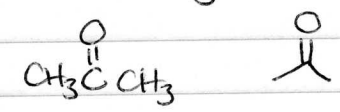
Chem 30B
Answers to Review Problems for Exam 2

Fossum
Chem 30B

1 a. N-ethylaniline
b. butyl formate
c. 3-iodobutanoic acid
d. 5-methyl-3-hexanone
e. 3-chlorobutanal
f. propylamine
g. N-methyl N-propylbutanamide
h. N-methylbenzamide

2. a.



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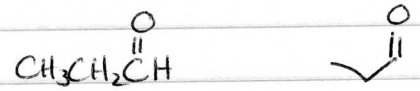

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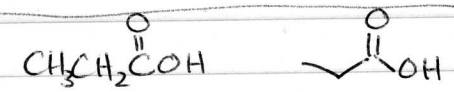

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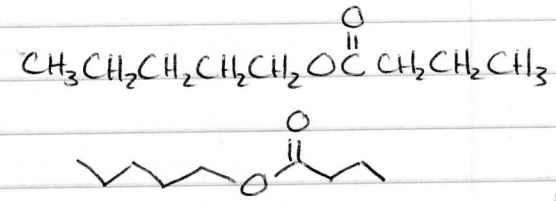

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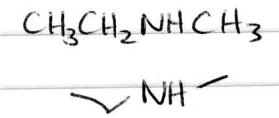

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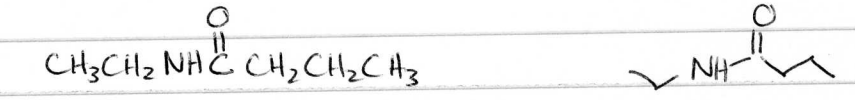
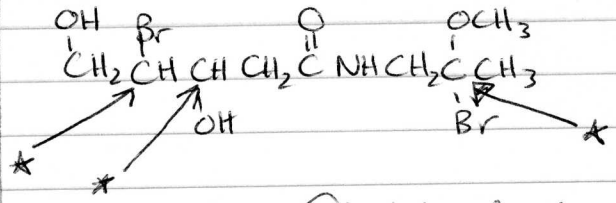


3. chiral C's - attached to 4 different substituents



4. most soluble (b) lots of OH groups. $\frac{3\,OH}{5\,C}$ can form lots of H-bonds to water.
2nd (a) 3-C carboxylic acid - can H-bond to water $\frac{1\,OH}{3\,C}$
3rd (d) can H-bond to water but has a larger nonpolar part than a.
$\frac{1\,NH_2}{4\,C}$
4th (c) ester - polar. can accept H-bonds, but no H-bond donating groups - not as soluble as (a)
(hard to decide between d and c which would be least soluble).

5. All of these have very similar molar masses, so similar London forces.
1. (a) highest bp - can form H-bonds to each other, very polar, can form "dimers" (2 stuck together)
2. (d) can form H-bonds to each other, but not as strongly as a.

3. c. polar but can't H-bond to each other, so weaker IMFs than d.
b. totally nonpolar - only London forces - weakest IMF's overall.

6. a. base hydrolysis of amide. Products:

$CH_3NH_2 + {}^{-}O\overset{O}{\overset{\|}{C}}CH_2CH_3\ K^+$

b. amidation $\rightarrow$ $CH_3CH_2\overset{O}{\overset{\|}{C}}NH_2 + H_2O$

c. ester hydrolysis $\rightarrow$ $CH_3CH_2OH + HO\overset{O}{\overset{\|}{C}}H$

d. esterification $\rightarrow$ $CH_3\underset{CH_3}{CH}\overset{O}{\overset{\|}{C}}OCH_2CH_3 + H_2O$

e. amine + SA $\rightarrow$ $(CH_3CH_2)_2NH_2^+\ Cl^-$

7. amines: weak bases, smell bad (fishy, decay, etc)
aldehydes - some smell good
ketones - excellent solvents
CA's - weak acids
esters - smell good (fruit flavors)
amides - not acidic or basic

8. $CH_3CH_2CH_2\overset{O}{\overset{\|}{C}}H + CH_3CH_2OH \xrightarrow{H^+} CH_3CH_2CH_2\underset{OH}{\overset{OCH_2CH_3}{C}}H + CH_3CH_2OH \xrightarrow{H^+}$

hemiacetal

$CH_3CH_2CH_2\underset{OCH_2CH_3}{\overset{OCH_2CH_3}{C}}H + H_2O$

acetal

acetal formation

9. a. $CH_3CH_2\overset{O}{\overset{\|}{C}}OH + CH_3CH_2OH \overset{H^+}{\rightleftharpoons} CH_3CH_2\overset{O}{\overset{\|}{C}}OCH_2CH_3 + H_2O$

esterification

ethyl propanoate

b. $CH_3CH_2\overset{O}{\overset{\|}{C}}OH + KOH \rightarrow CH_3CH_2\overset{O}{\overset{\|}{C}}O^-\ K^+$ potassium propanoate

neutralization

c. $CH_3CH_2\overset{O}{\overset{\|}{C}}OH + H_2O \rightleftharpoons CH_3CH_2\overset{O}{\overset{\|}{C}}O^- + H_3O^+$

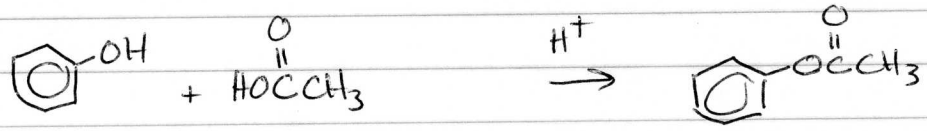
propanoate hydronium

d. $CH_3CH_2NH_2 + HBr \rightarrow CH_3CH_2NH_3^+\ Br^-$

ethylammonium bromide

9 e. $CH_3CH_2NH_2 + H_2O \rightleftharpoons CH_3CH_2NH_3^+ + OH^-$
(weak base rxn) ethylammonium hydroxide

f. $CH_3CH_2\overset{O}{\overset{\|}{C}}OH + CH_3CH_2NH_2 \xrightarrow{heat} CH_3CH_2\overset{O}{\overset{\|}{C}}NHCH_2CH_3 + H_2O$
amidation N-ethylpropanamide

10. a. 

b. $CH_3CH_2\overset{O}{\overset{\|}{C}}OH + HN(CH_3)_2 \xrightarrow{heat} CH_3CH_2\overset{O}{\overset{\|}{C}}N(CH_3)_2$

c. $CH_3\underset{\underset{CH_3}{|}}{CH}\overset{O}{\overset{\|}{C}}CH_3 \xrightarrow[2.\ H_3O^+]{1.\ NaBH_4} CH_3CH(OH)CH(CH_3)CH_3$

11. a. $CH_3\overset{O}{\overset{\|}{C}}CH_2CH_2CH_3 \xrightarrow[2.\ H_3O^+]{1.\ NaBH_4} CH_3CH(OH)CH_2CH_2CH_3$
2-pentanol

b. $CH_3\overset{O}{\overset{\|}{C}}CH_2CH_2CH_3 \xrightarrow{[O]}$ NR
Ketones can't be oxidized

12. a. Benedict's test
Cu^{2+} in basic solution ⊕ - red ppt
if positive, the starting compound got oxidized.
(it could be an alcohol or an aldehyde, but not a ketone)

b. I_2 test - deep blue if positive.
if ⊕, starch is present.

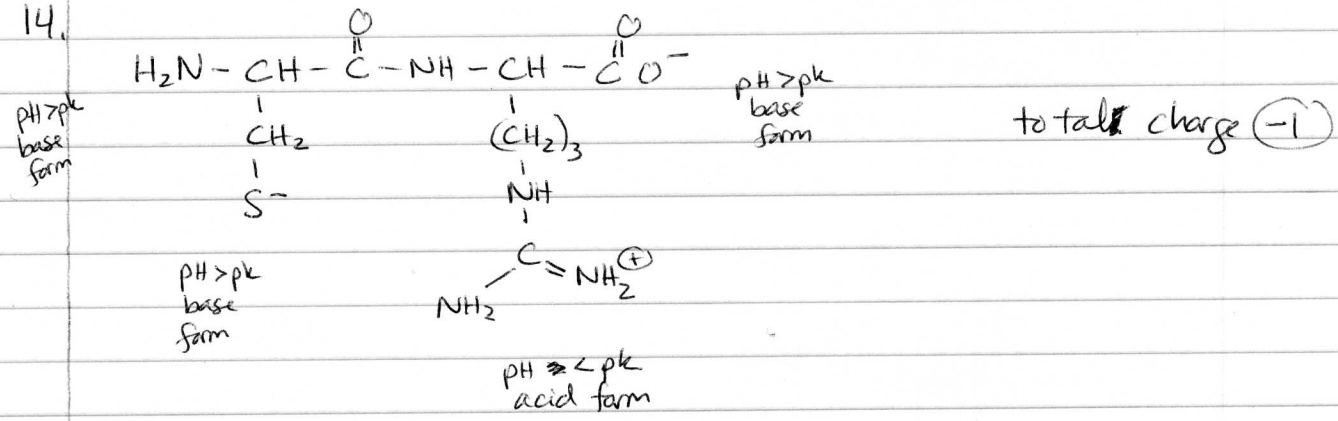
c. Br_2 test - if ⊕, orange color of Br_2 fades.
if ⊕, the compound has double or triple bonds that can react with Br_2 (it adds to double bond)

13. a. $CH_3CH_2O\overset{O}{\overset{\|}{C}}H + H_2O \overset{H^+}{\rightleftharpoons} CH_3CH_2OH + HO\overset{O}{\overset{\|}{C}}H$
ethanol formic acid

13 b. $CH_3CH_2O\overset{O}{\overset{\|}{C}}H + NaOH \longrightarrow CH_3CH_2OH + H\overset{O}{\overset{\|}{C}}O^- \; Na^+$

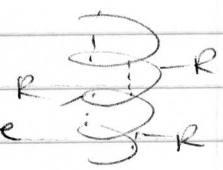
ethanol + sodium formate

14.

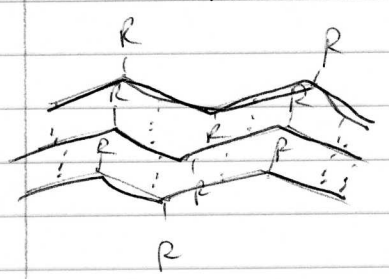


total charge (−1)

15. α-helix – a type of secondary structure – shape – helix or corkscrew.
held together by H-bonds along the back bone



β-sheet – another type of secondary structure
neighboring strands of amino acid chains
H-bond to each other along the back bone



16. acidic conditions (or certain enzymes)
complete hydrolysis yields amino acids.
incomplete hydrolysis yields smaller peptide chains (than before)

17. a. Asp ⊖ Arg ⊕ salt bridge ⊕ and ⊖ charges

b. Gln, Asn H-bonding both have H-bond donating and accepting groups.

c. Leu and Ile – both nonpolar hydrophobic interactions

d. Cys, Cys – disulfide bridges $-CH_2-S-S-CH_2-$

e. Thr, Lys polar ⊕ H-bonding both can donate or accept H-bonds

18. 1° structure - sequence of aa's (held together by peptide bonds)
2° structure - regular, repeating structures such as α-helix and β sheet. Held together by H-bonds between C=O and N-H groups along the backbone of the amino acid chain.
3° structure - overall folding of the entire protein. Stabilized by interactions among the R groups: H-bonding, hydrophobic interactions, disulfide bridges, salt bridges, hydrophilic interactions.
(also involves interaction of side chains with the solvent (water))

19. Denaturation - disruption of normal folding of protein / unfolding.
When a protein is denatured, it can no longer function.

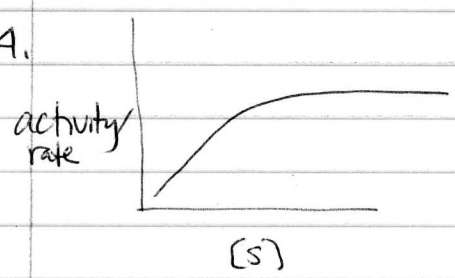
20. Normally, a protein folds so that the nonpolar side chains are on the inside of the protein, away from the water/solvent. Polar and charged groups are on the outside, facing the water/solvent. (There are also some polar and charged groups on the inside, interacting with each other.)
In the presence of an organic solvent, the protein would fold differently. The nonpolar side chains will point toward the outside, facing the solvent (because nonpolar substances are compatible). The polar and charged groups would face inside to be away from the nonpolar solvent. The protein would basically turn inside out and be completely inactivated.

21. If strong acid is added, it causes all acidic groups, which are normally ⊖ charged at pH 7, to become protonated and thus uncharged. This would disrupt all of the salt bridges that are stabilizing the 3° structure. (⊕ and ⊖ charges attract, but ⊕ and ⊘ charges don't!) Protein will unfold partially and become inactivated.

22. Each enzyme has an active site that is specific and fits one particular substrate. It's catalytic groups are positioned to help catalyze one very specific reaction. Other substrates won't fit and won't have the appropriate catalytic groups available.

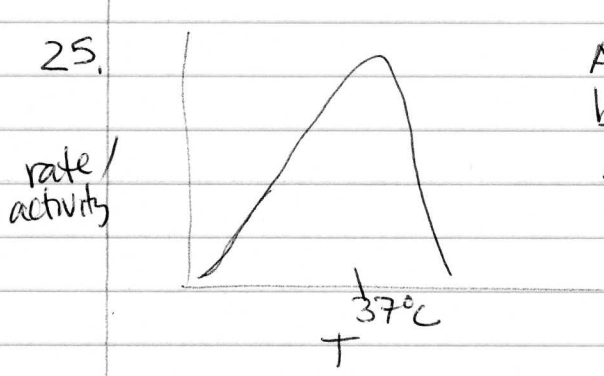
23. The enzyme active site is complementary to the structure of the substrate, so it only fits one type of substrate. As the substrate binds, it is often forced into a more strained shape. This destabilizes the substrate (so it has higher energy) and helps lower the activation energy of the reaction. Groups in the enzyme active site act as catalytic groups, providing whatever is needed for the reaction - (transfer protons, transfer e^-, stabilize charge, break/form new bonds, etc). The catalytic groups are positioned perfectly relative to the substrate in the active site - they give it exactly what it needs to react.
Rxn occurs, and product detaches from the enzyme.

24.



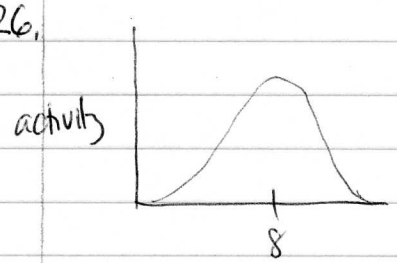
as [S] increases, the rate increases, since there's a greater probability that E and S will collide. After enough S has been added to bind a S to every E, the E active sites are saturated. The enzyme keeps working, but adding more S won't help to speed it up. The E molecules are working as fast as they can.

25.



All reactions are faster at a higher temp, because more molecules will have enough energy to react. As temp keeps increasing, the enzyme becomes denatured, and can't function any more, so rate of rxn slows or stops.

26.



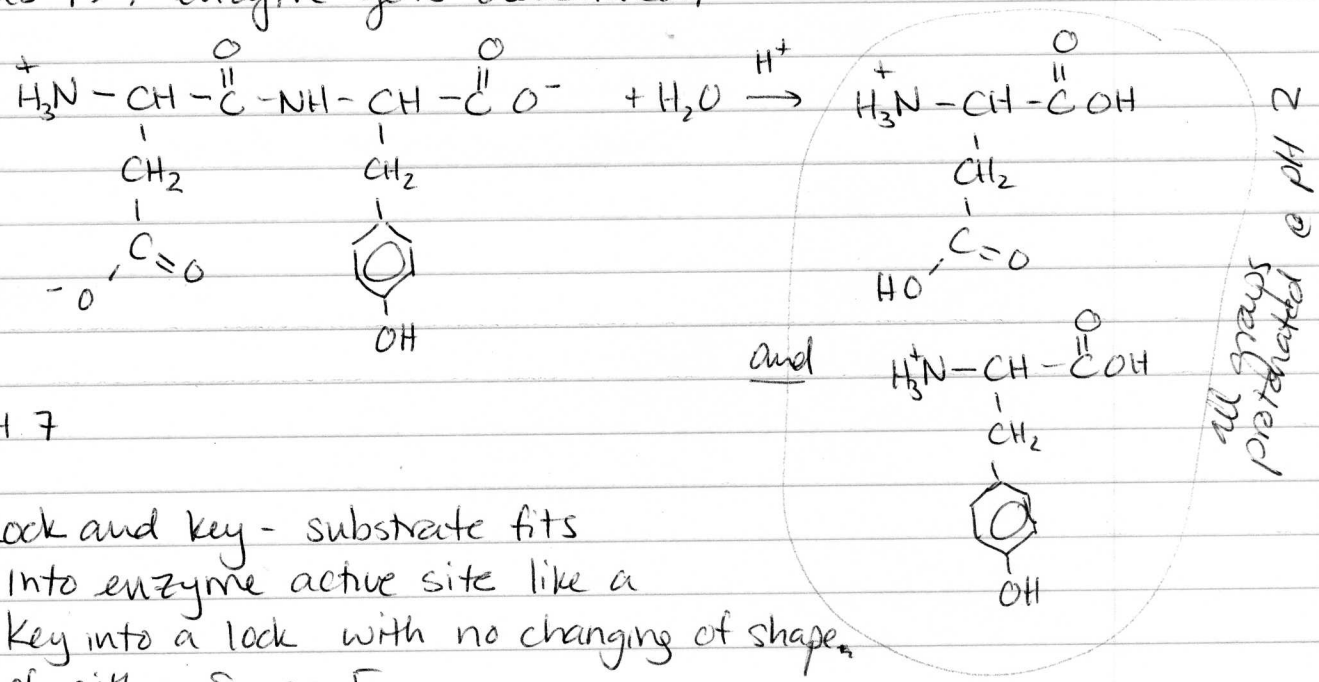
at low pH - very acidic solution - some side chains get protonated which changes ⊖ charges to ⊘ charges. This disrupts salt bridges and causes denaturation of the protein. a denatured protein can no longer function.

27 a. substrate loses H - being oxidized. — oxidoreductase
b. this is a hydrolysis Rxn — hydrolase
c. forming larger molecules, requiring energy — ligase
d. NH_2 group and OH group are switched/transferred between molecules — transferase

28. a cofactor is a non-protein part thats necessary for the protein to function.

29. as T↗, enzyme gets denatured.

30.



pH 7

31. Lock and key - substrate fits into enzyme active site like a key into a lock with no changing of shape of either S or E.
Induced-fit - S or E or both change shape slightly as the substrate binds.

32. lots of N, NH, O, OH - this is polar and would be able to H-bond to water in lots of locations - so water soluble.

33. glucose + Ⓟ → glucose-1-Ⓟ + H_2O — 5.0 kcal/mol
ATP + H_2O → ADP + Ⓟ — -7.3 kcal/mol

glucose + ATP → glucose-1-Ⓟ + ADP — $\Delta G = -2.3$ kcal/mol

ΔG is ⊖ so spontaneous overall.

34. competitive inhibitor – similar in structure to <u>substrate</u>.
This type of inhibitor will bind to the active site, but won't be able to react. When it's bound, the normal substrate can't bind. This will slow the rxn.
(At any time, some enzymes will bind inhibitor and some will bind substrate.)
If you add lots of excess substrate, enzyme activity can be restored.

35. A noncompetitive inhibitor binds to the enzyme somewhere <u>other</u> than the active site. It changes the shape of the enzyme, making the active site inaccessible so substrate can't bind. This will slow/stop the rxn.
(adding more substrate won't help.)

36. a.

$$CH_3CH_2N\overset{O}{\overset{\|}{C}}H + NaOH \longrightarrow \underset{\text{ethylamine}}{CH_3CH_2NH_2} + \underset{\text{sodium formate}}{H\overset{O}{\overset{\|}{C}}O^- Na^+}$$

$$CH_3CH_2N\overset{O}{\overset{\|}{C}}H + H_2O + HCl \longrightarrow \underset{\text{ethylammonium chloride}}{CH_3CH_2NH_3^+ \; Cl^-} + \underset{\text{formic acid}}{H\overset{O}{\overset{\|}{C}}OH}$$