Lecture 19A • 06/01/12

Amino acids

This is a subset known as alpha amino acids – it's the same kind of alpha we were talking about when we were talking about alpha protons. This is the simplest of all of them, which is glycine. Notice it has no stereocenter to it. All the other common amino acids [including the classic 20, plus others in extremophiles, such as sulfur- and selenium-containing amino acids founds in critters in hot springs] have this kind of structure to it. You still have that alpha amino group, but then you have an R group that's attached as well. These 20 amino are classified into 8 categories as to whether the R group is just an alkyl group or something with an alcohol or a thiol or another carboxylic acid or an amino or something aromatic or something that's a heterocycle. Let me show you one of the remaining amino acids.

The second-simplest amino acid does have a methyl group; this is alanine. Before I label which kind of alanine this is – there is a labeling system just like we had for carbohydrates – let's make a Fischer projection for this compound. We put the carbonyl up at top, the same way that we did for carbohydrates. Let's say that I fix my viewpoint down underneath the molecule so that the methyl group is pointed towards me, which it should be if it's going to be one of the sidearms. I'm going to make the amino the bottom part of the molecule, as I'm making the carboxylic acid the top part of the molecule. If I'm visualizing it in that manner, should the methyl group be to the left or the right of the Fischer projection? To the right, because if I'm looking up and the carboxylic acid group is up here, the amino group is down here relative to me. If that is a dash, that means it's going into the plane of the board, which, from my perspective, means that it is on the right. This is not the standard way to write it; there's going to me many instances in which it's more convenient for us to write the NH2 in the plane of the paper than to put it in the dash-wedge position. There'll be other times where it's easier to put the alkyl group in the plane of the paper, which is going to force the amino group into the dash-wedge position.

I'm going to rotate this around to put this in the standard way that amino acids are represented. This is just a redraw; it's not changing the molecule at all. The methyl group is going to end up at the bottom; the hydrogen that was on the left is now on the right; the amino that was on the bottom is now on the left. Because it is on the lefthand side, this is called an l-amino acid, so this is l-alanine. The d label would be the enantiomer. Since this only has one stereocenter to it, it means it's going to be a wedge instead of the dash, if we are writing the amino group in the plane of the paper. D-sugars are the ones that are biologically active; l-amino acids are the ones that are biologically active. All the rest of the amino acids have a stereocenter to them. Most of the rest of the amino acids are like this, where if you're focusing on the amino group, you would call it a primary amine. There's one and only one of the common amino acids which is a secondary amine; here's the structure of that compound, proline. Why do we need to know these classes and what does it have to do with acids and bases? We're going to talk about something called the isoelectric point, which is when you have the maximum amount of the neutral or zwitterionic form of an amino acid. Why do we care about that? Because if we're trying to analyze proteins, we need to be able to separate amino acids. One of the ways that we can separate them is to take advantage of their slightly varying acid/base behavior. [column chromatography – ion exchange chromatography, ninhydrin] In column chromatography, what you do is you load a separation material – for example, silica gel, which is the same stuff that's on the TLC place, except you have a whole lot more of it – you take a sample, push it through that gel, either by polarity, which would be a normal column, or by ions interacting, which is what goes on in this ion exchange column, some of the amino acids get held back, they linger longer on that column, so of them come off at different times. If you react it with the ninhydrin, you're able to visualize them, one, but if you're doing a spectroscopic analysis, using Beer's law, you could calculate the concentration of amino acids coming out, which as long as everything's standardized, that means that, given x amount of a protein, you can figure out what percentage of the various amino acids are in it. That can tell you the type, but not the order. [sequencing][polypeptide synthesis][proteins][lab]

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Structures – Identical to those from lab 12B (05/31/12)