



Department of Biotechnology	LP: BT18504 Rev. No: 00
B.E/B.Tech/M.E/M.Tech : Biotechnology Regulation: 2018A	Date: 04.07.2023
PG Specialisation : Not Applicable	
Sub. Code / Sub. Name : BT18504 / Protein Engineering and Proteomics	
Unit : 1	

**Unit Syllabus: BONDS IN BUILDING BLOCKS OF PROTEINS**

12

Covalent, Ionic, Hydrogen, Coordinate, hydrophobic and Vander walls interactions in protein structure. Amino acids (the students should be sithorough with three and single letter codes) and their molecular properties (size, solubility, charge, pKa), Chemical reactivity in relation to post-translational modification (involving amino, carboxyl, hydroxyl, thiol, imidazole groups).

**Objective:** To understand the properties of aminoacids and identify the protein structure

Session No *	Topics to be covered	Ref	Teaching Aids
1.	Interactions in protein structure	TB2 (139-166)	LCD/BB
2.	Covalent, Ionic Coordinate in protein structure	ATB1 (47-56)	LCD/BB
3.	Hydrophobic interactions in protein structure	ATB2 (24-25)	LCD/BB
4.	Vander walls interactions in protein structure	ATB3 (49-53)	LCD/BB
5.	Amino acids three and single letter codes	TB1 (6-7)	LCD/BB
6.	Amino acids classification size and charge properties	ATB2(74-81)	LCD/BB
7.	Amino acids size and solubility properties	ATB2(74-81)	LCD/BB
8.	Amino acids pKa properties	ATB2(74-81)	LCD/BB
9.	Chemical reactivity involving amino groups relation to post-translational modification	TB2(86-88)	LCD/BB
10.	Chemical reactivity involving thiol groups relation to post-translational modification	TB2 (98-99)	LCD/BB
11.	Chemical reactivity involving hydroxyl and carboxyl groups relation to post-translational modification	TB2 (88,96)	LCD/BB
12.	Chemical reactivity involving imidazole groups relation to post-translational modification	T2(96-97)	LCD/BB

**Content beyond syllabus covered (if any):** Raman Spectroscopy



Sub. Code / Sub. Name : BT18504/ Protein Engineering and Proteomics

Unit : 2

**Unit Syllabus : PRIMARY AND SECONDARY STRUCTURE**

12

Basic structural concepts- Primary structure: peptide mapping, peptide sequencing - automated Edman method & Mass- spec. Secondary structure: Alpha, beta and loop structures and methods to determine Super-secondary structure, tertiary and quaternary structures. Ramachandran plot, super secondary structures - Alpha-turn-alpha, beta-turn- beta (hairpin), beta-sheets, alpha-beta-alpha, topology diagrams.

**Objective:** To study about the arrangement and arrangement of protein biomolecules.

Session No *	Topics to be covered	Ref	Teaching Aids
13.	Primary structure: Peptide mapping and peptide sequencing	TB2 (31-34)	LCD/BB
14.	Primary structure: - automated Edman method, Mass- spectrometry	TB2 (35-42)	LCD/BB
15.	Primary structure: High-throughput protein sequencing setup	TB2 (28-30)	LCD/BB
16.	Secondary structure : Alpha structures	TB1 (13-18)	LCD/BB
17.	Secondary structure : Beta structures	TB1 (19-20)	LCD/BB
18.	Loop structures and methods to determine Secondary structure	TB1 (21-22)	LCD/BB
19.	Super-secondary structure: Alpha-turn alpha, beta-turn- beta (hairpin)	TB1 (24-25)	LCD/BB
20.	Super-secondary structure: Beta-sheets, alpha-beta-alpha	TB1 (26-29,57)	LCD/BB
21.	Nucleotide binding folds	TB1 (47-60)	LCD/BB
22.	TIM barrel structures	TB1 (47-54)	LCD/BB
23.	Up and down Beta barrel	TB1 (67-70)	LCD/BB
24.	Topology diagram	TB1 (13-32)	LCD/BB

**Content beyond syllabus covered (if any): Nil**

\* Session duration: 50 mins



Sub. Code / Sub. Name : BT18504/ Protein Engineering and Proteomics
Unit : 3

**Unit Syllabus : TERTIARY AND QUATERNARY STRUCTURE**

12

Motif and domain. Up and down & TIM barrel structures. Nucleotide binding folds. Tertiary structure: Domains, folding, denaturation and renaturation. Overview of X-ray, NMR and computational models in determination of 3D structures.

**Objective:** To gain knowledge about tertiary and quaternary structure of proteins.

Session No *	Topics to be covered	Ref	Teaching Aids
25.	Motifs of Protein Structure	TB1 (13-32)	LCD/BB
26.	Tertiary structure- Domains	TB 1 (27-29,31-32, 35-46, 49)	LCD/BB
27.	Tertiary structure- folding	TB 1 (96 - 100)	LCD/BB
28.	Denaturation and renaturation of protein kinetics	TB 1 (89-95)	LCD/BB
29.	Overview of methods to determine 3D structures	TB1 (373-391)	LCD/BB
30.	Quaternary structure-Modular nature	ATB5 (40-42)	LCD/BB
31.	Quaternary structure- formation of complexes	ATB5 (43-46)	LCD/BB
32.	Protein-Protein interactions - Suppressor mutations, Synthetic effects, , Dominant negatives	ATB4 (453-456) TB3 (134-136)	LCD/BB
33.	Protein-Protein interactions - Yeast two-hybrid system.	ATB4 (458-466)	LCD/BB
34.	Protein-Protein interactions - Fluorescence resonance energy transfer, Surface Plasmon Spectroscopy	RB1 (493-507, 527-529)	LCD/BB
35.	Overview of X-ray, NMR methods in determination of 3D structures	TB1 (373 – 392)	LCD/BB
36.	Overview of Computational methods in determination of 3D structures	RB2 (75-79)	LCD/BB

**Content beyond syllabus covered (if any): Nil**

\* Session duration: 50 mins



Sub. Code / Sub. Name : BT18504/ Protein Engineering and Proteomics

Unit : 4

**Unit Syllabus : STRUCTURE-FUNCTION RELATIONSHIP**

12

DNA-binding proteins: prokaryotic transcription factors, Helix-turn-Helix motif in DNA binding, Trp repressor, Eukaryotic transcription factors, Zn fingers, helix-turn helix motifs in homeodomain, Leucine zippers, Membrane proteins: General characteristics, Trans-membrane segments, prediction, bacteriorhodopsin and Photosynthetic reaction center, Immunoglobulins: IgG Light chain and heavy chain architecture, abzymes and Enzymes: Serine proteases, understanding catalytic design by engineering trypsin, chymotrypsin and elastase, substrate-assisted catalysis other commercial applications.

**Objective:** To realize the structure-function relationships in proteins.

Session No *	Topics to be covered	Ref	Teaching Aids
37.	Prokaryotic transcription factors, Helix-turn-Helix motif in DNA binding,	TB1 (129-135)	LCD/BB
38.	DNA-binding proteins: Trp repressor	TB1 (142-145)	LCD/BB
39.	DNA-binding proteins: Eukaryotic transcription factors	TB1 (151-161)	LCD/BB
40.	DNA-binding proteins: Zn fingers, Helix-turn helix motifs in homeodomain	TB1 (175-161)	LCD/BB
41.	DNA-binding proteins- Leucine zippers	TB1 (199-200)	LCD/BB
42.	Membrane proteins: General characteristics, Trans-membrane segments, Prediction	TB1 (223 -225) TB1 (244 -246)	LCD/BB
43.	Membrane proteins: Bacteriorhodopsin	TB1 (225-229)	LCD/BB
44.	Photosynthetic reaction center	TB1 (234-239)	LCD/BB
45.	Immunoglobulins: IgG Light chain and heavy chain architecture	TB1 (299-320)	LCD/BB
46.	Abzymes and Enzymes catalysis mechanism	TB1 (205-208)	LCD/BB
47.	Abzymes and Enzymes: Serine proteases, understanding catalytic design by engineering trypsin, chymotrypsin and elastase	TB1 (209-214)	LCD/BB
48.	Substrate-assisted catalysis other commercial applications	TB1 (215-219)	LCD/BB

**Content beyond syllabus covered (if any):** Commercial applications Ig G

\* Session duration: 50 mins



Sub. Code / Sub. Name : BT18504/ Protein Engineering and Proteomics

Unit : 5

**Unit Syllabus: PROTEOMICS**

12

Introduction to the concept of proteome, Analytical Proteomics - Protein digestion and separation technique, Functional Proteomics – Role of mass spectrometry in protein identification – peptide mass finger printing, Tandem MS, identifying protein - protein interactions and protein complexes, mapping – protein identification, protein arrays, cross linking methods, affinity methods, yeast hybrid systems and protein arrays. Mining proteomes, protein expression profiling, new directions in proteomics.

**Objective:** To practice the latest application of protein science in their research.

Session No *	Topics to be covered	Ref	Teaching Aids
49.	Introduction to Proteome & Components of Proteomics	TB3 (1-20) TB4 (15-24)	LCD/BB
50.	Analytical Proteomics	RB2 (1-3) TB4 (31-48)	LCD/BB
51.	Protein Protein Interaction – Cross Linking Methods	TB3 (140-145)	LCD/BB
52.	Protein Protein Interaction – Affinity Chromatography Methods	TB3 (37-46)	LCD/BB
53.	Protein Protein Interaction – Yeast two-hybrid system.	RB2 (47-57)	LCD/BB
54.	Protein Protein Interaction – Phage Display	RB2 (61-67) RB3 (237-255)	LCD/BB
55.	Protein Protein Interaction – Mass Spectrometry	RB2 (72-74) RB 3 (87-124)	LCD/BB
56.	Protein Protein Interaction – Computational Methods	RB2 (75-79)	LCD/BB
57.	Protein interaction maps	TB3 (158-163)	LCD/BB
58.	Protein Arrays	RB2 (81-89)	LCD/BB
59.	Protein Chips	RB2 (90-95)	LCD/BB
60.	Protein microarrays	RB2 (96-101)	LCD/BB

**Content beyond syllabus covered (if any): Nil**

\* Session duration: 50 mins



Sub. Code / Sub. Name : BT18504/ Protein Engineering and Proteomics

**TEXTBOOK:**

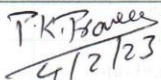

1. Branden C. and Tooze J., "Introduction to Protein Structures" 2nd Edition, Garland Publishing Inc, 1999.
2. Creighton T.E. "Proteins" 2nd Edition. W.H. Freeman, 1993.
3. Twyman, R.M. "Principles of Proteomics" 1st Edition, Taylor & Francis Group, LLC, 2004.
4. Liebler D.C., "Introduction to Proteomics – tools for the new biology", 1<sup>st</sup> Edition, Human

**REFERENCES:**

1. Wilson, K and Walker, J. "Principles and Techniques of Biochemistry and Molecular Biology", 7th Edition, Cambridge University Press, 2010.
2. Palzkill. T "Proteomics" Kluwer Academic Publishers, 2002.
3. Pennington, S.R and Dunn, M.J. "Proteomics : Protein Sequence to Function". Viva Books, 2002.

**ADDITIONAL TEXTBOOK:**

1. Lehninger, A. L, Nelson, D.L and Cox, M. M. "Lehninger Principles of Biochemistry", W. H. Freeman, 2005.
2. Voet, D.J, Voet, J.G and Pratt, C.W. "Biochemistry", 3rd Edition, John Wiley & Sons, Inc, 2008.
3. Bernhard Rupp "Biomolecular Crystallography: Principles, Practice, and Application to Structural Biology", Garland Science, Taylor & Francis Group, LLC, 2010.
4. Primrose, S.B. and Twyman, R.M. "Principles of Gene Manipulation and Genomics" 7th Edition, Blackwell Publishing, 2006.
5. Petsko, G. A. and Ringe, D "Protein Structure and Function" New Science Press Ltd, 2004.

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Date	04/07/2023	04/07/2023
Remarks *:		

