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ROLL NO.- 2021482

BIO211 – Cell Biology and Biochemistry

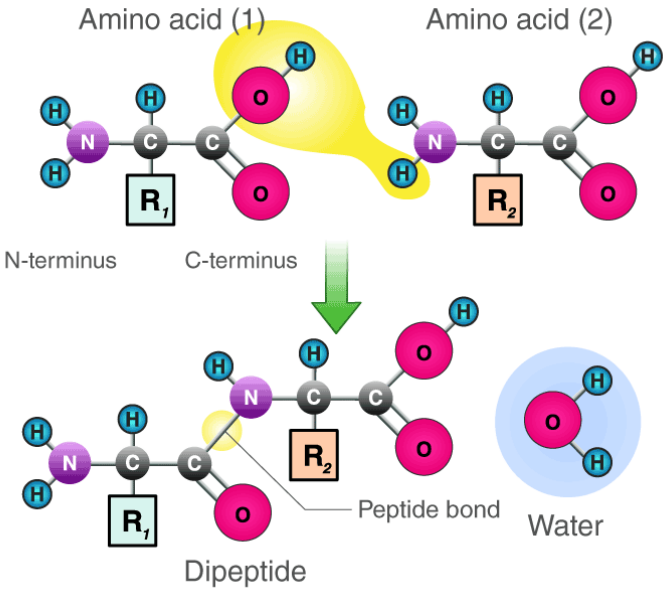
ASSIGNMENT-3 (December 16, 2022)

Sol 1

- The mechanism of peptide bond formation is a dehydration synthesis process.
- During the formation of a peptide bond, the carboxyl group of one amino acid moves towards the amino group of another amino acid.
- Subsequently, one hydrogen and one oxygen atoms are lost from the carboxyl group (COOH) of the first amino acid. In contrast, one hydrogen is lost from the amino group (NH_2) of the other amino acid.
- This results in the release of a water molecule (H_2O) along with the formation of an amide bond (C-N) between the two amino acids.
- The process of formation of a peptide bond between two amino acids results in a dipeptide molecule.
- Thus, a peptide bond is formed when the carboxyl group of one amino acid condenses with the amino group of another amino acid releasing in a water molecule.
- The formation of the peptide bond is an endergonic reaction that requires energy, which is obtained from ATP in living beings.
- Because this reaction involves the removal of a water molecule, it is called a dehydration synthesis reaction.

Sol 2

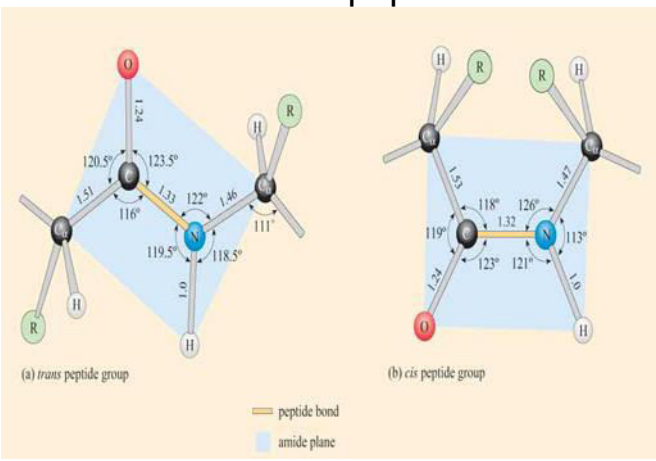
A peptide bond is basically an amide-type of covalent chemical bond. This bond links two consecutive alpha-amino acids from C-1 (Carbon number one) of ont alpha-amino acid and N2(nitrogen number two) of another. This linkage is found along a peptide or protein chain. A peptide bond is formed by a dehydration synthesis or reaction at a molecular level. This reaction is also known as a condensation reaction which usually occurs between amino acids.



The peptides are rigid and planar, which means that the C=O and the N-H bonds lie on the same plane, and the rotation of the peptide bond is **restricted**. The lack of rotation allows the peptide group to remain fixed in either a cis or trans configuration (stereochemistry), thereby stabilizing protein structure.

Sol 3

There are two possible conformations of the planar peptide bond: in the *trans* peptide group, the C_α atoms are on opposite sides of the peptide bond and in the *cis* peptide group, the C_α atoms are on the same side of the peptide bond

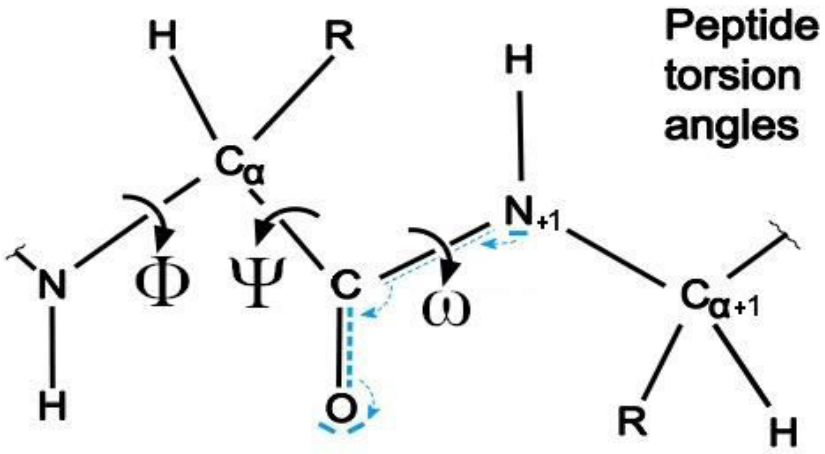


Bearing in mind the planar nature of the peptide group, a polypeptide chain can be seen to have a backbone that consists of a series of rigid planar peptide groups linked by the C_α atoms. Part

of a polypeptide with two planar peptide groups in the *trans* conformation.
peptide bonds are in the *trans* conformation. However, *cis* forms can occur in peptide bonds that precede a proline residue. In such cases, the *cis* form is more stable than usual since the proline side-chain offers less of a hindrance. Nonetheless, *cis* peptide bonds occur only in approximately 10% of instances of peptide bonds preceding proline residues.

Sol 4

The figure below shows the three main chain torsion angles of a polypeptide. These are phi, psi and omega.

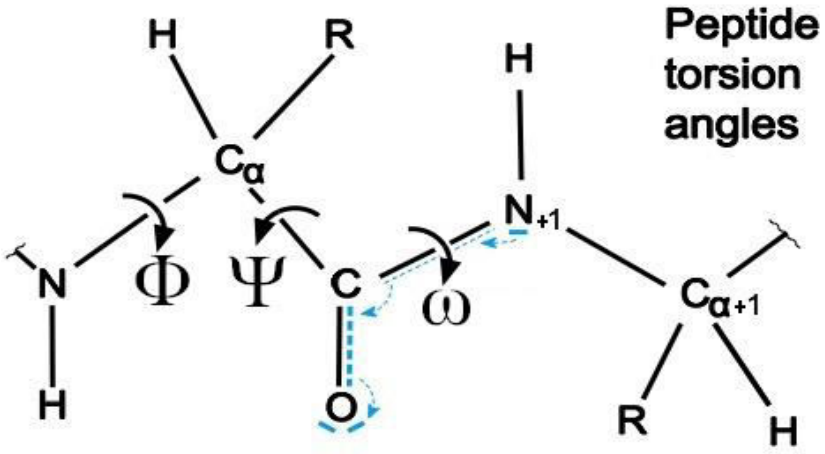


The planarity of the peptide bond restricts omega to 180 degrees in very nearly all of the main chain peptide bonds. In rare cases omega = 0 degrees for a *cis* peptide bond which, as stated above, usually involves proline.
The angles of rotation, termed **torsion angles** , about these bonds specify the conformation of a polypeptide backbone. The torsion angles about the C_α–N and C_α–C bonds are referred to as ϕ (phi) and ψ. (psi), respectively and they are defined as 180° when the polypeptide.

Sol 5

There are three main chain torsion angles of a polypeptide.
Phi (Φ; C, N, C_α, C) and psi (Ψ; N, C_α, C, N) are on either side of the C_α atom

omega (ω; C_α, C, N, C_α) describes the angle of the peptide bon essentially flat and fixed to 180 degree.
While Φ and Ψ have considerable rotational freedom, ω is planar. This is a result of the partial double bond character of the peptide bond which is caused by resonance effects, i.e. delocalized electrons (N-C=O <-> N+=C-O-). A trans configuration (≈180°) is preferred for steric reasons. Cis configuration (≈0°) is rare, except for prolines.

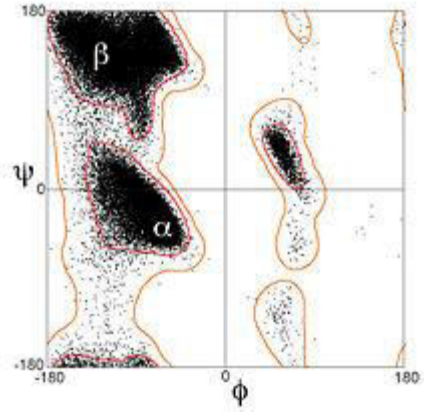


.
There is also one more that is termed as omega (ω) which is planar.

Sol 6

Bearing in mind the planar nature of the peptide group, a polypeptide chain can be seen to have a backbone that consists of a series of rigid planar peptide groups linked by the C_α atoms. Shows part of a polypeptide with two planar peptide groups in the *trans* conformation. Note that though rotation is not permitted about the peptide bonds, there is potential for rotation around the C_α–N and C_α–C bonds.

Sol 7

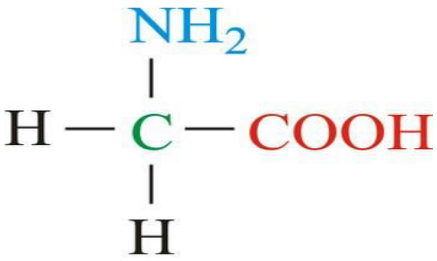


The Ramachandran plot shows the statistical distribution of the combinations of the backbone dihedral angles ϕ and ψ. In theory, the allowed regions of the Ramachandran plot show which values of the Phi/Psi angles are possible for an amino acid, X, in a ala-X-ala tripeptide (Ramachandran). In practice, the distribution of the Phi/Psi values observed in a protein structure can be used for structure validation (Ramakrishnan). The Ramachandran plot visualizes energetically allowed and forbidden regions for the dihedral angles. For poor quality homology models, many dihedral angles are found in the forbidden regions of the Ramachandran plot. Such deviations usually indicate problems with the structure. plot can be used in two somewhat different ways. One is to show in theory which values, or conformations, of the ψ and φ angles are possible for an amino-acid residue in a protein (as at top right). A second is to show the empirical distribution of datapoints observed in a single structure in usage for structure validation, or else in a database of many structures. Either case is usually shown against outlines for the theoretically favored region.

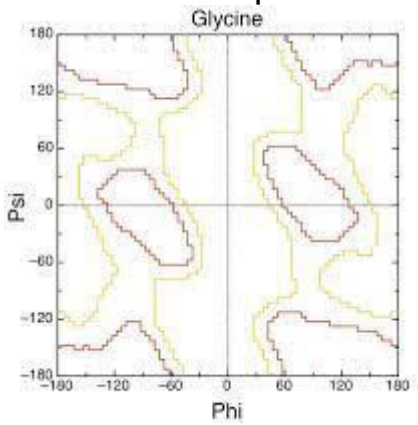
Sol 8

Glycine has no side chain and it is only a Hydrogen. Hence, Glycine can adopt many conformations than other amino acids and therefore Glycine containing peptides can take part in many phi and psi angles that are sterically forbidden for other amino acids. Therefore glycine containing peptide chains can adopt phi and psi angles in all four quadrants of the Ramachandran plot.

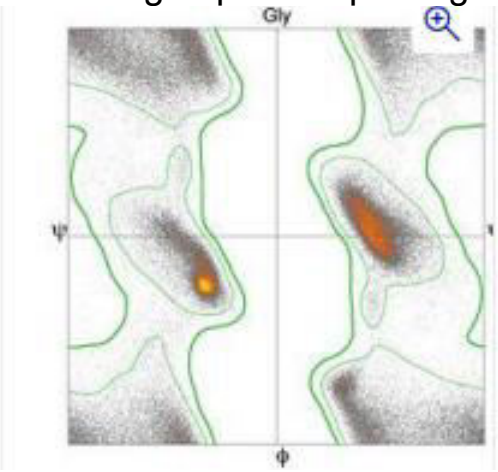
Struture of Glycine as follows:-



As from the structure we can see that glycine has H as the side chain.
Because of the lack of a big side chain Glycine contributes to the least steric hindrance in the peptide and therefore occurs frequently in turn regions of proteins where any other residue would be sterically hindered. Hence, glycine containing peptide chains can adopt phi and psi angles in all four quadrants of the Ramachandran plot.

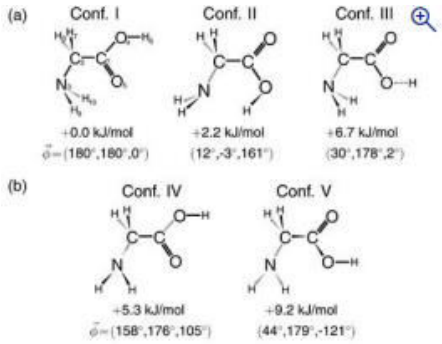


The areas surrounded by red lines indicates where the Glycine residues are. As you can see, the peptide can have conformations conferring to phi and psi angles in all 4 quadrants.



Glycine residues can take part in many conformations that are sterically forbidden for other amino acids. Hence, this increases

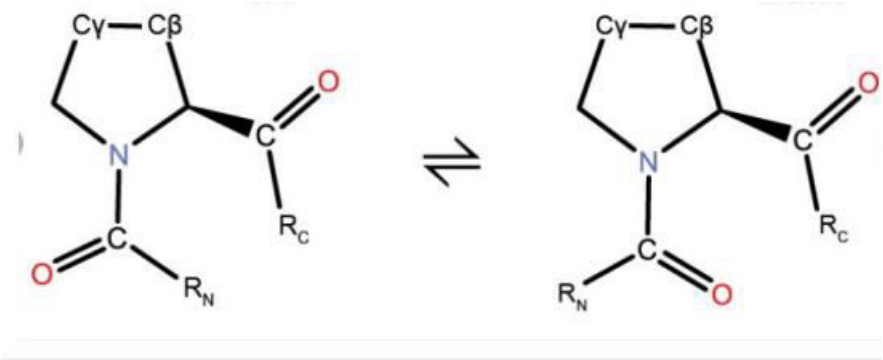
the flexibility of a Glycine containing peptide and this also contributes to the 4 quadrant distribution of phi and psi angles in a Ramachandran plot.
The different conformations of Glycine are shown below with there Gibbs free energy:-



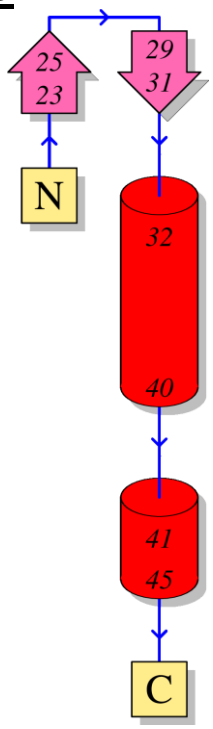
(a) Conf. I Conf. II Conf. III H H O H H C. C C- C Na O O N)-H H- N H H H +0.0 kJ/mol +2.2 kJ/mol +6.7 kJ/mol 6= (180,180,09) (12 ,-3 ,161°) (30',178 ,2') (b) Conf. IV Conf. V ... Show more

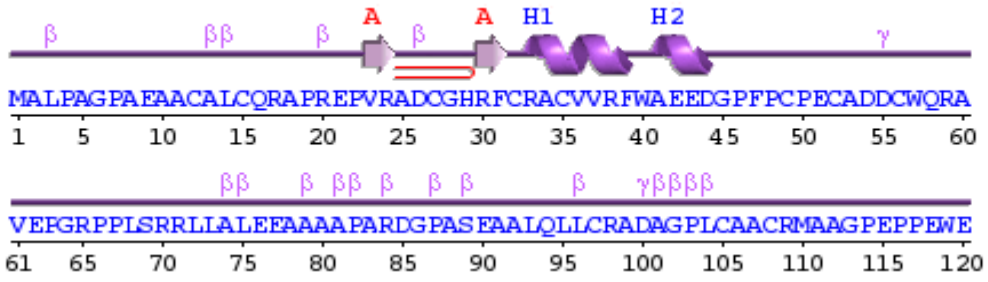
Glycine has many conformations as opposed to other amino acids. For example, Proline; a very sterically hindering amino acid found in peptide chains, has only 2 confirmations.

Cis **Trans**



Sol 9


25
23
29
31
N
32
40
41
45
C


β
ββ
β
A
β
A
H1
H2
γ
MALPAGPAFAACALCQRAPREPVRADCGHRFCRACVVRFWAEEDGPFPCPECADDCWQRA
1 5 10 15 20 25 30 35 40 45 50 55 60
ββ
β
ββ
β
β
β
β
γβββ
VEPGRPPLSRRLLALEFAAAAPARDGPASFAALQLLCRADAGPLCAACRMAAGPEPPEWE
61 65 70 75 80 85 90 95 100 105 110 115 120

PDBsum

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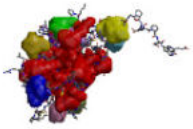
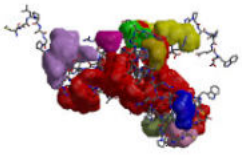
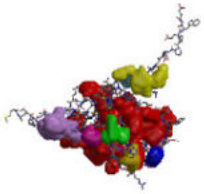
Top page | Protein | Clefts

Cleft analysis for: bnz2 | **PDB id** bnz2

View options

- (●) Binding-site(s)
- ( ) Binding-surface(s)

Coloured by

- (●) cleft (as in table below)
- ( ) closest atom type
- ( ) residue type

JSmol | RasMol

Clefts

	Volume	R1 ratio	Accessible vertices		Buried vertices		Average depth		Residue type							Ligands
1	5166.28	5.59	65.66	2	10.90	1	17.74	1	10	12	5	27	5	12	7	
2	924.75	0.00	55.61	8	10.42	2	12.10	2	3	2	0	5	0	4	0	
3	649.69	0.00	53.49	9	6.69	5	9.74	3	2	1	1	7	0	0	1	
4	284.77	0.00	59.65	5	9.21	4	5.52	8	0	2	1	2	0	3	1	
5	303.75	0.00	56.44	7	3.84	9	7.91	5	1	2	0	5	0	2	0	
6	239.62	0.00	58.39	6	5.37	6	4.68	9	0	1	0	6	0	1	0	
7	233.72	0.00	72.37	1	9.38	3	0.00	10	1	3	0	2	0	4	1	
8	211.36	0.00	59.74	4	4.60	7	8.04	4	3	1	0	2	0	3	0	
9	172.12	0.00	51.76	10	3.08	10	6.63	6	2	1	0	2	0	0	0	
10	174.23	0.00	64.54	3	3.96	8	6.35	7	1	0	0	5	0	0	1	

Protein structure

Residue-type colouring

Positive	Negative	Neutral	Aliphatic	Aromatic	Pro & Gly	Cysteine
H,K,R	D,E	S,T,N,Q	A,V,L,I,M	F,Y,W	P,G	C

PDBsum

Go to PDB code: bnz2 go

Top page | Protein | Clefts

No title | **PDB id** bnz2

PRIVATE: Custom-generated PDBsum page

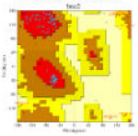
Theoretical model

PDB id: bnz2

Name: No title
Source: not given
Authors: not given
Date: 06-Dec-22

3Dmol | JSmol

PROCHECK



Headers

References

Protein chain

No UniProt id for this chain


Struc: 120 a.a.

Key: Secondary structure

Contents

Protein chain

120 a.a.

PDBsum

Go to PDB code: bnz2 go

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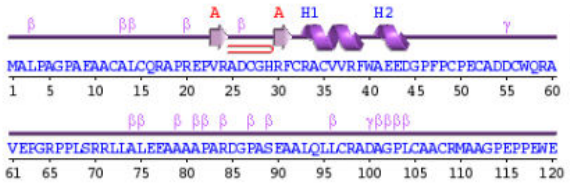
Protein chain A | PDB id bnz2

Chain A (120 residues)

Secondary structure:



FASTA file

Protein chain A highlighted (click to view)

JSmol

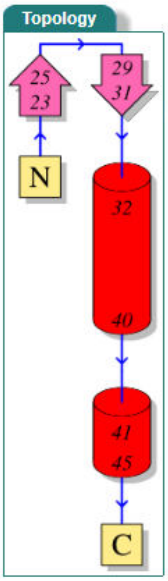
Key:

Sec. struc: Helices labelled H1, H2, ... and strands by their sheets A, B, ...

Helix Strand

Motifs: β beta turn γ gamma turn beta hairpin

Topology



Hera

Motifs

- Secondary structure
  - Wiring diagram
- ProMotif
  - 1 sheet
  - 1 beta hairpin
  - 2 strands
  - 2 helices
  - 1 helix-helix interac
  - 18 beta turns
  - 2 gamma turns

SAS **Related protein sequences in the PDB**

PDBsum entry bnz2

PDBsum

Go to PDB code: bnz2 go

Top page | Protein | Clefts

No title | PDB id bnz2

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REMARK   6 MODELLER BEST TEMPLATE % SEQ ID:  48.276
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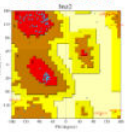
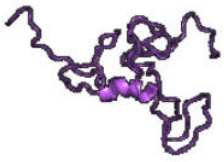
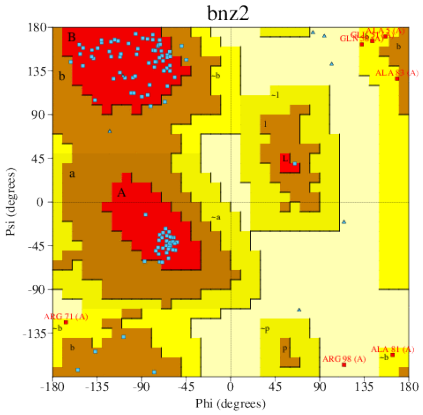


References



Contents

- Protein chain
  - A 120 a.a.



The database of highly refined protein structures and it plots a value graph of the position of the nine residue sliding window versus error function. This plot is based on nonbonded interaction statistics between different atom types that are calculated by its refined structure database. The result of the http://www.ebi.ac.uk/ server shows a graph between residues and error values**(the Ramachandran plot above)**. The overall quality score of this input structure is not considered good. If the input structure has good resolution, then it should have a quality score of greater than 95%. More than 90% score is observed for the protein structure with a resolution of 2–3 Å. In the Ramachandran plot, regions with red and yellow color represent the problematic part while the white color represents the normal part in the structure. Residues with error values more than 95% and 99% can easily be identified from the plot analysis. As we can see there is high amount of red and brown part we can say that this won't be a reliable structure to be used for other studies.

Referrences:-

Peptide bond- Definition, Formation, Degradation, Examples (microbenotes.com)

https://www.nature.com/scitable/definition/peptide-317/

https://byjus.com/jee/peptide-bond/

https://www.labxchange.org/library/pathway/lx-pathway/

https://www.open.edu/openlearn/science-maths-technology/biology/proteins/content-section-1.2/

https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/ramachandran-plot