Physics of Biological Systems
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Lecture – 25
Transcription and translation

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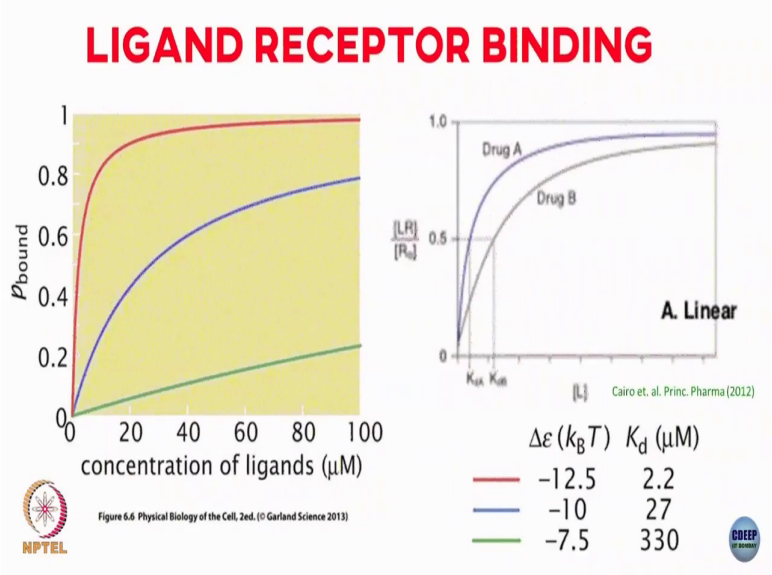

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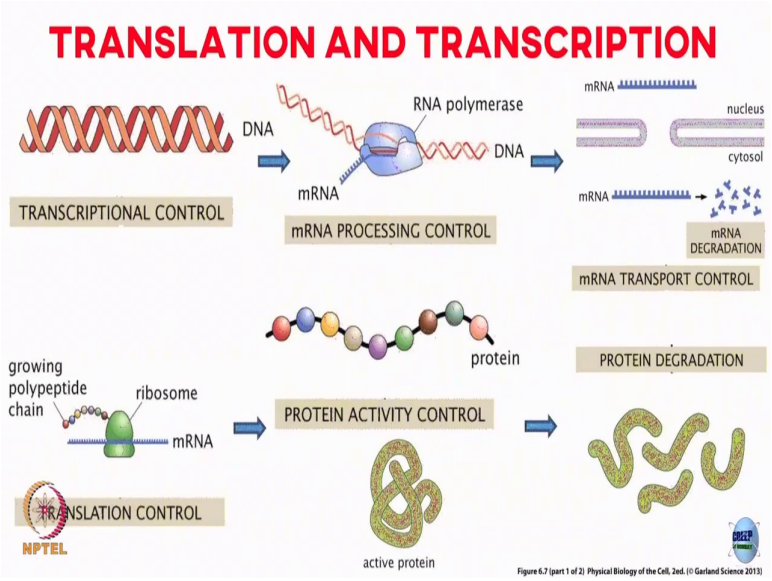

We can do a sort of. So, this is just sort of example for this ligand receptor binding. You can use a similar approach for different problems for example, if you think of this; let me come back to this RNA polymerase probe. So, this is the whole Transcription and translation process. We are just interested in this part, so, RNA polymerase.

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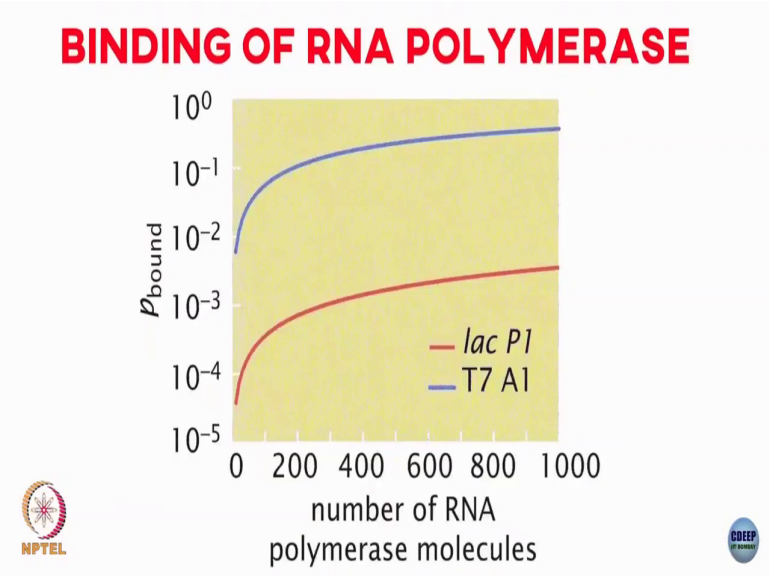

And again you can calculate this P bound right as a we calculated the entropy, but now, if you said that when this RNA polymerase ok. So, let me just say this little clearly. So, let us now consider a similar problem for this RNA polymerase binding. So, I have this one I have this 1 b DNA; which has these sites right. I forget about the physical 3D structure of the DNA and I consider that this RNA polymerase can come and bind and it can sort of hop around this,

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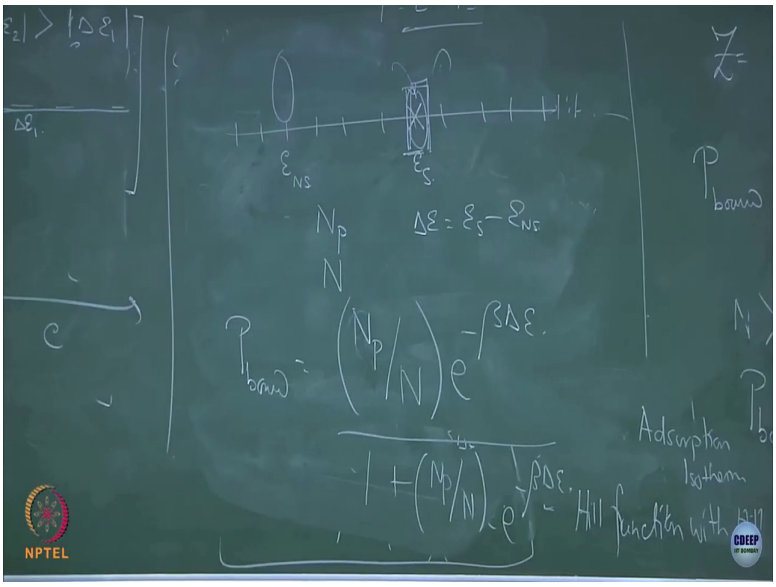

Maybe this site is a specific site, so this is the site where it wants to go and bind. So, it has some energy for going and sitting on this on this specific site let me call it specific.

But you can also bind non specifically to this sequence. So, it can bind weakly to this other sequences over here and let me call the energy for that as epsilon nonspecific ok. Again it is an approximation in that energy will depend on the exact sequence that you have, but let me say that all sequences as long as it is nonspecific binding will have some energy epsilon N S. When it goes and sits on the site that it wants to. So, that it can start reading the gene; that energy is lowered and that I will call as my epsilon S.

And then again we do; if you do the same business that you have N P number of polymerases, you have n number of available sites and. So, on you can calculate what is the probability that an RNA polymerase is going to be bound. Specifically to this site and that is again going to

look very similar. So, that is again going to look very similar to this whatever expression we had. So, again if you calculate what is P binding. So, this I leave because it is exactly the same sort of a calculation P bound is going to be P which is the or let me call it N P by N e to the power of minus beta delta e by 1 plus N P by N e to the power of minus beta delta e ok.

So, exactly what we had, but now delta e is the difference between the specific binding energy and the nonspecific binding energy. So, epsilon specific minus epsilon non specific. And again, if you go back and look at experimental data for different sort of a proteins binding on this DNA. So, this is lack protein in e coli this red curve; this is P 7, I think is a bacteriophage. So, this is another polymerase which is the blue one is a polymerase that is found in other bacteria Ph T 7

So, again these are experimental measurements of the probability that this polymerase molecule is bound in two different organisms as a function of the number of RNA polymerase molecules. And again you see that the curves look exactly as would be predicted by this sort of a language adsorption isotherm; you can read off what would be the values of this delta is what is the difference in the specific versus the nonspecific binding energies for these different polymerase is in different organisms.

So, it is true that these are very simple calculations, but even so you can often look at experimental data and get some information out about the underlying biological system using these very simple models like this. If one can of course, build more and more complicated models, but what I wanted to show at least for today was that; even these simple models often can be used to interpret real experimental data ok.

So, we will continue with this binding with little more maybe, little more biologically complicated models; where you can have multiple ligands and so on and so forth different complications which we look at, this is nice state.

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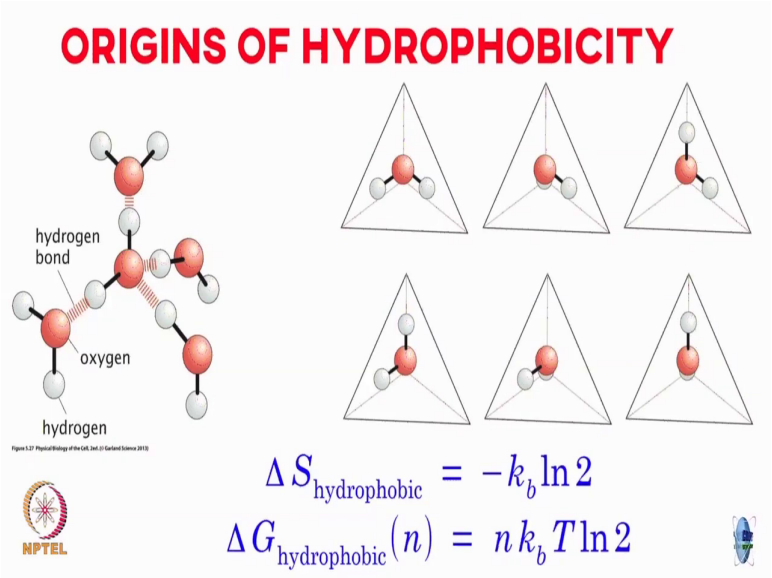

So, I just I will just take 2 minutes to describe this. So, you know that inside cells hydrophobic interactions are often a large or hydrophobic forces or a large or often a very important factor which determines. For example, even structure of protein folding and so on. This lipid bilayer formation; where you keep the hydrophobic tails inside and the hydrophilic parts outside and so on.

So, what is the origin of this hydrophobic forces? You can think of them in terms of a sort of entropic picture very hand waving picture, but nonetheless. So, here is water right H2O, the orange thing is the oxygen, the white ones are the hydrogens. Before the oxygen forms the hydrogen bond with a hydrogen molecule of a neighboring water right.

So, here is one oxygen, here is a hydrogen of a neighboring water molecule, it forms a hydrogen bonding between them. And similarly, so whenever you have an oxygen next to a

hydrogen you can form hydrogen bonding. Often you will find this sort of a tetrahedral structure; tetrahedral symmetry. So, this sits at the center of the tetrahedral and these are the four vertices of the tetrahedral ok, due to this oxygen binding sorry due to this hydrogen bond.

So, now you can think of this that let us say you have a c of such water molecules which are arranged in this sort of a tetragonal structure. So, if I think of this water molecule at the center it can form. So, this form sits at the centre of the tetrahedral and it can for these oxygen molecules depending on which way they are oriented can form hydrogen bonding with waters at the other vertices of the tetrahedral right.

So, these are the 6 possible confirmations depending on which way your oxygen molecule oxygen bonds point. So, here they are pointing along this axis; there one is pointing along this one is pointing along that and so on. So, these are the microstates in some sense corresponding to this hydrogen bonding network or this hydrogen bonding tetrahedral ok. For this one water molecule which sits at the centre of this tetrahedron.

So, you can say that the number of microstates that are possible. So, each of these confirmations is a microstate for that water molecule right. So, I can say that the number of microstates in this case; is going to be 6. Depending on which way this water molecule is oriented. Is that clear? So, now, let us say that you place you replace the water molecule and you place a molecule which does not like to form a hydrogen bond right ok. So, let us say you replace at any one vertex.

So, let us say you replace at this vertex instead of a water molecule you place a polar molecule ok. But, it should not like to form a hydrogen bond ok. Then what would happen? If there is no water molecule on this vertex, then this configuration is no longer allowed, because it cannot form a hydrogen bond. There is no water here, this configuration is not allowed that configuration is not allowed, is that clear. This all the central oxygen cannot form a hydrogen bond with the water here because there is no water here.

It cannot form a hydrogen bond with the new molecule here both the new molecule there. These ones are still fine; because, here this oxygen is forming a hydrogen bond with the water

which is present there that I have not replaced. So, if I replace the water molecule by a new molecule; which does not form a hydrogen bond at any one of these vertices ok. Then I reduce the number of available confirmations from 6 to 3, right.

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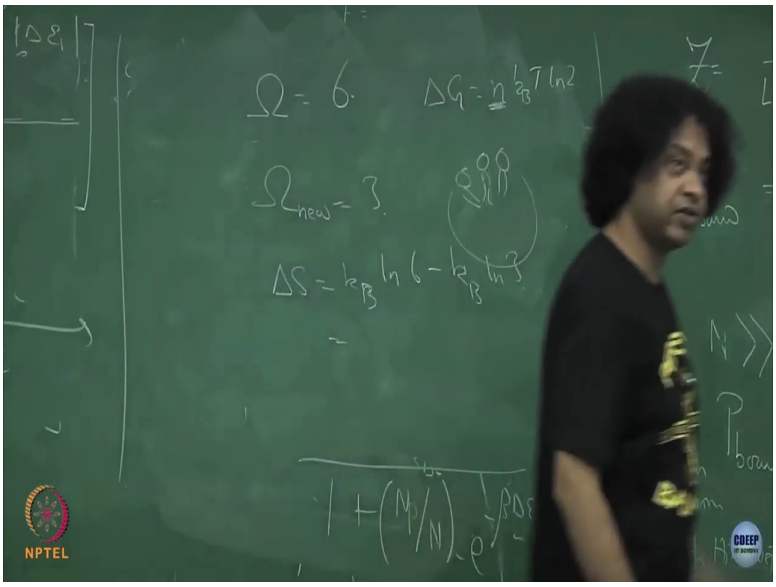

So, in this new case; I can call it omega new. I have only three available confirmations ok. So, by introducing a molecule which does not like to form a hydrogen bonding. I have reduced the number of available confirmations from 6 to 3, again this is very simple to take it with a pinch of salt, but the basic principle is this. So, if I now say that therefore, what is the change in entropy, right.

What is this delta S? That delta S is k B log 6 minus k B minus k B log 3 right; which is therefore, minus k B log 2. Per molecule of water that I have replaced ok. So, this is k B log 2 per molecule of water that I have replaced by this new molecule; which does not like to form a

hydrogen bond. Therefore, the total free if I wanted; the total free energy cost given that I had replaced n such molecules would go roughly as n k b T log 2, this n is in some sense.

So, if you are faced with a mixture of hydrophobic and hydrophobic molecules and water; what it would like to do is that, so this delta G is something like n k B T log 2; where n is the number of molecules which share an interface with water right. So, what it would like to do then is to minimize this number of n right. If it wants to minimize it is free energy, it would like to minimize the number of contact points of this molecule with water; which is what this hydrophobic interaction does right.

So, if I think of lipid membranes or whatever or vesicles it reduces the interaction of these hydrophobic parts with water. So, that this n this effective n which is the number of hydrophobic molecules which come into contact with water that gets reduced and therefore, that stabilizes the structure. So, the heart of it is this sort of you can think of it as this again of course, a very simple way, but you can think of it as this reduction in the number of available microstates when you place a hydrophobic molecule over here.

If you want to reduce; it reduces the number of available confirmations. And therefore, that has a change in the free energy. So, even this hydrophobic forces which are this fundamental forces you can think in terms of this changes in free energy of changes in entropy that are associated with the change with this.

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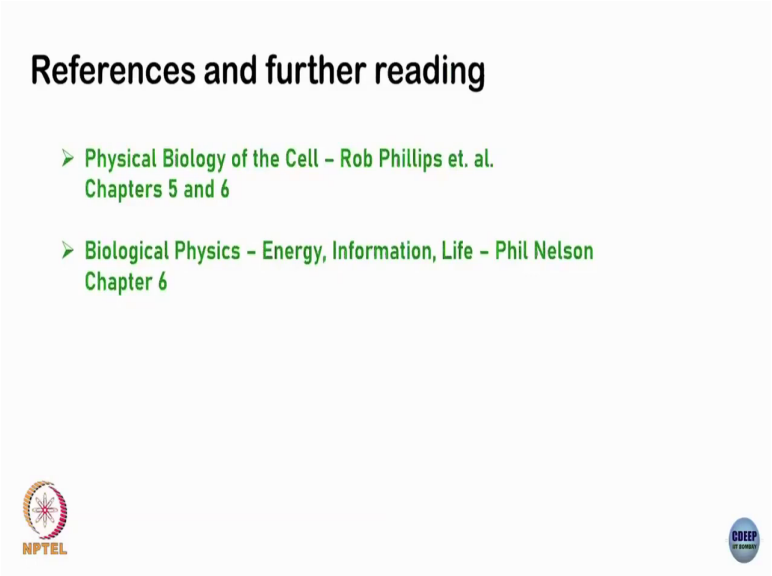

I think that is all I have yes; that is all I have. So, again these are the reference chapters from Nelson and from Phillips and of course, please if you have forgotten, please read up the stat mech path. We will be using a little more stat mech as we will go along today it is fairly simple.