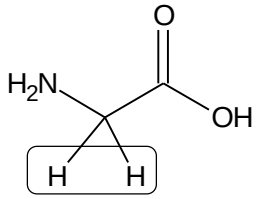
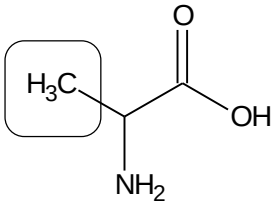
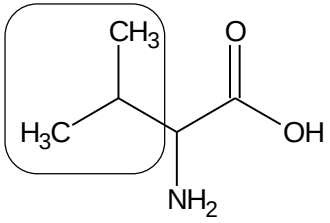
Interactions of amino acid side-groups on a protein backbone
and
Backbone hydrogen-bonding

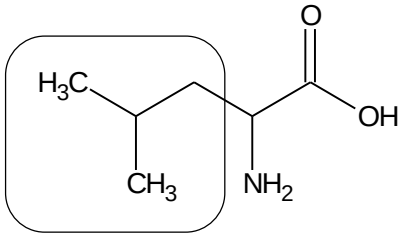
The groups are organized according to their constituent atoms and the type of interaction they are likely to experience. The rectangle encloses the interacting atoms of the side groups.

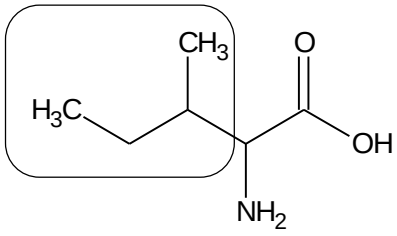
The aliphatic and aromatic groups experience weakly polar and hydrophobic interactions. Additionally, the aromatic groups can have pi-electron attractions. The alcohols and cysteine engage in dipolar/hydrogen-bonding interactions (cysteine weakly H-bonding). Methionine is hydrophobic but a potential hydrogen-bond acceptor. The amides are polar and engage in hydrogen-bonding. The charged carboxylates and aminium ions have electrostatic attractions and hydrogen-bonding.

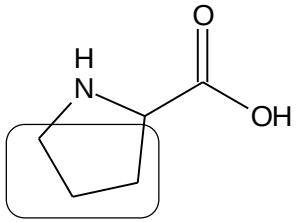
<table>
<tr><th colspan="3">Aliphatic [hydrophobic (attractive van der Waals)]</th></tr>
<tr>
<td> 

glycine</td>
<td> 

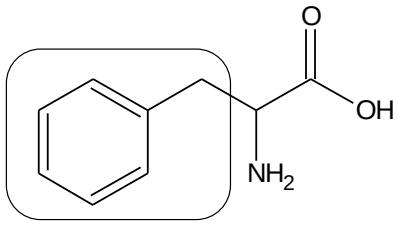
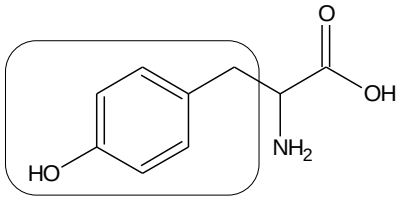
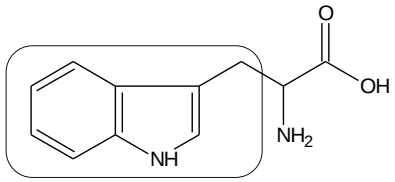
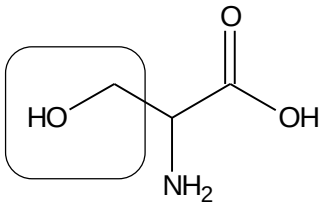
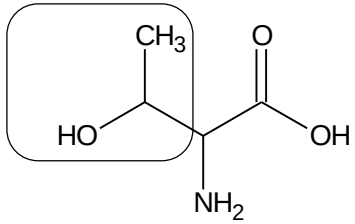
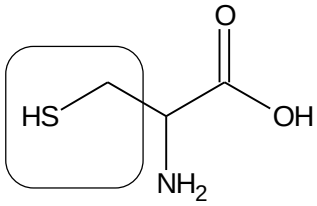
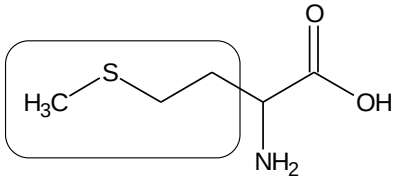
alanine</td>
<td> 

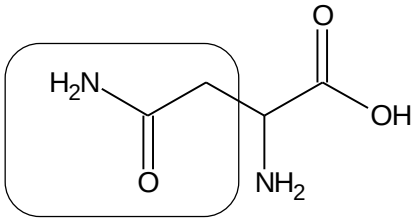
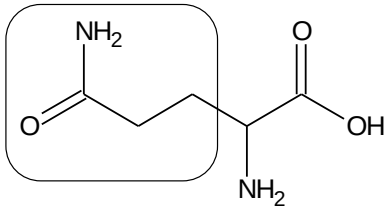
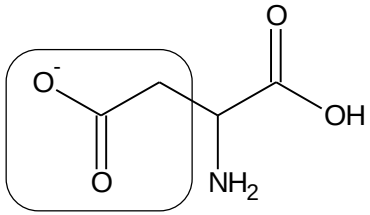
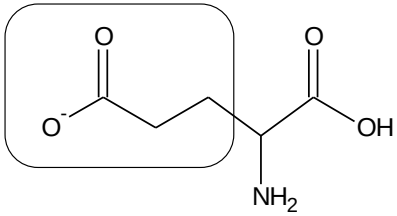
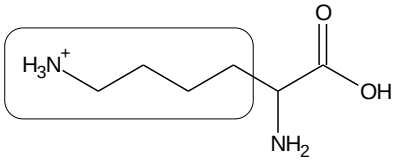
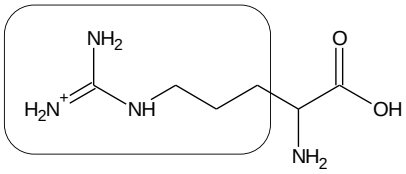
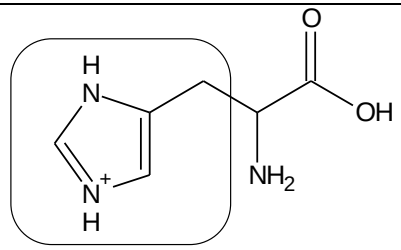
valine</td>
</tr>
<tr>
<td> 

leucine</td>
<td> 

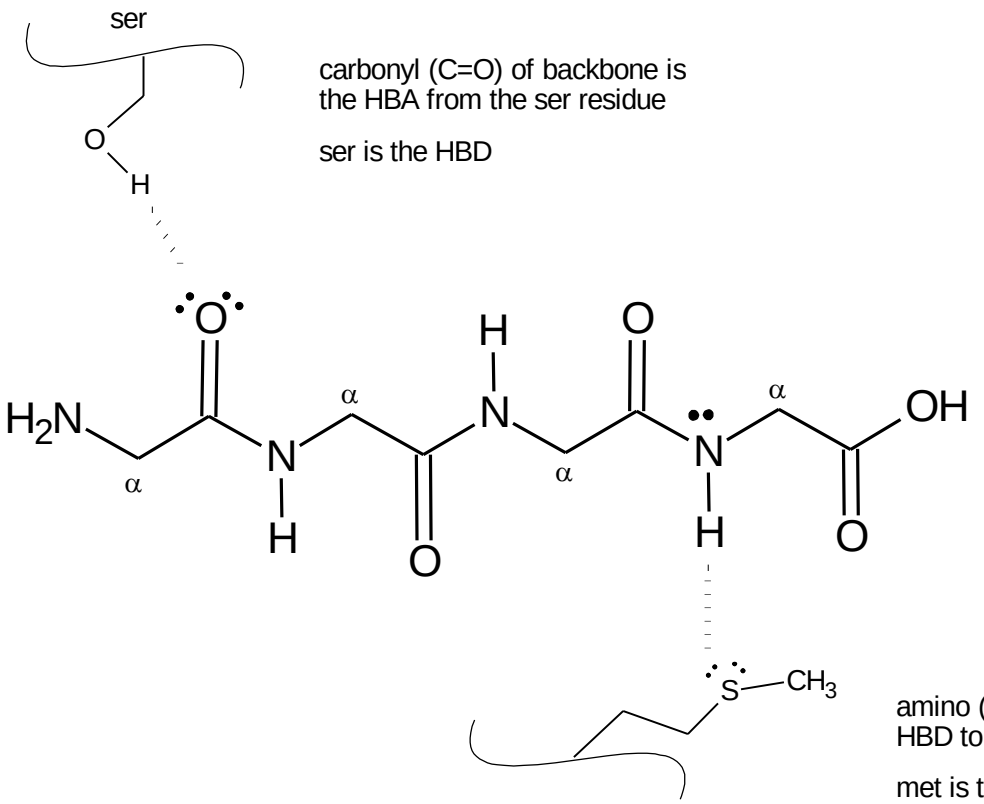
isoleucine</td>
<td> 

proline</td>
</tr>
</table>

Aromatic **[attractive π-interactions; hydrophobic]**		
 phenylalanine	 tyrosine (also an ***alcohol***)	 tryptophan
Alcohols **[hydrogen-bonding; H is hydrogen-bond donor/O is hydrogen-bond acceptor]**		
 serine	 threonine	
Sulfur-containing **[hydrogen-bonding; H is hydrogen-bond donor/S is hydrogen-bond acceptor]**		
 cysteine	 methionine	

Amides **[hydrogen-bonding; H is hydrogen-bond donor/O is hydrogen-bond acceptor]**		
 asparagine	 glutamine	
Carboxylic acids/carboxylate **[hydrogen-bonding, O is hydrogen-bond acceptor; electrostatic attraction to + charge]**		
 aspartic acid	 glutamic acid	equivalent resonance contributors for the carboxylate (CO_2^-)
Bases/aminium ion **[hydrogen-bonding, H is hydrogen-bond donor; electrostatic attraction to - charge]**		
 lysine	 arginine (3 resonance contributors for the $(CN_3H_5)^+$ group)	 histidine (2 equivalent resonance contributors in the ring)

The backbone itself can also engage in hydrogen-bonding interactions



carbonyl (C=O) of backbone is the HBA from the ser residue

ser is the HBD

amino (NH) of backbone is the HBD to the met residue

met is the HBA