hello everyone ah i welcome you all in ah bio ah
molecules lecture series today we are going to discuss ah lecture eight before going to the main
course of uh todays lecture i will ah give a recap to the last lecture in the last lecture
we talked about ah the amino acids and there we discussed about the you know different
type of amino acids based on their ah structures ah where we divided it in you know amino acids
with the aliphatic side chain amino acid with the you know ah acidic side chain amino acids with the
you know amides have acetic site chain that amino acids with the basic side chain that amino acids
with the you know heteroaromatic cores all these you know ah amino acids with the aerial ah
side chain and amino acids with the you know ah thial as a software containing side chain all
these you know ah you know classification we discussed in detail ah and then we talked about
ah are you know acidic and basic properties you know amino acids acidic and basic property ah and
where we learned ah that ah generally amino acid has you know ah tendency to be in its you know
ionic structure ah ionic form and that is you know ah in totality it is basically neutral but you
know ah in the scaffold ah amine tries to be in the ammonium form whereas the carboxylic group
tries to remain in the carboxylate form and ah the ph at which the population of these molecule
remains you know in the ionic form ah is known as the isoelectric point
so ah there we ah discussed
about the you know um how ah isoelectric point ah is important and we have also ah talked about
the ah how to calculate the isoelectric point that you know um you know if you know the p k of
ah you know particular functional ah group in the amino acid then we can easily evaluate the isolate
point which is basically if you know the two p k ah i mean the there are only two functional group
in mainly ah one is the carboxylic acid and other is the ah amine ah at the alpha position
so if
you know the p k of these two functional group ah by adding and then dividing by two one can get the
ah isoelectric point at which it tries to remain in the ionic form where amine remains in the
ammonium form and carboxylic acid remains in the carboxylate form basically what happens
that you know carboxylic acid proton gets transferred on the amines ah nitrogen and farms
ammonium ah we also discussed about ah how to ah determine the isoelectric point ah of the
amino acid with the different substituent substituents means you know if it has ah ah

proton receiving ah substituents like you know um heteroromatic cores ah ij substituent are
you know some you know hetero atoms are there in that case how we can evaluate they are also you
know basically if it is a it has like a unusual side chain then in case of base we consider that
you know ah basic group as well as the amine ah i mean p k we add and then divide it by two
whereas if it is like you know acidic amino acid then you know carboxylic acid p k and the acids
another substituent acids p k and and divided by two its a very simple way to determine we also
discussed about protein structure in the protein structure we learned that you know there are four
types of structures and in the primary structure ah protein of the protein basically we discuss
about the sequence of amino acid ah in the chain and ah you know the location of all the disulfide
ah bridges whereas in the secondary structure ah where regular conformations assumed by the segment
ah of the proteins backbone when it falls and it comes in a repetitive manner in the secondary
structure basically the secondary structures are regular conformations assumed by the segment of
ah you know ah proteins backbone when it folds so ah that that determined the second is a tertiary
structure you know is the three dimensional structure of the entire ah protein whereas in the
quaternary structure if the protein has more than one polypeptide chain then what is the what way
the individual polypeptide chains are arranged in the protein if it has more than one product that
that determines the quaternary structure ah
so ah i will start from the you know determining
the primary structure of polypeptide chain and ah how how to determine the primary
structure of a polypeptide or protein
so how to determine the primary structure of a polypeptide or a protein
so one way to determine the structure of a
polypeptide that you know we can break the disulphide bridges ah in the polypeptide
so that you know it can attain a basically a linear structure so
the important i mean transformation for ah determining the primary structure of
polypeptide is breaking the disulphide bridges breaking the disulfide bridges
how to do this how one can attain the you know breaking of disulphide bridges its
very simple the one way to do is reduce the disulfide bridges reduce the disulfide bridges this is in order to obtain a single
perpetration reduce the disulfide bridges in order to obtain a single polypeptide polypeptide chain
so how one can attain this transformation
ah for that we will use reducing agent ah two mercapto ethanol which will ah you know

break the disulphide bridge by the reaction with the you know reducing is a two mercepto ethanol
so here we are going to use a reducing agent that will basically oxidize the disulfide
functional group
so we will use we will we will achieve this transformation by applying a reducing agent agent two mercaptoethanol two two mercaptoethanol
so let me write here
the molecule with the disulfide bridge this is the representative you know structure of a polypeptide with the
disulphide bridge this is the disulfide bridge and we will react it with two mercaptoethanol two mercaptoethanol
so after reaction it will get converted to the corresponding
sulphide will indicate terms with thial it will get ah solid sulphide will get reduced to you know ah thial
so and tumor capture ethanol will
get converted to you know sulfide now the possibility that you know if these thials remain as it is you know as we know that they have tendency to again get you
know ah oxidized and get converted to disulphide
so it will be further reacted
with the iodoacid
so protein thiol group will be treated with the iodoacetic acid
so that it can convert it gets converted to to the corresponding two molecules of
so now after the reaction with after the reaction with iodostic acid this is hydroastic acid this thial group you know prevents from the again disulfide bridges ah as a result
of oxidation now again it can go for oxidation and form the you know disulfide but once you treat
this protein thial group with the iodo acetic acid iodo stick acid sulphur ah basically oxidations gets ah you know stopped and it
gets converted to the corresponding derivative
so now it is not available for again going
back to the and that way you can ah get the you know polypeptide chain without the disulfide
bridges now ah
so the this can also indicate that you know ah how many disulphide bridges are
there by the number of this ah you know i mean ah substituent one can determine now lets talk about
the determining the number and kinds of amino acid determining the number and kinds of kinds of amino acids to determine the number and kinds of amino acids number and kinds of amino
acids in the polypeptide chain in polypeptide chain it was dissolved in very concentrated hydrochloric acid it was dissolved in six molar its very strong hydrochloric acid and heated heated at hundred degree
centigrade for 24 hours basically we are here hydrolyzing all the amide ah linkages
all the amide you know functional group to convert it into the particular you know amino acid
the constituent amino acids which after the condensation they form the you know peptide chain
so by treating it with a very uh strong acid that is a six molar ah

hydrochloric acid and refluxing
it at hundred degree centigrade ah i mean hitting it at hundred degree centigrade not refluxing you
know ah i will say here ah to be more appropriate ah for the 24 hour all the pep basically amide
linkages gets hydrolyzed and it forms the carboxylic acid and the amine
so in totality
i will write here if you treat polypeptide polypeptide the six molar scl at degree
centigrade 24 hour it generates amino acids the constituent amino acids the mixture of amino acid is passed
through a amino acid analyzer now the mixture of this mixture of amino acid is passed through an amino acid analyzer amino acid analyzer to identify the amino acid to identify the amino acid ok now
so in the primary structure
as i mentioned that ah we need to know that number and ah type of amino acids as well as the
ah disulphide bridges in the peptide chain these are the requirement for primary structure which we
are evaluating ah by these two ah transformation first one we did that you know by treating the
polypeptide chain ah with the thio merceptol ah to ah you know reduce the disulfide bridge into
the corresponding thial and then ah um this ah thial since has ah you know kind of property
to go again ah you know ah basically ah oxidized to the disulfide
so again it is get
reacted with the ioistic acid ah to ah to form the corresponding you know um ah stick acid analogue
so that it cannot re ah you know oxidized to sulfur disulfide ah ah and
so that way we we we we
can ah easily identify in the polypeptide chain by this transformation how many you know disulphide
diseases are there another thing that you know how many amino acids are there that to ah and what
kind of amino acids are there that can be easily ah learned by ah treating it with the six molar
hcl ah and heat it ah at 100 degree centigrade for 24 hour ah one can ah get the ah all the
amino acid in the mixture and which can be easily identified through the mix amino acid ah
you know analyzer that what are the amino acids are there in that particular polypeptide chain now
i will talk about the you know secondary structure secondary structure
so secondary
structure describes the describes the repetitive conformations repetitive conformations assumed by segment of assumed by segments of the backbone chain of the backbone chain of a polypeptide protein in other words secondary structure describe
the segment of the backbone fold secondary structure this crives
how segments of the backbone how segment segments of the backbone fold segments of backbone fold three factors determine the
secondary structure of a segment of protein three factors basically three factors determine the

secondary structure of a segment determine the secondary structure of a segment of protein segment of a protein first one the regional planarity the regional planarity linear planarity about each peptide bond about each peptide bond the original planarity about
each peptidon why is it
so as a result as a result of the partial of the partial double bond character of the amide bond double bond character of the amide bond of the amide bond which limits basically which limits the
possible conformations of the peptide chain limits the possible confirmations possible conformations of the peptidogen
so what are the three factors for the secondary
structure that determine the you know structure of a segment of a protein first one is the
regional planarity about the each peptide bond you know how ah the every peptide bond is having
you know planarity and that occurs because of the double bond characteristic of the amide ah you
know functional group
so that basically restricts the you know conformational possibility
of the peptide chain
so that is one factor second is minimizing energy by
maximizing the number of hydrogen bond minimizing energy by maximizing the number of hydrogen bond by maximizing the number of hydrogen bond hydrogen bonds between peptide groups that is hydrogen bonds between the carbonyl oxygen hydrogen bond between carbonyl oxygen oxygen of one amino acid of one amino acid and the
amide hydrogen of another hydrogen of another
so how does it form let me through the structure
i will represent here
so as i mentioned carbonyl of one here i am
putting the carbonyl group and amide of other
so this is
one strand and the other stand is
so this is the as i mentioned you know ah carbonyl
of one you know amide chain with the amide of the other you know amid hydrogen of the other these
forms the hydrogen bond ok
so hydrogen form hydrogen bonding between peptide groups peptide groups hydrogen
bonding between peptide groups ok now the ah third thing is
the need of adequate separation the need for adequate separation between the neighboring r group adequate separation between neighboring r groups neighboring r groups to avoid steric strain steric strain and repulsion of like charges of like charges
so the need for educate separation between
neighboring r groups to avoid steric strain and repulsion of like charges
so again i
will like to repeat the secondary structure secondary structure describes the repetitive conformation assumed by segment of the backbone in other words
that secondary structure describe how segments of the backbone fold segments of the
backbone fold and to learn about it you know we need to know the three factors you know ah which
determine the you know structure of a segment of a protein what are the three

factors first one is
the regional planarity about each peptide bond and that how does it happen because of the you
know double bond characteristic double bond characteristic of the amide bond which limits
the possible conformation of the peptide gene because you know if the double bond characteristic
comes in because of the amide group it does not allow that flexibility which can occur in its
absence
so the conformational ah flexibility is lost in the peptide chain because of the double
bond characteristic second is minimizing energy by maximizing the number of hydrogen bonds as
we know that this is the nature law that every you know entity in this nature tries to
remain in the least energy state and ah to achieve that you know all kind of physical
processes happens and here basically the because of the hydrogen bonding you know its ah because
of the hydrogen bonding its minimizes its energy you know ah and that can easily occur in the
peptide chain ah particularly in in between the you know carbonyl group of i mean oxygen of the
carbonyl group and the ah amidic nh you know ah with the ah you know ah hydrogen bonding can
takes place
so ah carbonyl oxygen of one ah you know ah i mean m i d group and the nh of the
another mid group can engage in the hydrogen bond ah that is very clear from this you know schematic
presentation how how this carbonyl oxygen and the other ah amid nh are engaged
in the hydrogen burning also the need for adequate separation between neighboring r groups to about steric strain so that you know it cannot you know have a steric so
ah the folding takes place in a way ah
so that the all the you know neighboring ah r groups ah remain
far apart to have the minimal ah energy state ah and to about the sterics
so these are the you know
ah to add the steric repulsion basically
so ah ah also ah if charges are there like you know
as we know that you know um amine can be in the ammonium form or the side chain can can be
in the ionized state
so there also they need to remain far apart
so that they cannot have
you know ah repulsion between ah each other ah if the like charges are there then they can have
like repulsion
so ah this this is the the third ah you know um ah factor ah now ah based on that
i will like to ah talk about the you know ah you know different type of secondary structure

ah first one is alpha helix alpha helix alpha helix one type of secondary structure is
an alpha helix this is one and in alpha helic in alpha helix the backbone of the polypeptide the backbone of the polypeptide coils around the long axis of the protein molecule coils around the long axis of the protein axis of the protein molecule coils around the long axis of the protein molecule
so in alpha helix the backbone of the polypeptide
coils around a long axis of the protein molecule ah how does it happen to represent it let me draw
the structure
so this is the polypeptide chain
so this is the coiling and
since it is doubly extended
so basically the polypeptide
chain is coil around this axis the long axis of the protein molecule now because the amino acid have the l configuration because the amino acid have the l
control the alpha alex is right handed amino acid have the al configuration the alpha alex is a right handed helix alpha helix is a right handed helix right handed helix that is it
rotates in a clockwise direction that is it rotates in a clockwise direction clockwise direction as it spirals down
so this is the clockwise
so basically its coming
so this is the clockwise as it you can see
you can see here like as it spirals down eastern of the helis contain 3.
6 amino acid this eastern each turn of the helix contains 3.
6 amino acid contains 3.
6 amino acids and the repeat distance of the helix is
five point four angstrom you can see here the repeat distance of the helix is five
point four angstrom five point four angstrom and three point eastern of the helix
content three point six amino acid exactly and basically it has the hydrogen bond as i
told that you know in the secondary structure basically four amino acid away this hydrogen
bonding take is taking place four amino acids away four amino acid away and the repeat distance of the helic
so each turn of the helix contains 3.
6 amino
acids and the repeat distance of the helix and the repeat distance and the repeat distance of the helix repeat distance of the helix is 5.
4 angstrom this is important information
basically now let us talk about
so this is one alpha helix is the one ah secondary structure
and the second second one is beta pleated seed beta pleated seed the second type of secondary structure is beta pleated sheet how does it look like
in the bleed operator sheet i will make the pictorial ah representation through which you will understand so in the beta pleated sheet two seats
are anti parallel
so let me draw first anti parallel as i told you
so that is why i am you know making this opposite
orientation of these two seeds and basically these are the two seeds just i am

with the solid lines i am representing
that the two seats are there which are folded in anti parallel to each other
so this
is a anti parallel beta pleated seeds and then i will draw here the other
so other secondary structure the
polypeptide chains are parallel parallel
so this is the parallel beta plated seed
so parallel beta pleated seed here the hydrogen bonding in a beta plated seed
in a beta pleated seat occurs between neighboring peptide chains
these are the two peptide sense
so basically this is the you know in between the hydrogen bonding is taking
place similarly this is
the anti parallel and in the case of parallel also i can represent here
so the hydrogen bonding in a beta plated
seed occurs between neighboring peptide chain between neighboring peptide chains
between neighboring peptide chains a beta pelleted seed is almost fully extended
a beta pleated seat is almost fully extended and the average two amino acid
repeat distance is seven angstrom average two amino a two amino acids repeat
distance is submitting a stump the part of the backbone is structure of a
protein
background that exist in a plate pleated seed the part of the backbone structure
backbone is structure of a protein background that exist in a pleated seat is
see it is indicated by indicated by a flat arrow pointing
so this is i am talking about the flat arrow
flat arrow pointing in the end to c direction flat arrow pointing in the and to
c direction again i will repeat here in the beta pitted sheet the hydrogen
bonding in a beta plated seed
between the neighboring peptide chains occurs that i have shown here in these
two ah you know in one case it is anti parallel
another case the you know parallel
so a beta plate sheet is almost fully extended the
average two amino acid repeat ah distance is seven angstrom and the part of
the backbone structure
of a protein background that exist in a beta plate seed is indicated by a flat
arrow that that is
the flat arrow pointing in the end to c direction for example silk contains a
large
proportion of relatively small amino acids silk contains a large proportion of
relatively small amino acid relatively small amino acid and therefore has large
segment of beta plate received therefore has large segments of beta plated
segment of beta plated shift the number of side by side is strained in a beta
pelleted seed ranges from two
to fifteen in a global protein side by side strain i am particularly this
talking about this side by side strain the number of side by side
stains in a beta pleated seed in a beta plated seed ranges from two to fifteen
in a global protein globular protein the average stent in a beta plated
seed section contains six amino acid average is trained in a beta plated c
section seed section contains six amino acid
so these are the another wool and fibrous portion of
the muscle have secondary structure fibrous protein of muscle cool and fibrous
protein of muscle have secondary structure that are
almost all alpha helix alpha helix beta plated seeds are ordered
in the silk and spider way are occurred in silk and spider waves we are seeing
spider wave in our houses also and

you know spider wave ah and it cannot be staged cannot be stretched
so i will stop here reelector
and i will again continue with the you know um structure of protein ah
particularly the secondary
structure in the next class thank you very much you