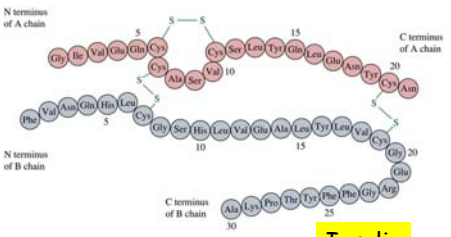
Amino Acids/Peptides



Insulin

- The DL nomenclature, one last time.
- Acid/base behavior of amino acids.
- Racemic syntheses of aa's.
- Methods for resolving racemic mixtures of aa's.
- Determining the primary structure of peptides. Edman & Sanger, MS-MS.

Announcements

Quiz 4 is scheduled for Friday, May 31. The focus of this quiz will be carbohydrates (Chapter 24). The 'think deeply' topic (10 pts) will be *Structures of the Monosaccharides* (Loudon, pages 1173-1182). The only structures you need to remember are D-glyceraldehyde and D-glucose. The remainder of the quiz will consist of suggested Chapter 24 problems (10 pts), problems of our own design (10 pts), and the usual series of bonus questions (5 pts).

It's time to prepare for our final exam! The take-home final exam questions will focus primarily on 41c material, but material from earlier quarters is certainly fair game. You will be allowed to only use the following when working your final exam: a calculator, molecular models, Loudon's text & solutions manual, and any class notes associated with 41a-c. A final exam review session will take place on Friday, June 4th from 4-5:30 PM in Crellin 151.

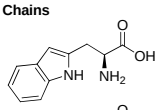
TA Office Hours: Mon 7-8 pm: Rob Craig - 302 Schlinger (x4056); Tue 3-4 pm: Kelly Kim - 302 Schlinger (x4047); Tue 7-8 pm: Corey Reeves - 302 Schlinger (x4056); Wed 5-6 pm: Adam Boynton - 139 Noyes (x3202); Wed 8-9 pm: Ben Suslick (UTA) - Lloyd Lounge; Thu 8-9 pm: Evan Zhao (UTA) - Fleming Lounge; Thu 9-10 pm: Crystal Chu - 202 Schlinger (x3634); Sun 3-4 pm: Chung Wan Lee - 302 Schlinger (x4056).

Suggested Problems for Chapter 26: 26.42, 26.46, 26.48, 26.62(a-g), 26.66(a-d), 26.70.

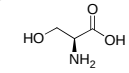
20 amino acids

Neutral Side Chains

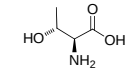
Glycine Gly **G**

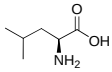

Tryptophan Trp **W**


Alanine Ala **A**

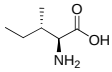

Serine Ser **S**

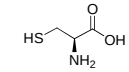

Valine Val **V**

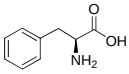

Threonine Thr **T**

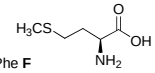

Leucine Leu **L**

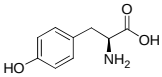

Proline Pro **P**

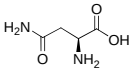

Isoleucine Ile **I**

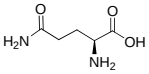

Cysteine Cys **C**


Phenylalanine Phe **F**

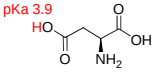

Methionine Met **M**


Tyrosine Tyr **Y**

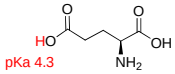

Asparagine Asn **N**


Glutamine Gln **Q**

Acidic Side Chains

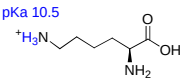


Aspartic acid Asp **D**

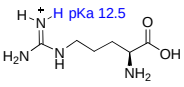


Glutamic acid Glu **E**

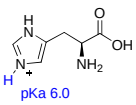
Basic Side Chains



Lysine Lys **K**

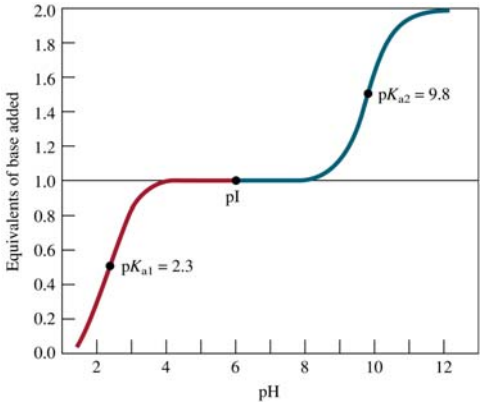


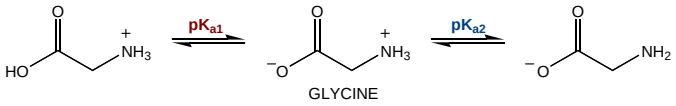
Arginine Arg **R**



Histidine His **H**

Isoelectric Point (pI)



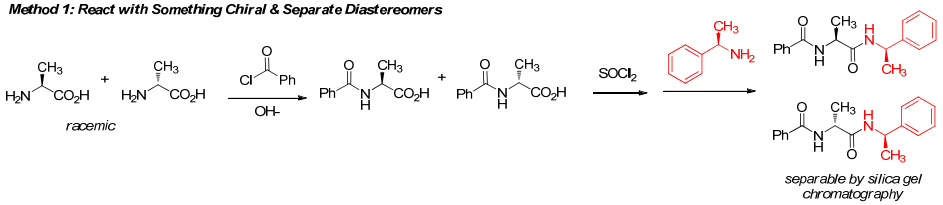


GLYCINE

pI = pH at which the primary species in solution is zwitterionic

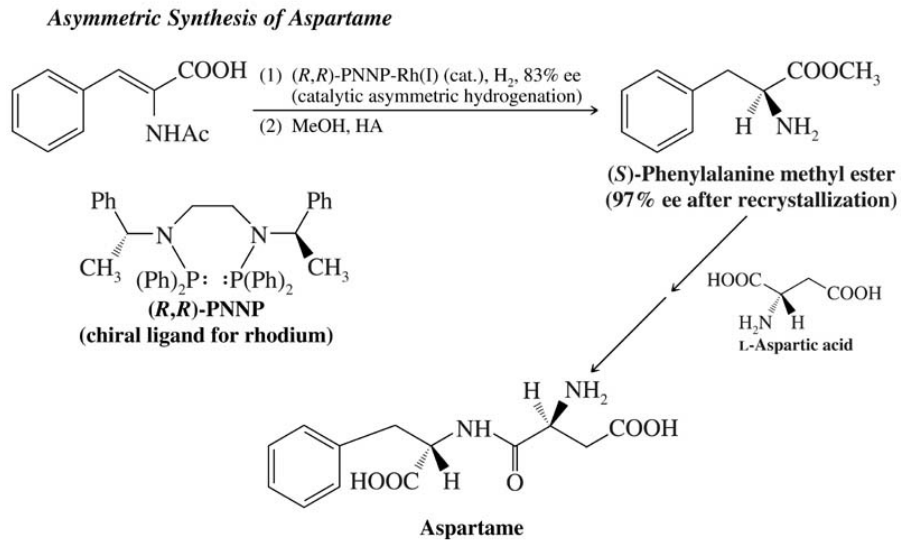
Two Methods for Resolving a Racemic Amino Acid Mixture

Method 1: React with Something Chiral & Separate Diastereomers

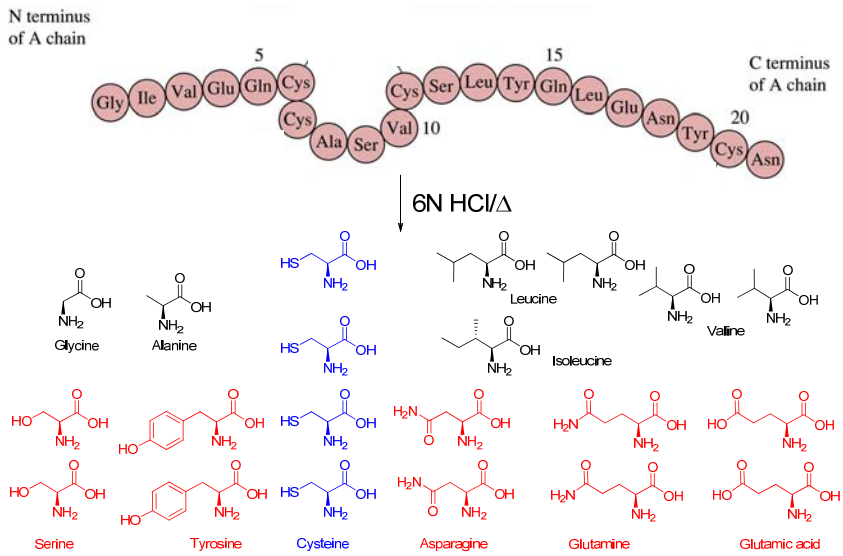


Method 2: Use an Enzyme to Selectively Hydrolyze One Enantiomer

Catalytic Asymmetric Hydrogenation



Determination of amino acid sequence: INSULIN



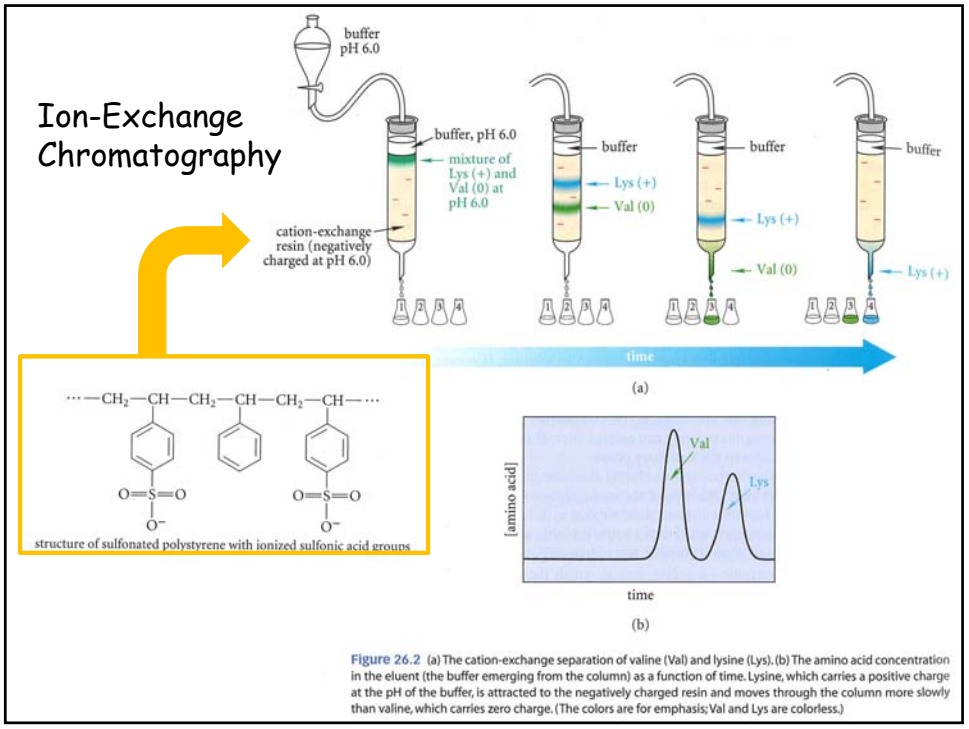
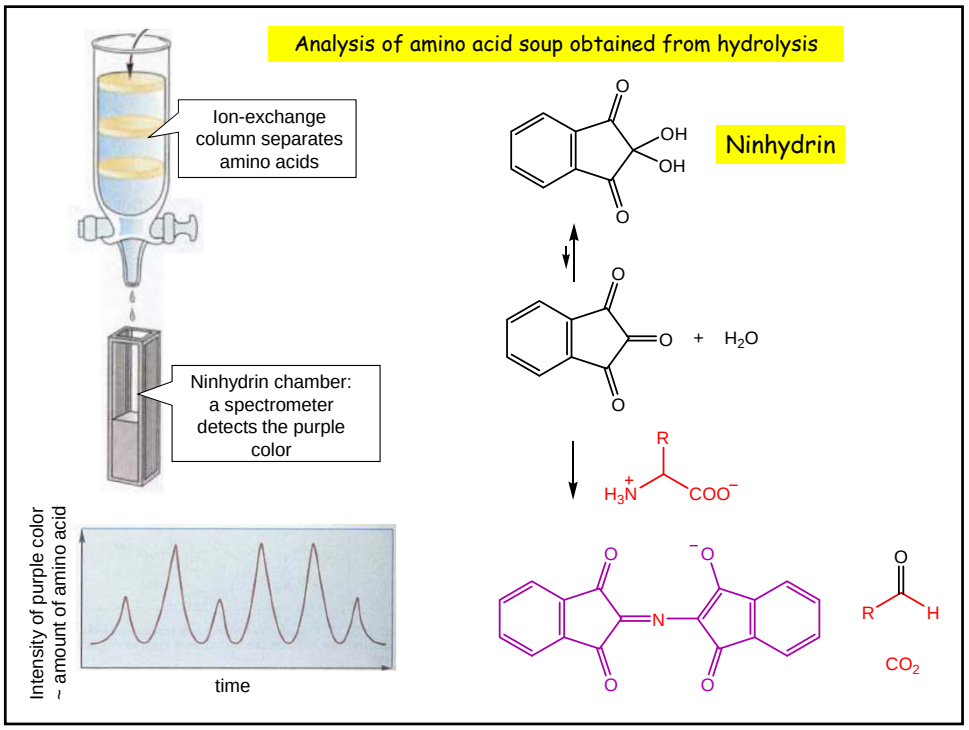
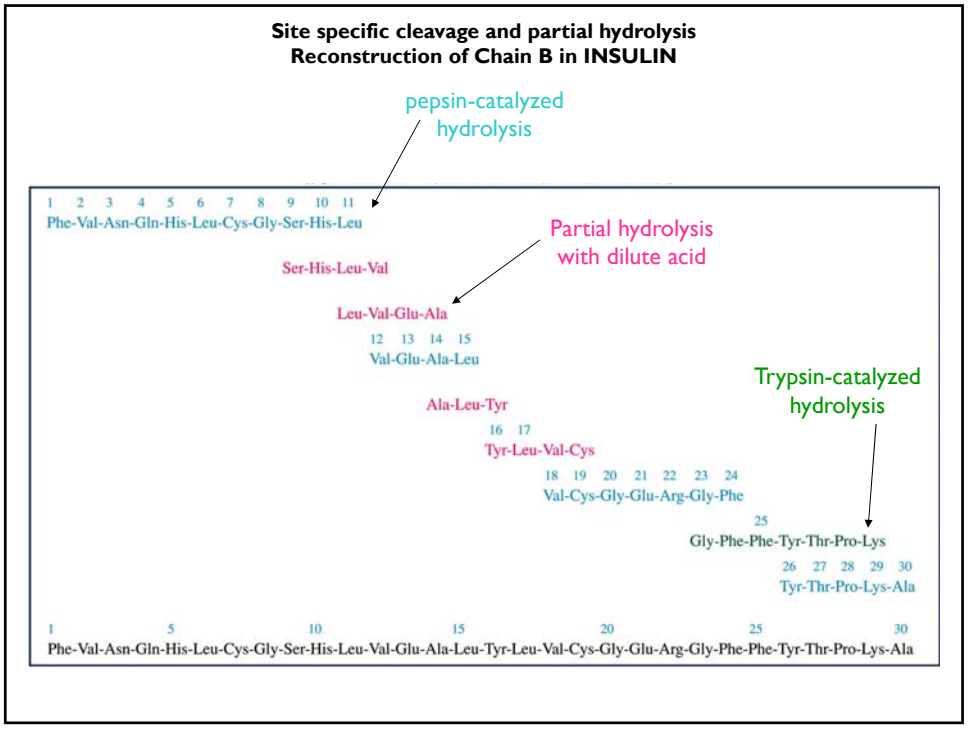
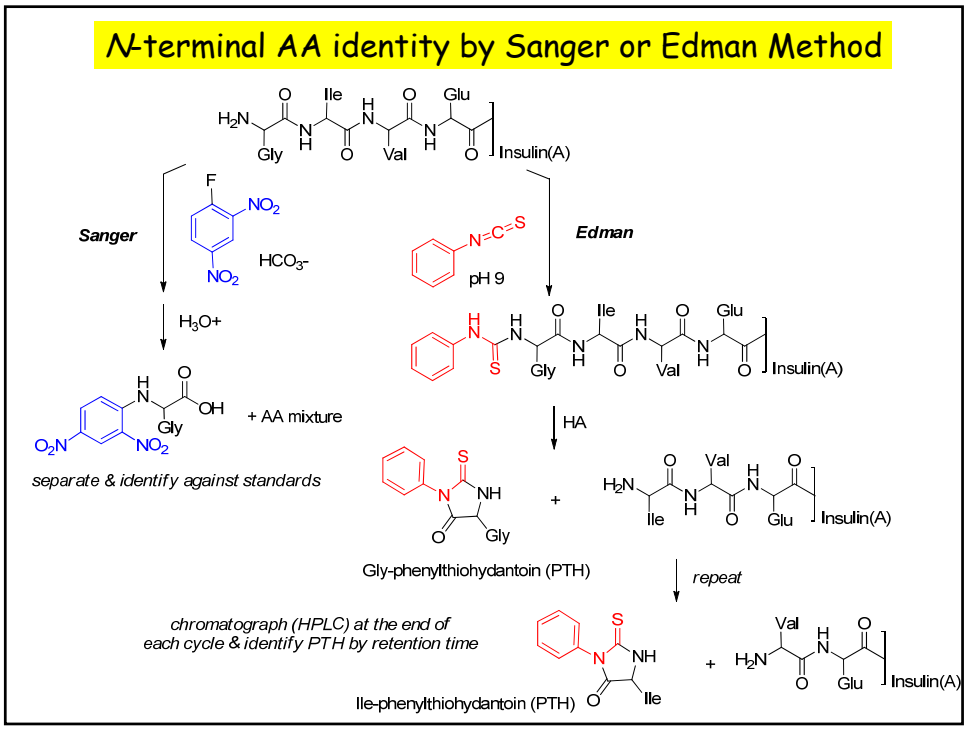


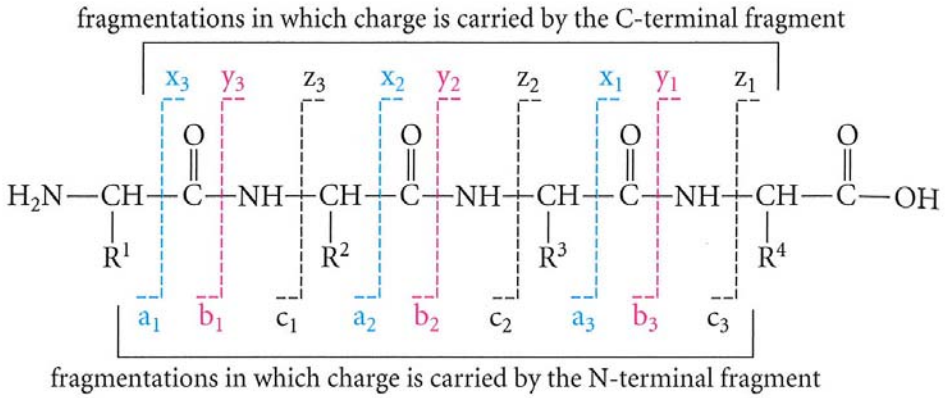
Figure 26.2 (a) The cation-exchange separation of valine (Val) and lysine (Lys). (b) The amino acid concentration in the eluent (the buffer emerging from the column) as a function of time. Lysine, which carries a positive charge at the pH of the buffer, is attracted to the negatively charged resin and moves through the column more slowly than valine, which carries zero charge. (The colors are for emphasis; Val and Lys are colorless.)




Site specific cleavage and partial hydrolysis
Reconstruction of Chain B in INSULIN
pepsin-catalyzed hydrolysis
1 2 3 4 5 6 7 8 9 10 11
Phe-Val-Asn-Gln-His-Leu-Cys-Gly-Ser-His-Leu
Partial hydrolysis with dilute acid
Ser-His-Leu-Val
Leu-Val-Glu-Ala
12 13 14 15
Val-Glu-Ala-Leu
Trypsin-catalyzed hydrolysis
Ala-Leu-Tyr
16 17
Tyr-Leu-Val-Cys
18 19 20 21 22 23 24
Val-Cys-Gly-Glu-Arg-Gly-Phe
25
Gly-Phe-Phe-Tyr-Thr-Pro-Lys
26 27 28 29 30
Tyr-Thr-Pro-Lys-Ala
1 5 10 15 20 25 30
Phe-Val-Asn-Gln-His-Leu-Cys-Gly-Ser-His-Leu-Val-Glu-Ala-Leu-Tyr-Leu-Val-Cys-Gly-Glu-Arg-Gly-Phe-Phe-Tyr-Thr-Pro-Lys-Ala


N-terminal AA identity by Sanger or Edman Method
Insulin(A)
Sanger
Edman
HCO3-
pH 9
H3O+
+ AA mixture
separate & identify against standards
HA
Gly-phenylthiohydantoin (PTH)
repeat
chromatograph (HPLC) at the end of each cycle & identify PTH by retention time
Ile-phenylthiohydantoin (PTH)

MS-MS Peptide Fragmentations



Loudon, p. 1300.

MS-MS Peptide Sequence Analysis

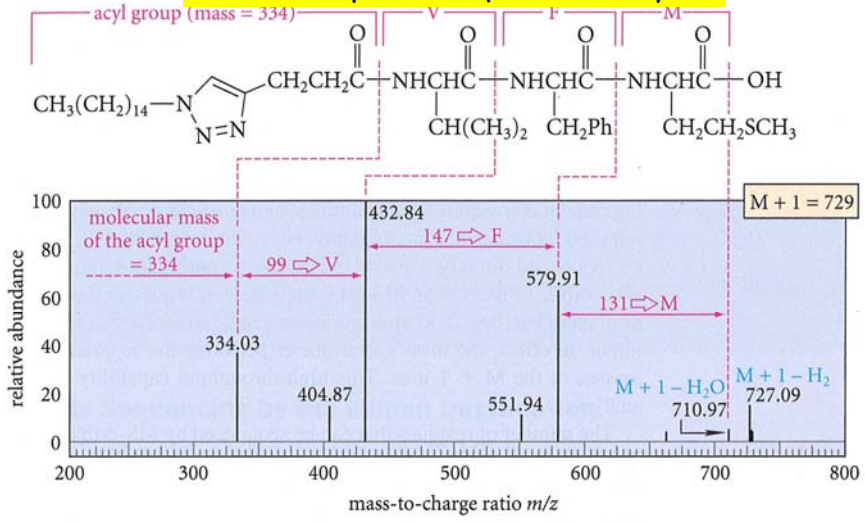


Figure 26.5 The MS–MS of an *N*-acylated tripeptide, V-F-M. The M + 1 ion was observed before it was subjected to fragmentation and found to have a mass of 729. The mass differences between the major peaks correspond to the residues between successive b-type fragmentation points. The fragmentation points are marked with dashed lines. The mass differences correspond to the residue masses in Table 26.2.

Loudon, p. 1301.