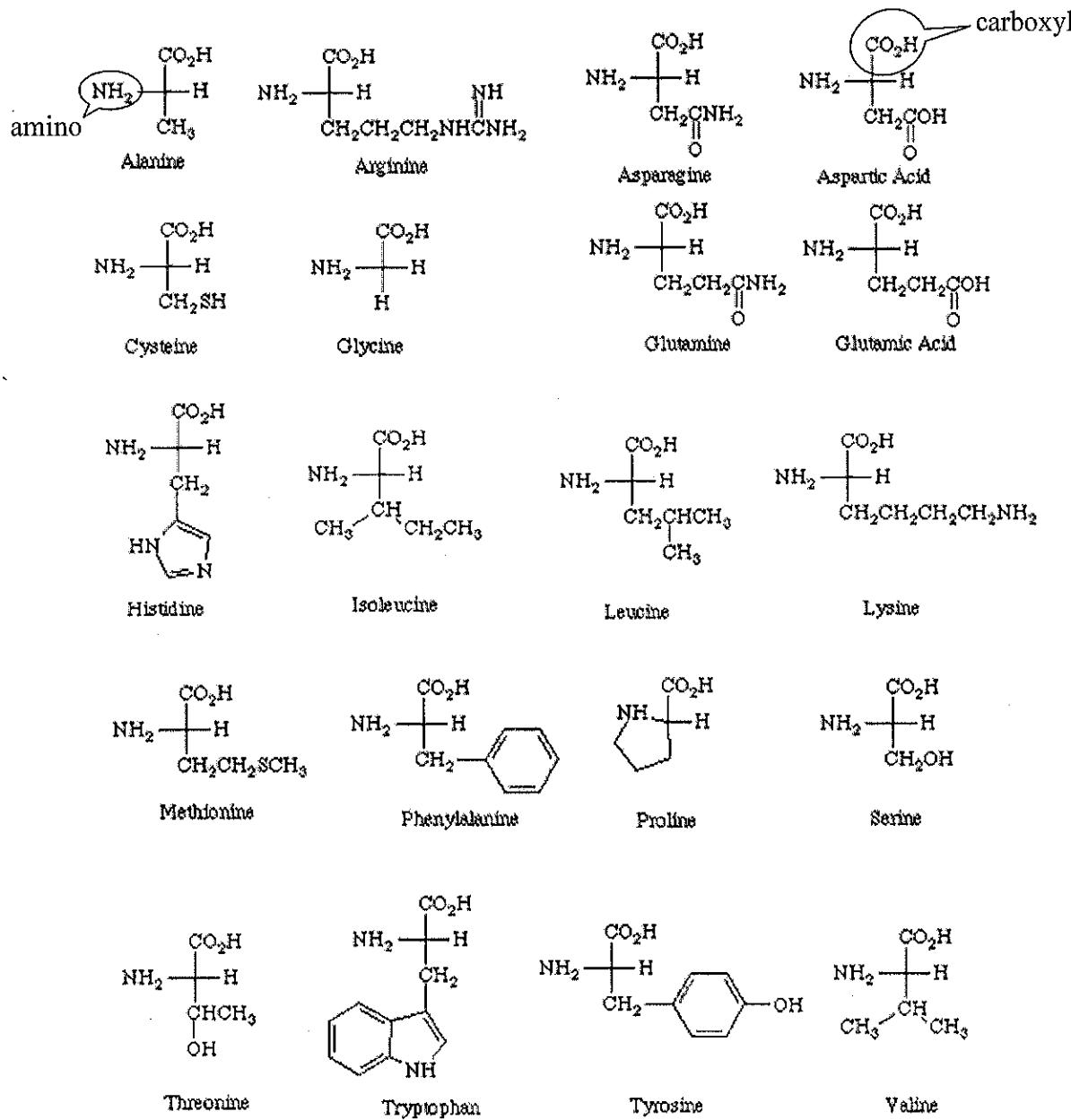


## Amino Acid Structures

These are L- $\alpha$ -aminoacids shown in their Fischer projections.

The structures are listed in alphabetical order. Ionizable groups (amino and carboxyl) are shown in their neutral form - this implies absolutely nothing about the predominant form at any particular pH. These neutral forms DO NOT exist at any pH.



The following table gives the pKa values for the  $\alpha$ -carboxylic acid group, the  $\alpha$ -amino group, and any ionizable side chains.

**Amino Acid pKa Values**

Amino Acid	$\alpha$ -carboxylic acid	$\alpha$ -amino	Side chain
Alanine	2.35	9.87	
Arginine	2.01	9.04	12.48
Asparagine	2.02	8.80	
Aspartic Acid	2.10	9.82	3.86
Cysteine	2.05	10.25	8.00
Glutamic Acid	2.10	9.47	4.07
Glutamine	2.17	9.13	
Glycine	2.35	9.78	
Histidine	1.77	9.18	6.10
Isoleucine	2.32	9.76	
Leucine	2.33	9.74	
Lysine	2.18	8.95	10.53
Methionine	2.28	9.21	
Phenylalanine	2.58	9.24	
Proline	2.00	10.60	
Serine	2.21	9.15	
Threonine	2.09	9.10	
Tryptophan	2.38	9.39	
Tyrosine	2.20	9.11	10.07
Valine	2.29	9.72	

*Last modified 2/4/97*

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<ul style="list-style-type: none"> <li>• Non-polar</li> <li>• <b>Hydrophobic</b></li> </ul>	<ul style="list-style-type: none"> <li>• No charge (non-acidic amino acids)</li> <li>• Polar</li> <li>• <b>Hydrophilic</b></li> </ul>	<ul style="list-style-type: none"> <li>• Negatively charged (acidic amino acids)</li> <li>• Polar</li> <li>• <b>Hydrophilic</b></li> </ul>	<ul style="list-style-type: none"> <li>• Positively charged (basic amino acids; non-acidic amino acids)</li> <li>• Polar</li> <li>• <b>Hydrophilic</b></li> </ul>
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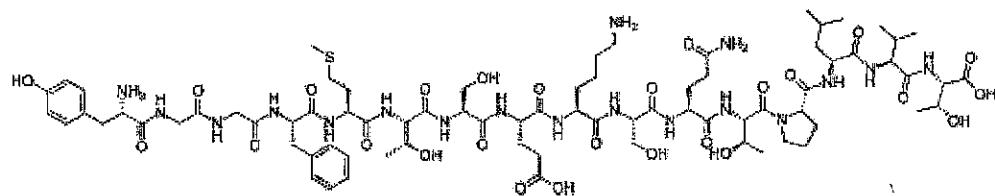
Amino acid	pI	Amino acid	pI	Amino acid	pI	Amino acid	pI
<u>Phenylalanine</u> phe f	5.48	<u>Cysteine</u> cys c	5.02	<u>Aspartic acid</u> asp d	2.77	<u>Histidine</u> his h	7.47
<u>Methionine</u> met m	5.74	<u>Asparagine</u> asn n	5.41	<u>Glutamic acid</u> glu e	3.22	<u>Lysine</u> lys k	9.59
<u>Tryptophan</u> trp w	5.89	<u>Glutamine</u> gln q	5.65			<u>Arginine</u> arg r	11.15
<u>Isoleucine</u> ile i	5.94	<u>Threonine</u> thr t	5.64				
<u>Valine</u> val v	5.96	<u>Tyrosine</u> tyr y	5.66				
<u>Leucine</u> leu l	5.98	<u>Serine</u> ser s	5.68				
<u>Alanine</u> ala a	6.00						
<u>Glycine</u> gly g	5.97						
<u>Proline</u> pro p	6.30						

## Protein Structure and Function

Proteins are the most versatile macromolecules in living systems and serve crucial functions in essentially all biological processes.

FUNCTION	EXAMPLE
structural support	keratin, collagen, and elastin
bodily movement	muscles
defense against germs.	antibodies
membrane component	integral or surface membrane protein
hormones	insulin or oxytocin (messenger molecules)
Enzymes	Biological catalysts (CHP 10)-digestive enzymes
Transport	Hemoglobin
Storage (amino acids of N)	ovalbumin and casein
neurotransmitter	endorphins (peptides)

IN CLASS EXERCISE concerning protein structures (9.3)



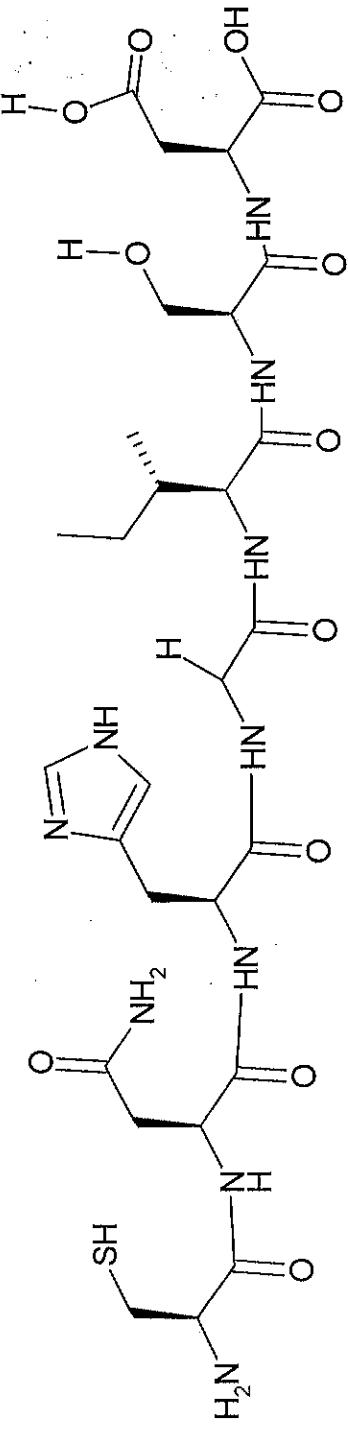
Try writing the primary sequence of this.

N-terminal  
C-terminal  
peptide bonds

PROTEIN STRUCTURE WORKSHEET

1. Fill in the primary structure and show with arrows where the peptide bonds are.

2. Show the bonding (with dotted lines) in the secondary structure of an alpha helix.
3. Draw a parallel polypeptide using amino acid fragments that show all of the possible tertiary structure bonding
4. Describe how these tertiary structure bonds could be disrupted (denature this polypeptide you have made)



## TERTIARY STRUCTURE INTERACTIONS

hydrophobic bonds	between non-polar sidechains
hydrophilic	between polar side chains and water
hydrogen bonds	between polar side chains
ionic bonds	between an ionic acid side chain and an ionic base side chain
disulfide bonds	between sulfurs in two cysteine amino acid residues

## DENATURING PROCESSES (disrupts the 2°, 3°, or 4° structure):

Heat	hydrophobic, hydrogen bonding
pH change (acid or base)	salt bridges
heavy metals	salt bridges, disulfide bonds
oxidation	disulfide bonds
agitation	hydrophobic, hydrogen bonds

## PRIMARY STRUCTURE DESTRUCTION

hydrolysis	destroys primary structure
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