture}}$$

Problems 31-33. Melting points and yields of the products

Problem #	Product	Melting point, °C	Yield, %
31	<i>N</i> -[(<i>E</i>)-Phenylmethylene]aniline	51-53	85
32	Osazone of <i>D</i> -glucose	205-207	62
33	Acetone derivative of mannose	118-120	79
33	Acetone derivative of cysteine	148-150	68

Problem 31. Formation of double carbon-nitrogen bond

1. Hemiaminal.



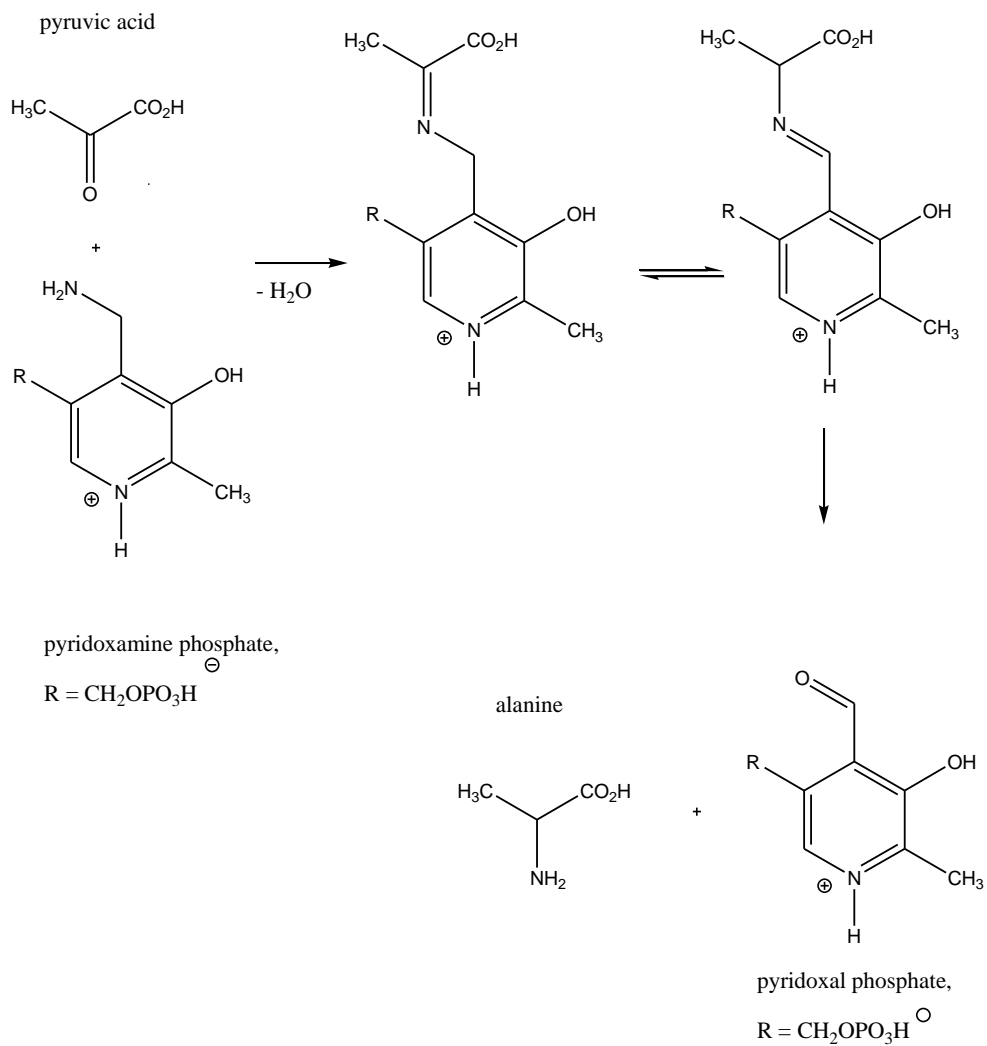
The rate-determining steps are:

The amine attack at the carbonyl carbon atom at low pH, since most of the amine molecules are protonated;

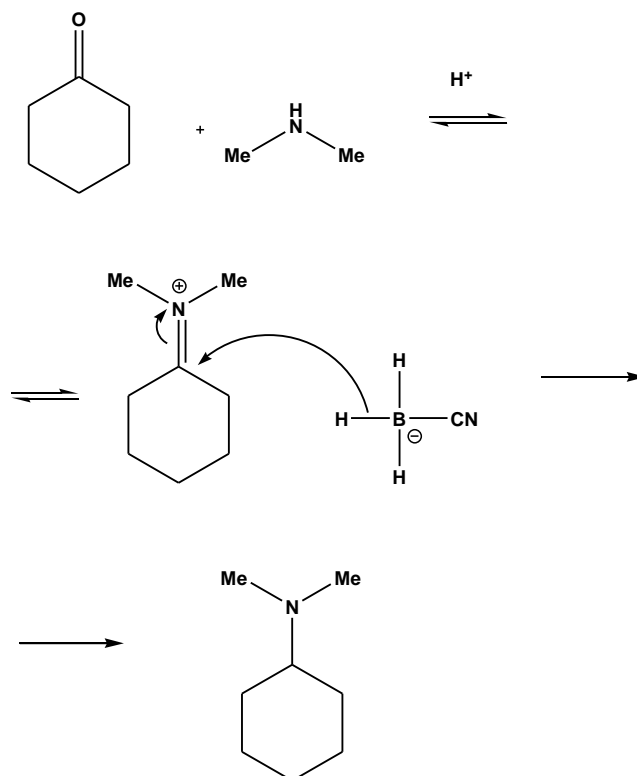
Dehydration of the tetrahedral hemiaminal intermediate at high pH, since this requires protons.

2. Both reactions proceed through the positively charged intermediates, iminium and oxonium ions, respectively. While the former just loses the proton to form the final product, the later acts as an electrophile adding another molecule of alcohol to become the full acetal.

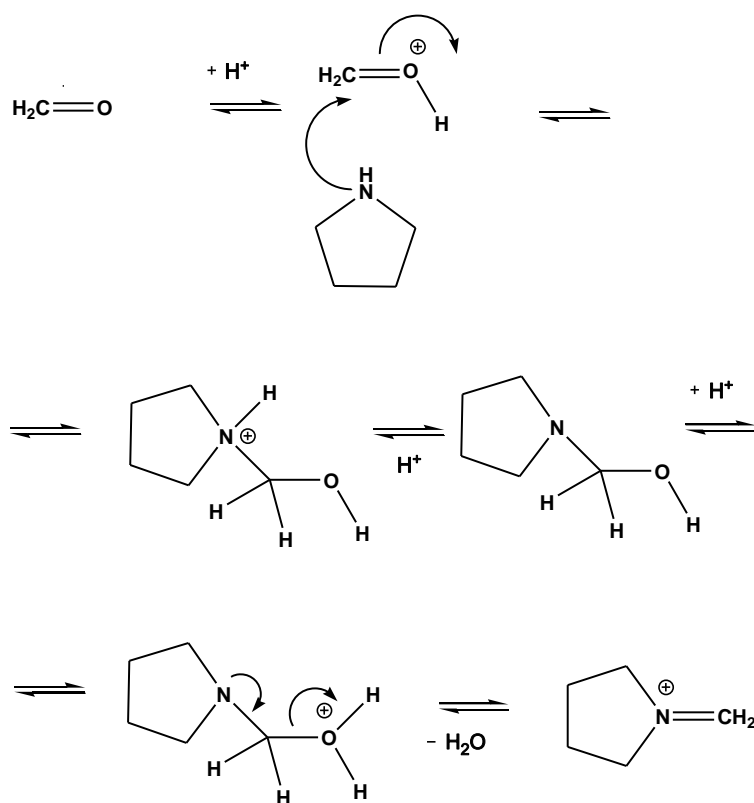
3.

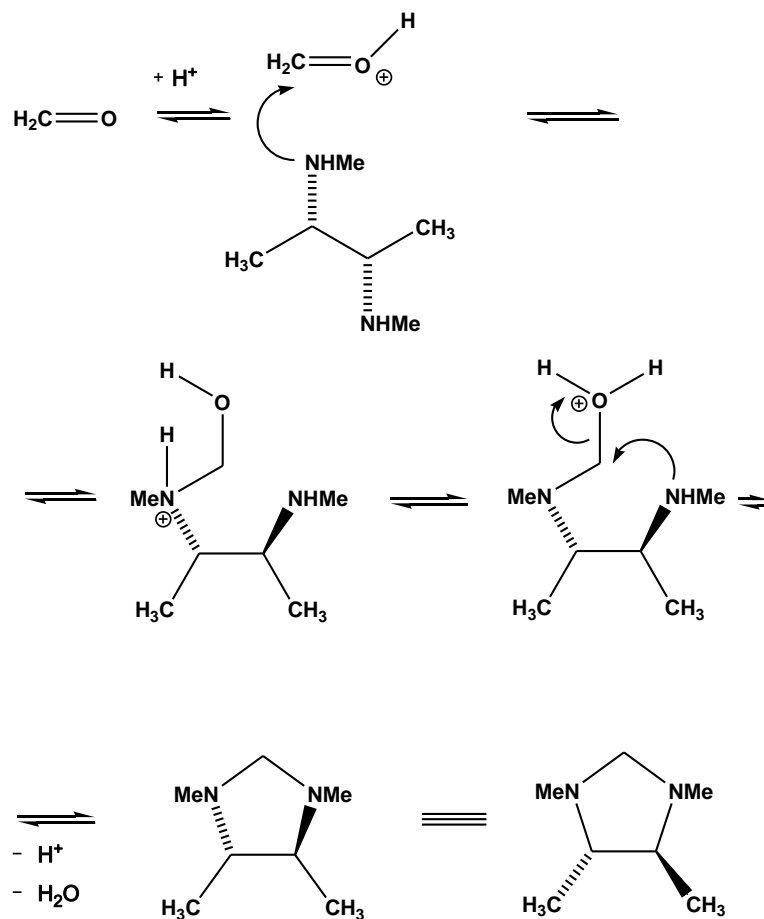


4.



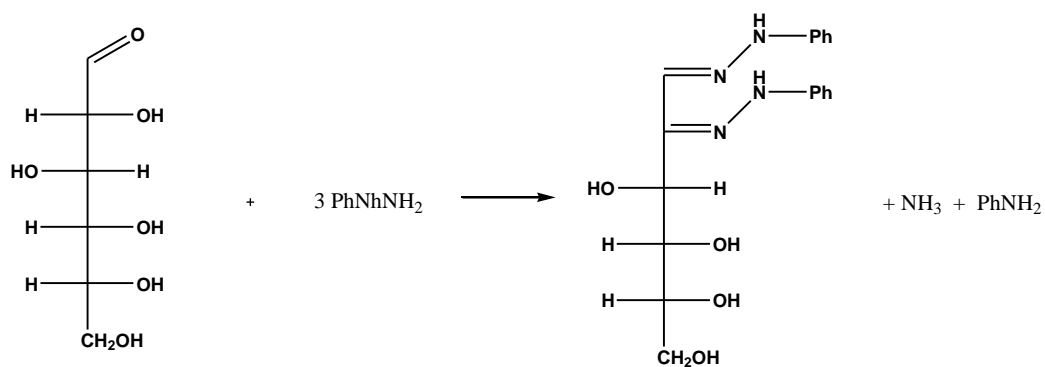
5.





Problem 32. Osazone of glucose

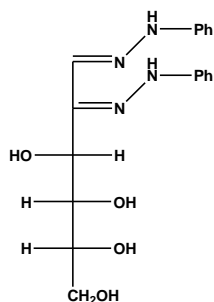
1.



2. *D*-Glucose, since phenylhydrazine is taken in an excess.

3. The appropriate phenylhydrazone of aldehyde.

4.



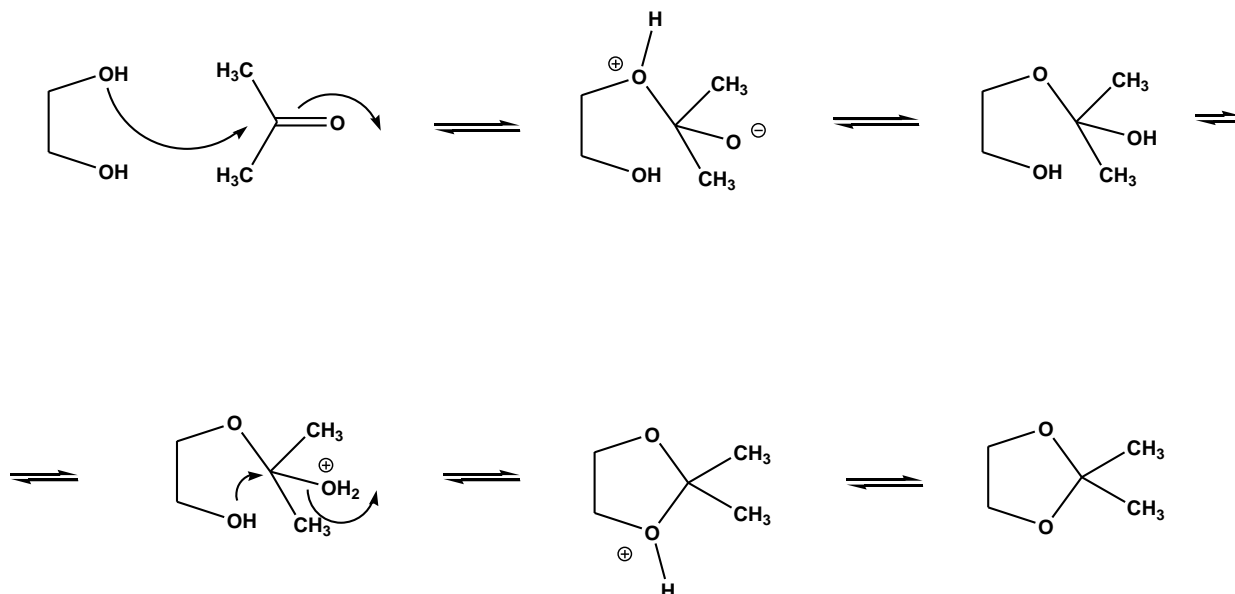
It is one and the same product for all the starting substances. These means the stereochemistry of C3, C4 and C5 of the starting sugars is the same. The initial difference in nature and/or stereochemistry at 1st and 2nd carbon atoms of the monosaccharides is equalizes by hydrazone formation.

5. a), b), d) are different; c) are the same.

Problem 33. Acetone as a protecting agent

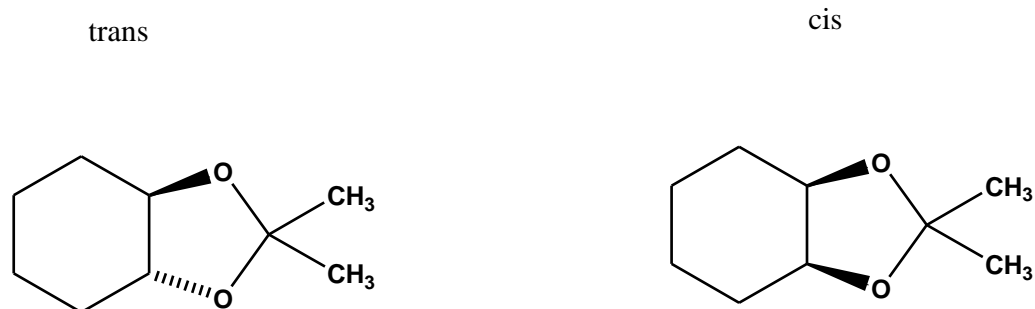
Ninhydrine test. The spot with the product will show no color change, whilst that with the starting amino acid will become colored (blue-violet to brown-violet).

1.



Transformation of hemiketal into full ketal needs the acid catalysis to protonate hydroxyl group, which is further removed in the form of water molecule. The resulting positively charged carbocation-type intermediate is stabilized by electron donation from oxygen lone pair.

2.

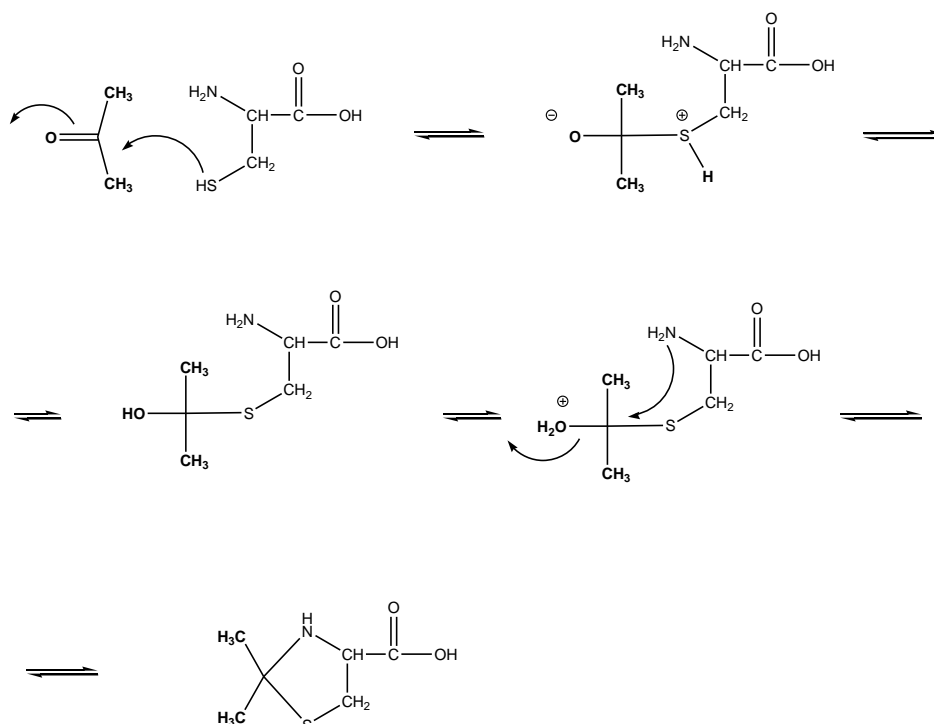


cis-Fused six- and five-membered rings in the resulting product of *cis*-cyclohexane-1,2-diol are more stable than *trans*-fused rings. The reason is the higher bond and angles distortion in *trans*-fused bicycles.

3. In the furanose form of *D*-mannose, there is a possibility to form two rather than one (in the pyranose form) 1,3-dioxolane rings, which is more thermodynamically favorable. Pyranose – furanose transformation proceeds via the open aldehyde form of the carbohydrate.

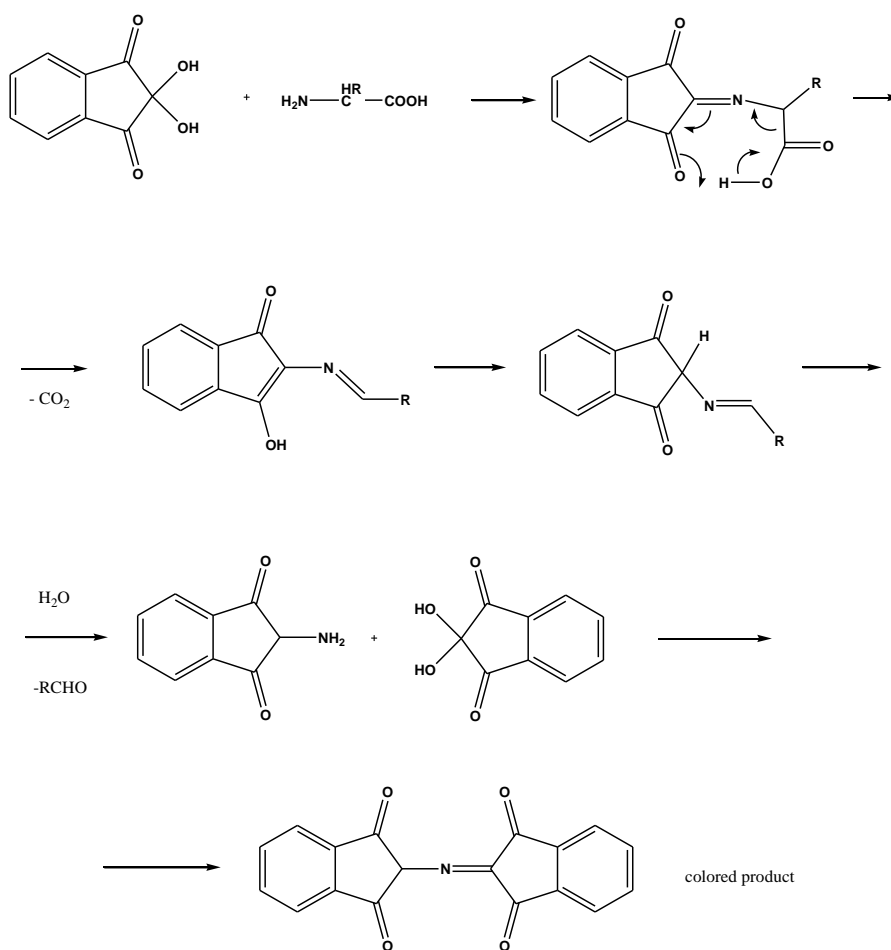
4. Aqueous hydrochloric acid.

5.



Acid catalysis enhances the electrophilicity of carbonyl carbon atom (enhancing carbonyl activity). Thiol group reacts first due to higher nucleophilicity compared to that of amino group.

6.



Problem 34. Determination of molecular mass parameters (characteristics) by viscometry

1. The viscosity values calculated from the flow times of polystyrene solutions (2 to 10 g/L) determined with the Ubbelohde viscometer at 25 °C are given in the hereunder tables. Each flow time value is an average of three measurements. Note that your experimental values may significantly differ from those in the tables, since the flow times depend on the molecular properties (mainly molecular weight distribution) of a particular polystyrene sample.

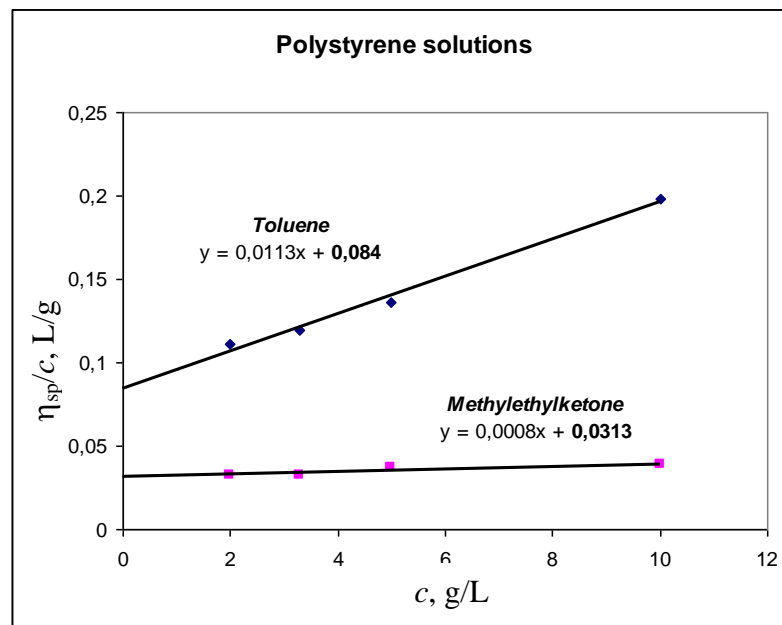
Polystyrene/toluene, the solvent flow time $t_0 = 24.4$ s

Concentration of the polymer c , g/L	Flow time t , s	$\eta_{rel} = \frac{t}{t_0}$	$\eta_{sp} = \frac{t - t_0}{t_0}$	$\frac{\eta_{sp}}{c}$, L/g
10	72.8	2.98	1.98	0.198
5	41.0	1.68	0.68	0.136
3.3	34.0	1.39	0.39	0.119
2	29.8	1.22	0.22	0.111

Polystyrene/methyl ethyl ketone, the solvent flow time $t_0 = 26.0$ s

Concentration of the polymer c , g/L	Flow time t , s	$\eta_{rel} = \frac{t}{t_0}$	$\eta_{sp} = \frac{t - t_0}{t_0}$	$\frac{\eta_{sp}}{c}$, L/g
10	36.0	1.38	0.38	0.0385
5	30.8	1.18	0.18	0.0369
3.3	28.8	1.11	0.11	0.0326
2	27.7	1.07	0.07	0.0327

2,3,4. The intrinsic viscosity $[\eta]$ can be found by either graphical extrapolation to 0 concentration (as the Y-intercept), or by linear fitting (as an absolute term) of the reduced viscosity data.



Analysis of the data given in i. 1) leads to $[\eta]$ equal to 0.0840 and 0.0313 L/g for the toluene and methyl ethyl ketone solutions, respectively. (Three significant digits are left in both cases based on the typical amplitude of the measured flow times).

5. The viscosity-average molecular weights as calculated from the Mark-Kuhn-Houwink equation are of 226000 and 125000 g/mol for the toluene and methyl ethyl ketone solutions, respectively.

6. The polydispersity index equals $226000/125000 = 1.81$.

Problem 35. Cooperative interactions in polymer solutions

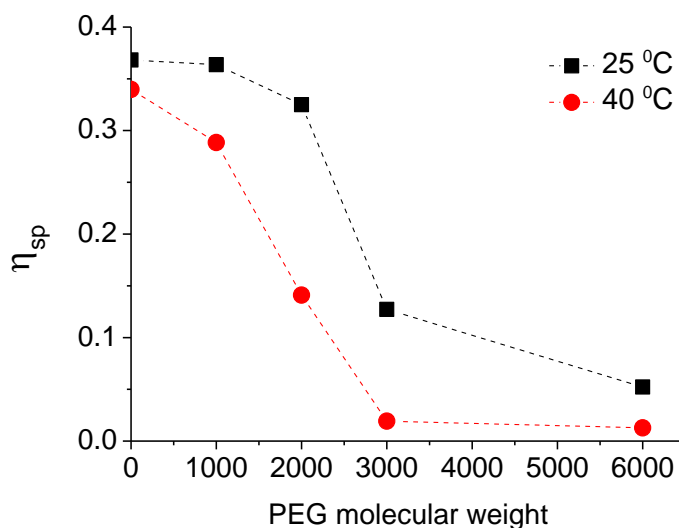
1. Experimental flow times and the calculated specific viscosities are given in the hereunder table.

Note 1. The molecular weights of the repeating units of PMMA and PEG are of 86.06 and 44.05 g/mol, respectively. Mixing of equal volumes of a 2 g/L PMMA and a 1 g/L PEG (of any molecular weight) solutions results in a reaction mixture with the molar ratio of the PMMA and PEG units of approximately 1:1.

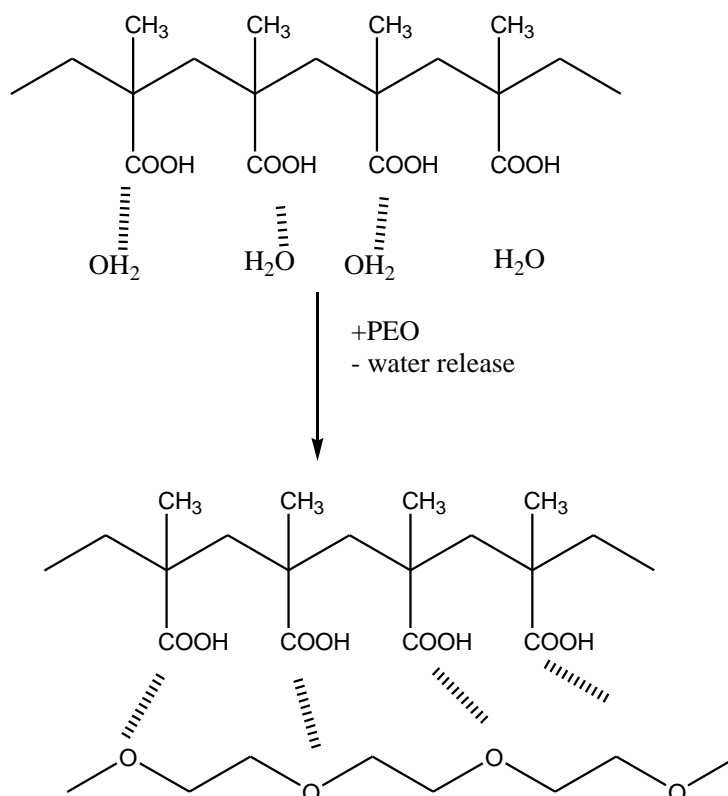
Note 2. The final concentration of PMMA in the resulting mixtures and its aqueous solutions is of 1 g/L.

Composition	Temperature, °C	Flow time t , s	Specific viscosity of the solution η_{sp}
Water	25	44.0	-
PMAA, 1 g/L	25	60.2	0.368
PMAA+PEG-1000	25	60.0	0.364
PMAA+PEG-2000	25	58.3	0.325
PMAA+PEG-3000	25	49.6	0.127
PMAA+PEG-6000	25	46.3	0.052
Water	40	31.2	-
PMAA, 1 g/L	40	41.8	0.340
PMAA+PEG-1000	40	40.2	0.288
PMAA+PEG-2000	40	35.6	0.141
PMAA+PEG-3000	40	31.8	0.019
PMAA+PEG-6000	40	31.6	0.013

2.



3. The reaction scheme of the complex formation is given below. A decrease of the specific viscosity of the PMAA solution upon addition of the equimolar amount of PEG is observed, which reflects that that polymer coils in the interpolymer complex are more compact than those in the initial solution. The compaction is due to hydrophobization of the PMAA chain with PEG.



Dramatic changes in the density of the complexes are observed within a rather narrow range of PEG molecular weights (of about 1500 g/mol at 40°C and 2500 g/mol at 25 °C). Such processes are often referred to as cooperative.

The enthalpy change in PMAA-PEG complex formation being negligible, the entropy gain due to the release of water molecules is the driving force of the reaction.

As positions of the repeating units in a polymer chains are constrained, the total entropy of the polymer coil is less than that of the same number of unbound monomer units. For longer polymer chains such entropy loss is more significant. Consequently, the entropy gain as a result of PMAA-PEG complex formation ($\Delta S = S(\text{complex}) + S(\text{water}) - S(\text{PMAA}) - S(\text{PEG})$) is increasing with an increase of the PEG chain length (total entropies of released water molecules, the complex, and the initial PMAA molecules are nearly the same). This is why the PMAA-PEG interaction proceeds efficiently only starting with a certain molecular weight of PEG (<1000 g/mol at 40°C and of about 1000-2000 g/mol at 25 °C).

Higher efficiency of the complex formation at elevated temperatures (PEG with a lower molecular weight is needed to provide for a noticeable viscosity drop) contributes to the consideration that the entropy gain is behind the process.