CHEM1611 Chemistry 1A (Pharmacy) - June 2008

2008-J-2

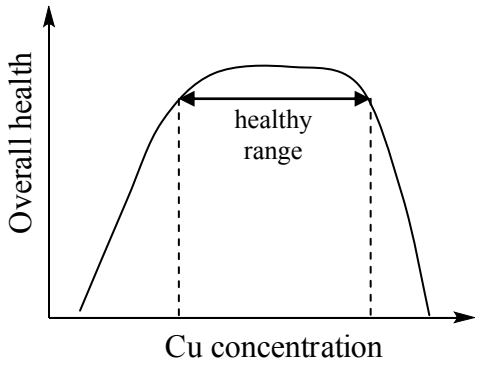
-

	sulfur dioxide
	cobalt(II) chloride-6-water
Ag_2CrO_4	
$KHCO_3$	

-

$1s^2\ 2s^2\ 2p^5$
$1s^2\ 2s^2\ 2p^6\ 3s^2\ 3p^6$
$1s^2\ 2s^2\ 2p^6\ 3s^2\ 3p^6\ 4s^0\ 3d^5$

-



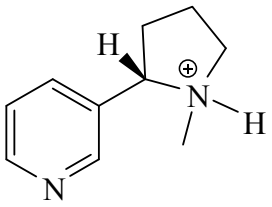
Copper can participate in electron transport systems due to multiple oxidation states.

Treat with complexing agent such as EDTA which forms very stable water-soluble complex that can be excreted from the body.

2008-J-3

- **A**: H-bonding, dipole-dipole
  B: dipole-induced dipole, dispersion forces

N1	trigonal planar	sp^2	bent ~120°
N2	tetrahedral	sp^3	trigonal pyramidal
C3	tetrahedral	sp^3	tetrahedral
C4	trigonal planar	sp^2	trigonal planar

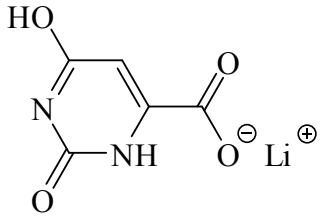


2008-J-4

- $Li_2CO_3(s) + 2H^+(aq) \rightarrow 2Li^+(aq) + H_2O(l) + CO_2(g)$

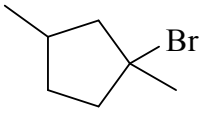
  There's no difference. The lithium orotate dissolves to give lithium ions and orotate ions.

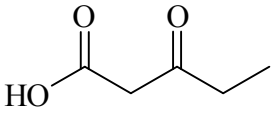
  $LiC_5H_3N_2O_4(s) \rightarrow Li^+(aq) + C_5H_3N_2O_4^-(aq)$



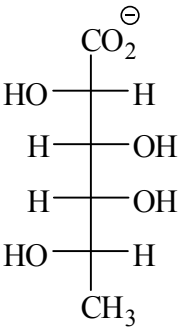
2008-J-5

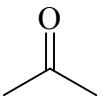
-



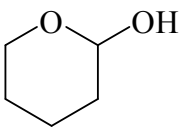


CH_3CH_2OH / catalytic H^+



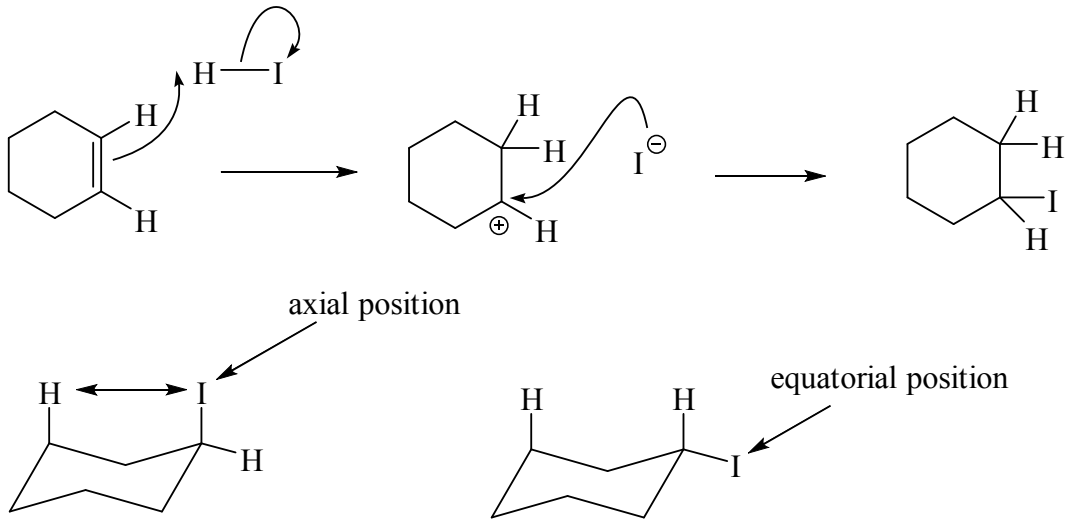


+ CH_3CH_2OH



2008-J-6

•

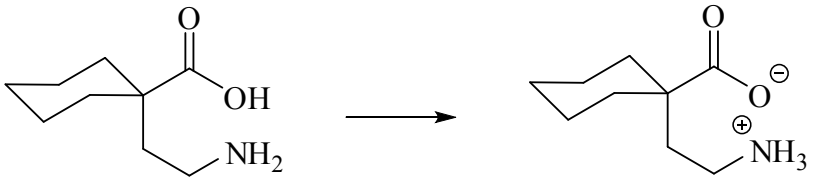


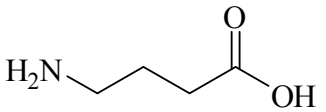
The conformation with the iodine in the equatorial position will be the more stable. Iodine is a big atom and there are significant 1,3 steric interactions with axial hydrogens when iodine is in the axial position.

2008-J-7

- Gabapentin has both an amine and a carboxylic acid functional group, so it is an amino acid. It is not an α-amino acid (like those found in proteins) as the amino group is not attached to the carbon next to the COOH group.

  Salt formulations are mainly used to prevent oxidation of the free amine group. The amine group is converted to a quaternary ammonium salt which is more stable. Gabapentin would exist in a zwitterionic form where the amine group is already converted to the more stable quaternary ammonium ion.



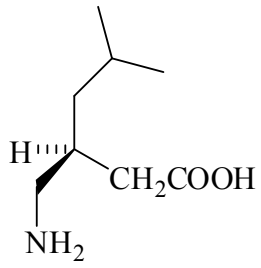


Both GABA and gabapentin have the same basic features - a four carbon chain with a terminal NH_2 and a terminal COOH group. These functional groups are likely to be involved in receptor binding through interactions such as H-bonding.

2008-J-8

The bulky cyclohexyl group interferes with the binding of gabapentin at the GABA receptor site. This could be due to either steric reasons (the group is too large to fit into the receptor site) or its hydrophobic nature is a poor match for the equivalent part of the receptor.

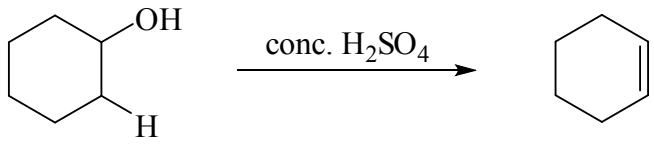
$-CH_2NH_2 > -CH_2COOH > -CH_2CH(CH_3)_2 > -H$



2008-J-9

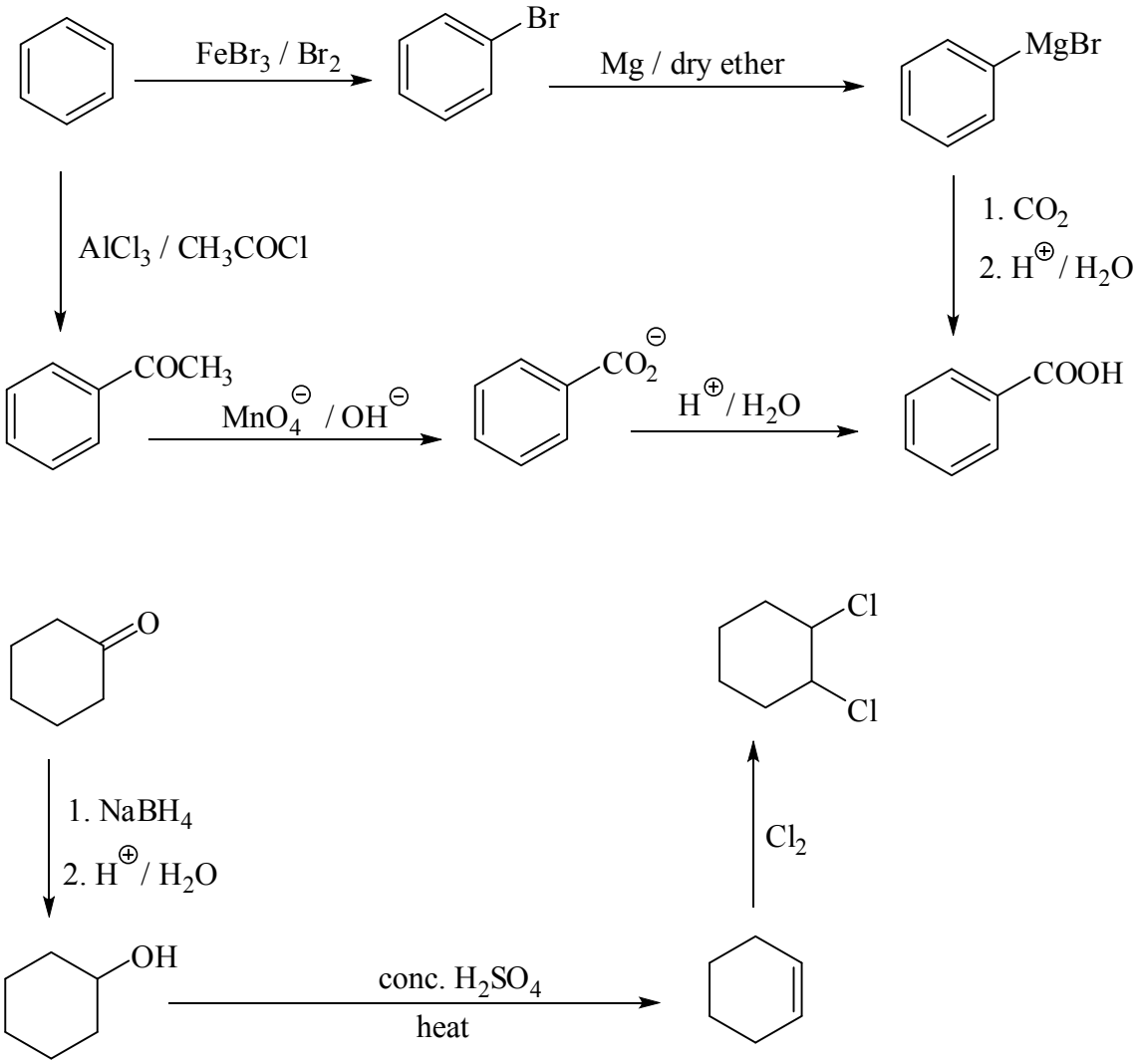
- **A**: NaOH
  B: $CH_3CH_2CH_2Br$
  C: I_2
  nucleophilic substitution
  reduction

- Elimination is the removal of an H^+ and a nucleophile from adjacent atoms and the concomitant formation of a double bond between those atoms.
  eg



2008-J-10

•

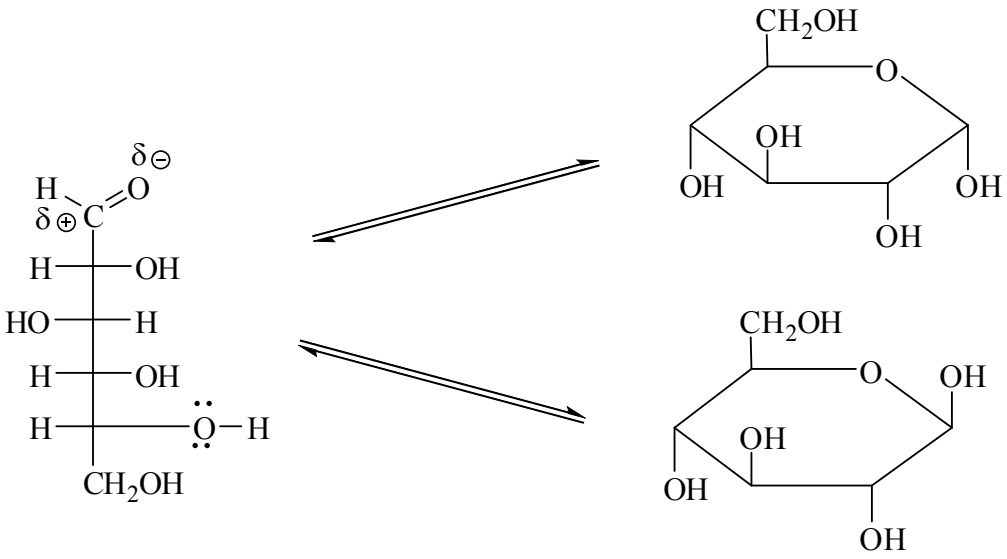

FeBr3 / Br2
Br
Mg / dry ether
MgBr
AlCl3 / CH3COCl
1. CO2
2. H⊕ / H2O
COCH3
MnO4⊖ / OH⊖
CO2⊖
H⊕ / H2O
COOH
O
1. NaBH4
2. H⊕ / H2O
OH
conc. H2SO4
heat
Cl2
Cl
Cl

2008-J-11

- salt

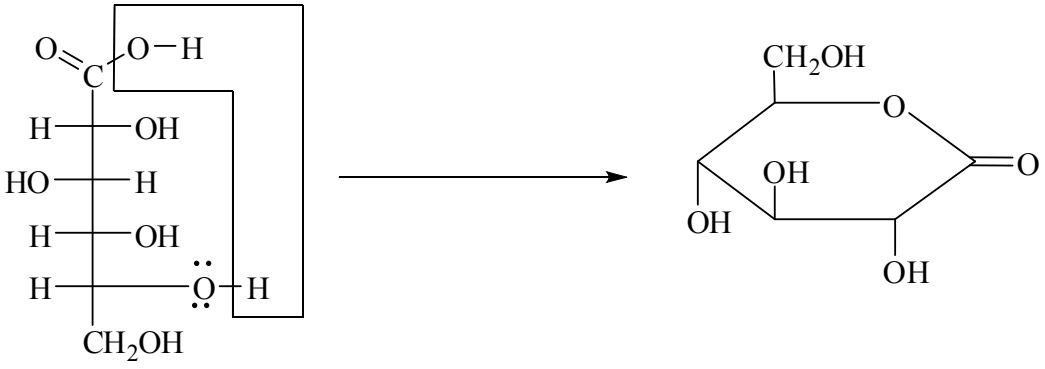
  So that the correct dosage can be delivered.
  The ester form may need to be given orally to allow it to hydrolyse (to give the free quinine) in the digestive tract.

2008-J-12



Formation of cyclic forms of glucose is due to the reversible reaction between the OH on C5 and the aldehyde group on C1 to form the hemiacetal function group.

Carboxylic acids do not form hemiacetals, so no similar cyclic forms exist for glucoronic acid. However, acids and alcohols can form esters, so a different type of cyclic compound is possible. (Cyclic esters are often called lactones.)



2008-J-13

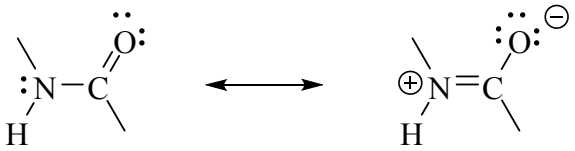
- The primary structure is the order of sequence of the amino acids in the chain. The amino acids are linked with covalent bonds, specifically by the formation of amide functional groups. (Shown in structure on left.)

  The secondary structure refers to the way segments of the peptide chain orient themselves into regular patterns such as α-helices and/or β-pleated sheets because of H-bonding. The structure on the right shows some α-helices connected together by sections of amino acid chains with neither of these structures. There are no β-pleated sheets in insulin.

  The tertiary structure refers to the way the entire protein coils into a 3-dimensional structure. This is due to disulfide bridges between cysteine (cys) residues, hydrophilic interactions between the protein and solvent (water) and dispersion forces between separate hydrophobic parts of the protein. The positions of the two disulfide bridges is clearly shown in the structure on the left. The basic 3D shape of the protein is shown in the ribbon diagram.

2008-J-14

Resonance occurs when two or more Lewis structures can be drawn for the same compound. In such cases, the true structure is none of those drawn, but rather a weighted average of all of them.



The amide functional group has two major resonance contributors as shown. As a consequence of resonance, the peptide bond is rigid and planar.

Consequence for structure: This rigidity and the charge on the oxygen are ideal for the formation of α-helices and β-pleated sheets via H-bonding.

Consequence for chemistry: The involvement of the N lone pair in resonance, means that the N is unavailable for protonation and non-basic. The peptide bond is therefore relatively inert.

Changing surface amino acids (eg charged to uncharged or polar to non-polar) will alter the pI and hence the protein's solubility. As long as the residues changed are not near the active site and do not change its shape, the mode of action of the enzyme won't be affected.