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3.091SC Introduction to Solid State Chemistry, Fall 2010
Transcript – Session 32

PROFESSOR: All right. It's 11:05. OK, let's get started.

Last day we talked about protein structure. We talked about composition, which is the primary structure of proteins, and that's the instant R group sequence, as you go down the backbone. The secondary structure proteins is all about packing, and we saw that there were three different structures, the alpha helix, the beta pleated sheet, and the random coil. And the gambit here is to maximize hydrogen bonding. And why you choose alpha, beta, or random coil depends upon the instant R group sequence, which is why in some instances, you can't form the coil. Because the R groups won't allow it. And then lastly, we talked about tertiary structure, and that's conformation, and that talks about our group interactions, and ultimately explains protein folding.

Today I want to talk about denaturing of proteins, which is disruption of secondary and tertiary structures. But before we do so, I wanted to show you. I found another movie reference to chemistry. This comes from 1957, and the movie is called Silk Stockings. It's based on an old Cole Porter play. And this stars Cyd Charisse and Fred Astaire, who were both fantastic dancers. And I want you to see in this film clip how she carries herself. And she actually sings this. She didn't have somebody dub it over. So the singing is OK. It's not great, but you've got to see her posture. She's so graceful. And Fred Astaire is a terrific dancer, but he doesn't dance in this sequence.

And last thing you need to know here is, this is set during the Cold War. So she's playing Ninotchka Yoschenka, a good Ukrainian name, and she's a Soviet representative. And she's fighting with Fred Astaire, who is an American agent. And they're talking about the differences between the Soviet and the American systems. So that's the background. It's 1957. I guess we better get some volume up here so we can hear it. And she will explain to you-- and remember, just parenthetically, that my particular interest in chemistry is, of course, electrochemistry, which is the highest form of chemistry. Now she'll explain it to you.

[BEGIN FILM PLAYBACK]

-If you studied, Kamachev, you would know what I am talking about.

-Who's Kamachev?

-He was one of our greatest scientists. He has proved beyond any question that physical attraction is purely electrochemical.

-You don't say.

-Kamachev has proven it!

-For 30 years, he worked.

-I happen to have worked on the same subject for about the same amount of time, and I have very good reasons for believing otherwise.

-Facts are facts

[SINGING]

-When the electromagnetic of the he-male meets the electromagnetic of the female, if right away, she should say, this is the male, it's a chemical reaction, that's all. And though you Fascists may answer with kisses, the same applies when your Mr. And Mrs. Hey-diddle-diddle with middle-class kisses, it's a chemical reaction, that's all. Say in love, with you, I fall. And in love, with me, you also fall. Though the uninstructed faction calls it mutual attraction, it's a chemical reaction, that's all.

[END SINGING]

-You don't believe in Kamachev?

-No, ma'am.

[END FILM PLAYBACK]

PROFESSOR: See the posture? It's just unbelievable. Fantastic.

OK. So let's talk about denaturing of proteins. So we want to talk about how we can alter the structure. And we do so by invasive means. So let's get to the next slide.

So here's the tertiary structure, and I can point to that. The first thing I wanted to draw attention to, is we can disrupt that structure by change in temperature. So temperature is the first agent that we can use in disrupting, or denaturing, protein. And the whole idea here is to break bonds. But we're only going to break secondary or tertiary bonds. We're not going to do anything to the backbone.

And a good example is what happens when we fry an egg. The egg has protein in it. One of them is ovalbumin. It's about 90% water, about 10% protein. And its native state, its natural state, conformation is a tight ball. And the diameter of that ball is small enough that uncooked egg is transparent to visible light. Egg white is transparent to visible light in its natural form, but when we heat beyond the denaturing temperature, that changes the bonds in here, and it unpacks. And when it unpacks, two things happen. First of all, the length scale changes to be great enough that it scatters light. So now the egg white appears white. And secondly, those various chains entangle, and that gives it its rubbery character. So all of that is happening as a result of the increase in temperature.

So second way that we can operate, is to change pH. And what that does, is it changes hydrogen bonding and electrostatic interactions. Now I draw your attention to zone two here. In zone two, imagine if we take that proverbial drink of cola, and now the pH in here goes way, way down. You can see this N has got a hydrogen

bond over to here. Now, if there's a proton excess, the proton can cap, because this is a proton attachment site. If the proton caps this carboxyl, then this hydrogen bond is broken, and now this thing can unfurl.

Over here, you see, this is an electrostatic attraction. Again, the carboxyl could be kept by a proton, and now the plus minus electrostatic attraction is lost. So by change of pH, we could denature what we see here. So there's a good example. And in fact, I think we do this. We pickle our foods.

And then this one I have, because of my interest in high temperature electrochemical processing of metals, I've been to Norway many times. And this is a food that they will never let me eat, because they're afraid if I ever taste this, I'll never return to Norway. But this is lutefisk, which literally means lye fish. And lye has high pH. And this is an example of denaturing protein by going to very, very high pH. And then you soak it and draw back out and so on. So there's a good example of food.

Now the third one I want to talk about is oxidizing reducing agents to denature proteins. And what they do, they can either create or destroy the sulfide linkages, the sulfur-sulfur linkages. So for example, you see at position number one. Position number one, we can use oxidizing and reducing agents.

And a good example, that comes from hair. So first of all, I want to talk to you. Hair is protein. And this first example is just, how protein can, one strand can bond to the other by hydrogen bonding. So up here you have one strand and a second strand, and there are hydrogen bonds in your hair. Now, what you do when you want to change your hair by blow drying is first you wet the hair. And the water goes in and interrupts these hydrogen bonds between strands. So now each of these cross-links that want to form instead terminate with a water molecule. And now with the water molecules, now you can move the hair one strand versus the other, hold it in place, blow dry, get rid of the water, and form new hydrogen bonds.

So what, on the basis of what I've just told you, how can you account for a bad hair day? What is a bad hair day? A bad hair day is a day in which it's rather humid. And so water can get in from the atmosphere and interrupt these bonds, and then the hair will relax, and go back to a native state that is unfavorable vis-a-vis what you tried to achieve with the blow dryer in the mirror.

So you want to combat this. So what do you do? Well, you bring out covalent bonds. So here's two strains of hair, and there are disulfide linkages between the strands of hair. So now with a reducing agent, reducing agent is going to be a proton donor. And can you see, these disulfide linkages are capped with hydrogen, and now they're terminated. And so now the two strands of hair are free to move relative to one another.

And now when you're at the beauty parlor or the hairdresser, now you can take this hair, for example, and wrap it around-- what do you call this thing? It's a mandrel in the metallurgical word. What do you call this thing? Curling iron or something? Yeah. OK. So here you are. You wrap this around-- I know what it does. I don't know the terms, all right.

So now you see, we've got the hair now wrapped around in this fashion, and now we use an oxidizing agent. The oxidizing agent is peroxide here. You know the

derogatory term, peroxide blonde. There it is, right here. So the peroxide goes in, and now it removes these hydrogens. The peroxide takes the hydrogens away and reforms the disulfide linkages, but now the hair is in this curled state. You know, you might have the opposite. Maybe in your native state, your hair, because of the way the R groups are formed along the length of your hair, you know, it's always, the ones with the curly hair want the straight hair, the ones with the straight hair want the curly hair. And so, you know, maybe you could be running this sequence in reverse. But in this case, somebody obviously wants curly hair. Now they form the disulfide linkages.

So this is the object, here, of denaturing. So now when we go over to here, we have a disulfide linkage, which is forcing this run of the random coil to stay straight. But if we get, in this case, the oxidizing, the reducing, and what will happen is that we will break this. So the reducing agents will destroy disulfide linkages, and the oxidizing agents will create disulfide linkages, and thereby we can distort the natural form of the protein.

And here's a fourth example. There are many others, but I'll just give you four here. In the fourth one, we can use detergents. And last day, I showed you the example of how to do your laundry. And so you've got this long aliphatic tail and the hydrophobic head, and you can imagine if you take such species and you've got this hydrophobic pocket, the species will operate in such a way as to pull these non-polar entities out, and then destabilize this hydrophobic pocket.

So depending on what the nature is of the protein, these various chemical and thermal actions can lead to denaturing. So this destabilizes hydrophobic pockets. All right. So that's pretty good.

All right. Well, I think this is where I want to leave it with the treatment of proteins. And I want to move on to a second biomolecule, and that's the lipid. We'll say a few words about lipids.

Lipids are not classified on the basis of their composition, but rather by their properties. So they are defined their properties, which is kind of unusual. Normally we define things in terms of their chemical compositions. And in particular, they're soluble in solvents of low polarity. Some of the books say nonpolar solvents, but even something that's polar but only mildly so will work, in solvents of low polarity. So that's the example. They're insoluble in water, they're oily to the touch. And this includes things like fats, oils, these are all lipids. Cholesterol, hormones. These are all members of the lipid class.

And so let's look at some examples. We've got some slides. So if you start over here with the glycerol, this is a trialcohol. And you can see the OH. We're going to drop the H's, and we're going to put these long aliphatic chains on. There's 14 carbons here, plus the two, so it's 16 carbons long. And this also is seven plus seven, and then the two carbons. And the difference here is that in this case, it's all straight chain.

In this case, we go for seven, then we put in a double bond. And by doing so, when we get to the double bond, that forces everything to go into planar 120 degree arrangement. So you go for seven however you want, and then there's this rigid 120 degree placement, and then you go for seven however you want. Well, clearly, the one in the middle is going to pack better than the one on the left. And so even

though they have seemingly the same chemical composition, the one in the middle is a solid. It's a fat. The one on the right is a liquid, because it doesn't pack well enough. The bonds aren't strong enough.

So these are both examples. And this is called a palmitic acid. And you can see here oxygen acting as a bridge, as an ester. So oxygen, over and over again, acting in this way to give us the ability to make these other longer structures.

Now we can replace that oxygen bridge with a dibridge. So instead of having just an oxygen here, we're going to put a phosphate. So with the phosphate, we've got a phosphodiester linkage. There's one ester, there's a second ester. And why we doing this? Because nature wants to get the spacing right. And remember what I just said, because by the end, you're going to see that spacing is everything.

So we can use this, and we can even lose that oxygen, and put something else here. So here's a-- I'm not expecting you to know these by heart. I would give you the structure and tell you what it is, tell you its name, and then we can go on from here.

So what do you see here? Well, this is called a phosphatide. And this one is a phosphatidylethanolamine, because there's the amine here. And look at this thing. Well, you've got a phosphate in the center that's the bridge. This is the glycerol, the three carbons. In its most primitive form, we could just have hydroxyls here. This is the fatty acid off the one end. Long chains here, not to scale. So these things should be way, way over to here. And over here, we have an ethanol amine.

But look more closely. Well, this is a hydrophilic head, this is twin hydrophobic tails. Look, this is just hydrocarbon. It's not soluble in water. So now you've got this amphipathic molecule. It looks like a detergent, doesn't it? This long, hydrophobic tail could stab the grease, and this hydrophilic head can bond to the water. And now if we shake things up, we'll release the grease that's binding the soil to your T-shirt. Got the phosphate bridge here, and look even more closely. There's a minus, and there's a plus! This is zitterionic, on top of everything else. So this can function as a zwitterion, too. And everything we learned about zwitterionic chemistry and buffering, this thing can do. That's cool.

All right. So now I want to show what happens when I take a whole bunch of those. All right? So let's go back. I want to keep this one up, and I want to want to do is take a whole bunch of those, and show how lipids can actually operate in order to build complex structures for us.

So what I'm going to do, is I want to represent that molecule. So here's the hydrophilic head. That's the amine, right? And then we've got twin hydrophobic tails. And that's your carbon sp3 chains. And I don't want to write that so much. So I'm just going to simplify that as simply hydrophilic head and hydrophobic twin tails. So this now represents the twin tails.

Now if I put a whole bunch of these in water, what's going to happen? First of all, this is hydrophilic. And what if I were to just pour this into a beaker? What do you think would happen if I introduced this into a beaker of water? Well, this is hydrophobic, this is hydrophilic. Can you imagine that they would all sort of line up like this? We're trying to stick the hydrophobic tails up into the air. Because they don't want to be down in here. This is hydrophobic. Doesn't want to be here.

So now suppose I put a whole bunch of these in water. More than four, right? With only four, that's the best can do. What if I put some molar? So then what it does, is it forms a pocket. It's going to do this. All the heads are going to find each other, and all of the tails are going to find each other. Because now they're going to form a hydrophobic pocket. So they'll do it this way, because they can-- can you see how the heads can sort of make a wall against the water? And you go on and on and on, not to scale, and then finally you have some end effects here.

So what have I formed here? I've got something, first of all, I've got a lipid layer here, and a lipid layer here. So together, I have a lipid bilayer. In here, there's a pocket. And now, what I can do with this whole thing, is I can build a cell wall with this. I've got a cell wall. I've got an outside and an inside.

So what happens is, when we put all these things together, because of the clustering of the hydrophobic and hydrophilic, we say this thing is endowed with the property of self-assembly. Very hot topic in material science. And that leads to cellular structure, and I think we've got a nice cartoon here. So this is taken from one of the readings. So you can see this with the plurality of these. They're actually showing the twin tails. Now, this was taken from another text. I like this one, because it shows the hydrophilic top, hydrophilic bottom, and the hydrophobic interior.

And then this thing is called an integral protein. Why? Because it's integrated into the cell wall. And let's think about this protein for a second. What must be the nature of the R groups in this vicinity of the protein, that it sits where it does? The R groups around here must be dominantly hydrophilic, otherwise it would get dumped out of that zone. And in here, it must be dominantly hydrophobic, so that it feels at home with all of these hydrophobic tails. And over here, it must be hydrophilic.

Now imagine what happens. I'm going to go back to that drink of Coca Cola. Forgive me, no brand names. Cola. And now the this zone here gets flooded with protons, because the pH is dropping. So that could cause conformational changes, because pH changes the conformation of the protein, and it could cause this thing to change shape. It could unfold, or it might unfold in such a way as to open a channel down the center here. And so in response to a change in pH here, we open up a channel, which means this is acting as a chemical gate. This is how things are animated! It responds. And then once the proton concentration has been depleted and you're back to a more neutral pH, then this thing changes back to its old confirmation, and the gate closes. It's that simple! The secondary bonding explains animation. That's what's happening.

And there's one other cool thing. Look at this. If they all have the same head, They're going to close pack! It's fantastic. Everything. Everything you need to know, 3.091 here.

All right. So what is the key to animation? The key to animation is self-assembly. And why do we have self-assembly? Because we have these molecules with the hydrophilic head and the hydrophobic tail. These molecules are called amphipathic. OK. So this has hydrophobic and hydrophilic components. So if you take amphipathy, you end up with self-assembly. That's the key. All right, good.

All right. I think that's all I want to say about lipids. That's all you need to know about lipids, is lipids will give you cellular structure.

Now we've got a little bit of time left, and we're going to talk about nucleic acids. So what do I want to say about nucleic acids? Nucleic acids carry information. They carry information that directs metabolic activity, including replication. And something can be animated, but it doesn't count as a life form unless it replicates. That's the characteristic of life forms. So nucleic acids carry information that directs metabolic activity, including replication.

So these are macromolecules. Not polymers, but macromolecules. We'll take a look in a moment at their structure. They're macromolecules, and the basic structural unit is called a nucleotide. And it's got three building blocks. Every nucleotide has three building blocks.

See, what we're doing right now, is we're really tying together all of that chemistry you've been learning the entire semester. And it's fun to see it actually go to use.

So what are the three building blocks? Every nucleotide has a sugar. And we didn't study carbohydrates, but I'll just show you the structure the sugar. It's got an amine. You know what that is. That's the NH something group. And it's got a phosphate. So the nucleotide has those three components,

So let's take a look at the sugar. There's really two types of sugars found in amino acids. There's the ribose-- and the only reason I'm showing you this, is so that you'll understand the terminology. There's the deoxyribose. So if you look here, the sugar on the left has this five-fold symmetry, the five-fold ring. And there's hydroxyls at the number one position, number two position, number three position. The deoxyribose is missing the hydroxyl at the number two position. That's the difference. The reason I'm showing you this, is this is called deoxyribose, and ultimately this is the D in DNA. So you'll be able to at least hold your own with your course seven major friends, if you have any friends in course seven. And you can say, I know what the D is. It's deoxyribose. OK.

So then the amines. The amines we've got, there's five of these. And they split for RNA and DNA. And they're shown here. So it's interesting. There's two of them that are called purines, because they've got this ring structure. And then the six fold, and then the five fold. So these are the purines, and then the pyrimidines have just the six fold structure. There are three of those. So A, G, C, U, and T. Those are the five different amino acids. And the difference is that in DNA, you only have A, G, C and T, whereas in RNA, you have A, G, C, and U. This is the chemistry. If you take 7012, you'll figure out how all of this other stuff goes.

And this thing here is phosphate. And why is phosphate present? Because it's acting as the bridge and a spacer.

So let's take a look at the structure. OK. There's more of the amines in nucleic acid. So this is what it looks like. So you have a backbone that consists of sugar phosphate, sugar phosphate, sugar phosphate, shown here. So in this case, you've got the deoxyribose. So there's the sugar, there's the five-fold symmetry. Then the spacer, the phosphate, then the sugar, and then the spacer, the phosphate.

And you can see that the sugars are acting as hangers for these amine groups. And they're called bases, because in fact they act as Bronsted bases. They're proton acceptors, and in the early days of molecular biology, people determine the chemical composition by wet assay, and these were determined to be Bronsted bases. And so

to this day, people refer to them as base pairs, et cetera, et cetera, even though now we know they're amines, et cetera.

So this is the structure going up. And you see, at one end, you've got the three, and going up to the five. The three is, you have the carboxylic acid end, and at the other end you have the amino end. OK. So there the structure.

And you have a choice here. So again, the sugar hanger, the phosphate spacer, the sugar hanger, the phosphate spacer. And you have a choice of one of these four. Any one of these four is what's found in a DNA strand, as you go up the strand.

Now, how is information encoded? Well, the information is encoded-- first of all, we have to recognize what the structure is. Know that the structure, turns out that it forms a double helix, which is the first secondary structure, right? It doesn't have. The primary structure is this instant A, C, G, T sequence all along. And then the secondary structure is, in order to maximize hydrogen bonds, this forms a double helix with a second chain. And furthermore, the pairing is such that A always pairs with T, because they have two hydrogen bonding sites between them, whereas C pairs with G, because they have three hydrogen bonding sites between them.

And furthermore, look at the spacing here. This always just stuns me. If you look down the center of the strand-- so I've got two strands of nucleic acid. The center to center spacing is 1.085 nanometers between A and T, and it's 1.085 nanometers to four significant figures between C and G. And you might say, well, is it possible that I could take two of these hydrogen bond sites and line them up to two of the three hydrogen bond sites? And the answer is no, because the spacing is wrong. You can't, these two are far enough apart that they won't line up here. So it's guaranteed that it's always A to T, C to G.

All right. So now you see the double strand. You have one strand moving up. You see the pentagon is pointing up, and here you see the pentagon is pointing down, and we have the base pairs in between. C pairs to G, and T pairs to A. And down here is the basic end, the acidic end, the basic end, the acidic end. And so the secondary structure is the double helix. Why? To maximize hydrogen bonds in between, and then to keep maximizing hydrogen bonds. Hydrogen bonds between the galleries. Maximize, maximize, maximize.

So there's what they call the base pairs, and et cetera, et cetera, et cetera. This distance is all prescribed by the fact that we have the phosphate present.

OK. Now where's the information here? I said this encodes metabolic information. Well, suppose I want to direct protein synthesis. I want to put amino acids in a sequence. So I have to be able to call. You know, I'm sitting here as nature, and I'm saying, I want to make this protein. So I need this amino acid, and then I need this amino acid, and then maybe that amino acid, and put them in sequence. So I need 20 different words to call 20 different amino acids. Well clearly, clearly if I have just A, C, G, and T-- so if I have one-letter words, it won't work. Because I need to call out 20. I need 20 amino acids.

So how am I going to get to 20? I don't have 20 of these. I'm only using, there's only four of these. So I say, oh. I know what to do. I can use this idea. The number of words will equal the number of letters that I have in my alphabet, raised to the power, number of letters per word. OK? So if I use this idea, then I can say-- what if

I have two-letter words? So in other words, to call out an amino acid, I have to take two base pairs in sequence. That means I'll have-- there's only four letters. But if I have two letters per word, that's 16, which is still less than 20, and that's no good, because I can only call 16.

So what does nature do? What if I had three-letter words? Three-letter words, then, is a 64, which is greater than 20, and that works.

So now I've got, in point of fact, 61 of these three-letter words. So I go down the sequence. First base pair, second base pair, third base pair. That triad represents one amino acid. I've got 61 to call out 20, And I've got three left over. For what?

Well, let's think about this. See this? How do you know to read this, defined by their properties? You know to read from left to right. You know that there's a space here between words. So if I just give you this strand of DNA, where do I begin? Do I take these three, or do I start counting from here or here? So built into this, it tells you to read either from left to right, or right to left. It tells you where to start, and it tells you where to stop. These three-letter words, by the way, are called codons. So we've got sixty-one to call out 20 amino acids, which means, some amino acids have more than one name. There's one of them that has six different names. There's six different codons that can call it a given amino acid. For some of them it's only one, for some it's two, three, et cetera.

OK. So that's the information. Look! Here it is! There's the information! It's all in there. Just hydrogen bonds like this, hydrogen bonds like this. It's all bonding.

So here's the codon. So somewhere here, see, we take this, this, and this. This triad represents one piece of information.

All right. So let's go back and look at some of the history. Who got us to this point? This is fresh! A lot of this happened in my lifetime.

All right. So Oswald Avery-- this is before my lifetime. He was working at the Rochester Institute. And he was the first person-- he was born in Halifax, actually. And he worked professionally here in the United States. And he was the first person to recognize that nucleic acids store and transmit genetic information. Up until the 1940s, people thought nucleic acids-- are you ready for this?-- are too complicated. Their structure was too complex to contain information. It's precisely the complexity that gives us the abundance of information! The prevailing belief was that proteins contained the genetic information. But people couldn't figure out how to make it work. So he was the first to make the argument that the nucleic acids have the information.

And then the second giant is Erwin Chargaff. Erwin Chargaff worked at Columbia in New York, and hospitals in the vicinity. And he was a painstaking analytical chemist. He did all of this work by analytical chemistry, and he gave us Chargaff's Rules, 1949. And he said that in any biological system, the concentration of a-- remember, they didn't know the structure of DNA yet. I'm going to lead up to how we get to the structure of DNA. So we're going back, this is like a flashback in a movie. Now we're going back to see how we got to the double helix, all right?

People knew that the concentration of A in any nucleic acid was equal to the concentration of T. They knew that there were sugar present, they knew there were

amines present, and they knew there were phosphates present. That's all they knew, based on chemical analysis.

And now he tells us that, of the amines, concentration of A always equals concentration of T, concentration of G always equals concentration of C. And then the sum of concentration A plus G is the sum of C plus T. That's Chargaff's rule.

And so here we are, Homo sapiens. 31, 31, 19, 19, a little bit of statistical error, et cetera. But look! Corn! Yes! Corn reproduces using this same code. All living organisms on this planet use the same code.

Which makes sense! If I eat corn, and I'm going to get nutrition from it, and it's going to help me build cells, and regenerate my body, and get energy from it, it has to be made of this same stuff, otherwise my body can't recognize it! Because I'm a biological machine. This is not a fireplace in here, right? If it's a fireplace, you can drink something combustible and boom! You've got energy. But we can't derive energy from something combustible. We can only derive energy from something like this. So, you know, when you think you're really hot stuff, your DNA is not that different from that of an ear of corn. So a little bit of humility might be in order.

All right. And then the last person we want to talk about is Rosalind Franklin. Rosalind Franklin worked at the King's College in London, and her specialty was x-ray diffraction. And she made painstaking experiments where she could take a strand of DNA with a stainless steel needle and pull it out of an aqueous solution, and hold it in a chamber where the chamber was humidified so that the DNA didn't dry out. And while it was humidified in this chamber, take an x-ray diffraction exposure for hours, because all of the recording was done by film. By halide photography, and you had to have long exposure time.

This is one of the most famous images of the 20 century. This is the image of the DNA from calf thymus, the beta structure. And this is a Laue pattern. So the symmetry of this pattern is reflective of the symmetry in the DNA structure, which people don't know yet. And what you see is five positions. One, two, three, four, five. Four is missing. There's no reflection there. But it's where you would expect a position to be. So it's sort of Bragg-like, isn't it? Not all of the lines are reflecting.

On the basis of this image, this is what we learned. We learned, first of all, that the Laue pattern is indicative of a double helix. Based on X pattern. Remember, they had no computers in those days! All they had was a pencil and paper. So to do the Fourier transform, and go back out of K-space, and discern what the pattern is-- you know, today it's trivial! They did this all longhand.

Number two. On the basis of that pattern, you learn that it's 3.4 angstroms between nucleotides along the backbone. We don't know what the backbone is! We just know that there's sugar, there's amine, there's phosphate. There's different ways of putting this together to make a chain.

And the third thing that you learn, because the strong, clear lines indicate that the heaviest elements must lie outboard. What does that mean? If you've got a double helix, based on the first finding, what's the heaviest element? Phosphorus. Because otherwise you've got carbon, oxygen, nitrogen. Nitrogen is atomic mass 14. Phosphorus is atomic mass 30. So it must be outboard. Otherwise, if it were inboard, there would be other elements farther out, and you wouldn't get the clear lines.

Because the heavy elements are the ones that give the reflection, and if the heavy elements are obscured by lighter elements that are shielding them, you get a lousy reflections. Blunted reflections, blurry reflections. So all of that comes out of her findings.

So what happens next? So there's the 3.4, and 10, and et cetera, et cetera. All of that happens based on the pattern that I just showed you. So I'm going to read to you what happens in those days, back in the 1950s.

There was intense competition. You know, Linus Pauling had proposed a triple helix, and people in the UK were working hard on it, and so on. A lot of competition. So what happens is that Watson goes down to King's College in London, and he meets Rosalind Franklin in the hallway, and they get into a big argument. And she really chews him him out, and he goes running away. She was very tough. And so he goes to Maurice Wilkins, who was her boss. And I'm reading, now, from Freeman Judson's book.

"Wilkins told Watson as they went down the hall that Franklin had found that DNA fibers, when kept wet, yielded a different x-ray pattern, suggesting a second structure. Fourteen months after the King's colloquium, despite repeated correspondence and conversations, visits, meals together between Wilkins, Watson, and Crick, the possibility of a second structure was news to Watson, he wrote."

Now, this is quoting from Watson's own book, The Double Helix.

'When I asked what the pattern was like, Maurice went into the adjacent room to pick up a print of the new form they called the beta structure. The instant I saw the picture, my mouth fell open, and my pulse began to raise. The pattern was unbelievably simpler than those obtained previously, the a-form. Moreover, the black cross of reflections which dominated the picture could arise only from a helical structure. With the a-form, the argument for a helix was never straightforward. With the b-form, however, mere inspection of its x-ray picture gave"-- listen to this-- "several of the vital helical parameters."

I'm going to come back to that.

"The picture that Wilkins showed Watson was Rosalind Franklin's, without her approval."

So then Watson goes on the train back to Cambridge, and sits down with Crick, and in no time, they've put the structure together. And this is a famous picture. This is Crick. This is Watson. And I don't know if you can see really well. These are lab clamps that they're using. This is a lab stand. They're using lab clamps to put the structure together.

So here's the paper. The paper as it comes out, Molecular Structure of Nucleic Acids. And this was the first image of DNA. And I submit to you that if the earth were to end in a giant explosion, and we were to only send two images in a spaceship out to let some other race discover what we're all about, it would be this image, and the image of the atom. That's all you need. Because you have the simple atom, and you've got this, and everything else is just detail in between. So there's the first image. All right.

"We wish to suggest a structure for the salt of deoxyribonucleic acid. The structure has novel features which have considerable biological interest. The structure for nucleic acid has already been proposed by Pauling and Corey. They kindly made their manuscript available to us in advance."

These guys never made their manuscripts available to Corey and Pauling.

"Their model consists of three intertwined chains with the phosphates near the fiber axis and the bases on the outside."

See, they got the positions wrong.

"Without acidic--" da, da, da, da, da, and so on. Whatever.

Now here's-- remember, I've quoted from Watson's book.

"The previously published x-ray data on deoxyribonucleic acid are insufficient for a rigorous test of our structure."

Really?

"So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it's been checked against some more exact results."

Remember, he's writing this after having seen Rosalind Franklin's x-ray pattern.

"Some of these are given in the following communications."

Yeah, the next paper is Rosalind Franklin's paper.

"We were not aware of the details of the results presented there when we devised our structure,--"

That's a lie.

"--which rests mainly, though not entirely, on published experimental data and stereochemical arguments."

You know what? once I've given you the data, and you know what the structure is, you can give me a very, very strong stereochemical argument. But that's hindsight. If you don't know what the structure is, you have no idea what the stereochemical arguments are, because you can justify anything. So this is just absolute lies.

Who are the authors? Watson and Crick, even though it's based on data that was taken from other people.

So here they are. This is the acknowledgments.

We're indebted to-- blah, blah, blah. The experimental results in ideas of Wilkins, Rosalind Franklin, and their coworkers at King's College. And one of us, Jim Watson, he was the American, and I think there's an irony here, was aided by a fellowship

from the National Foundation for Infantile Paralysis. And I think there's a joke there, if you know anything about Jim Watson.

And now contrast that with this. This is the publication of the human genome. And look at all the names here. Everybody who was involved in the enterprise was named. This is not the paper. This is just the names of the authors.

Now, to be literate, there's this one phrase. Typical British understatement. Remember, this was about the structure of DNA. But there's this passage.

It has not escaped our notice. This is the litotes. Understatement, right?

"It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material."

That is the understatement all time. We've got the structure of DNA, and parenthetically, I think this is how you direct replication in all living creatures, by the way. So when this paper was published. and they rolled out the human genome as a sort of a literary-- what's the word-- allusion, thank you. The literary allusion was-- there's a passage in this paper that at one point begins "It has not escaped our noticed," da, da, da, da. So if you're ever with some Course 7 people, and you want to really get under their skin, you know, you could be at a party or something, and finally, you say you know, it's not escaped my notice. And they know what you're saying. It'll make you less popular then you are now.

So let's fast forward. This is Stockholm, December 10, 1962, the Nobel Prize ceremony. Here is the King of Sweden. This is Francis Crick. This is James Watson. This is Maurice Wilkins. No Rosalind Franklin. This is Kendrew, and I'm drawing a blank. These two guys were getting the Nobel Prize in Chemistry for hemoglobin structure. This, if you look carefully, is John Steinbeck, getting the Nobel Prize in Literature.

Over in Oslo is Linus Pauling, getting his second Nobel Prize, but for peace. So ironically, he's getting his Nobel Prize. They're getting the Nobel Prize not in Chemistry, not in Physics, but in Medicine. You know, what's medicine? I mean it's not really a science. But anyway. Here it is. It's worthy of a Nobel Prize.

So what really happened here? What really happened? Why was there no Rosalind Franklin? She was marginalized as a woman. She was mistreated by these men. It was 1955. You realize in the 1950s-- and I'm not talking about the England of Charles Dickens. I'm talking about the England after World War II. Women were not allowed in the common room. And the common room is where everybody congregates at 4:00 p.m. to drink coffee and exchange ideas. So she couldn't go into the common room and so on.

And it was just a terrible, terrible story of misuse, of information, lack of attribution, and so on. If this story were unfolded today, I guarantee you these guys would not be getting a prize, and in fact, the publication would probably be rescinded on the grounds of its fraudulent claims, that they were unaware of the previous information.

So after the paper was published, she was so brokenhearted that she resigned her position at King's College, and took a job at another college in London. Her terms of severance included her signing a document in which she agreed to abandon all future

work in biochemistry. I mean, imagine that you leave your job, and they tell you what you cannot do! I mean, obviously, if you were privy to intellectual property and so on, you're bound by confidentiality. But no one can tell you, you can't go to work for somebody! And so she changed fields, and made seminal discoveries in two other fields outside of the DNA work.

So why isn't she here? She died of cancer in 1958, very young. And you can't get the Nobel Prize posthumously. So some people are quite outraged by this story. But there's a symbolism here to have Wilkins. It's basically saying that you two guys are not the authors of this. And so some people say that Wilkins is standing in for Rosalind Franklin, and the Nobel committee at least acknowledged that.

So what's the message here? The message here is, I hope nobody in 3.091 is ever embroiled in a controversy like this. We have to acknowledge our collaborators. All of us are here because somebody helped us.

Don't go away. You haven't been dismissed yet. This is important. What I'm telling you is far more important than that structure. I'm telling you how to stay out of jail. See, here, you know, 50 years ago, you cheat and steal, you get a Nobel Prize. Today you go to jail. It is a Nobel Prize in Medicine, of course, but anyway.

So this is a book, if you're interested in Rosalind Franklin's story, it's fantastic reading. Real page-turner. This is James Watson's book. If you read this, you know, have your you-know-what sensors on all the time. And here's a picture of Rosalind Franklin on vacation in France.

And we'll leave with The Twist by Hank Ballard, who was another person who was marginalized, because he was black! And so you couldn't listen to this music, and so there was a cover made. The version of The Twist that you have heard is probably by Chubby Checker. This is the original one by Hank Ballard. It's gritty. It's very gritty.

All right. Treat each other well. Get out of here.