**BIRLA INSTITUTE OF TECHNOLOGY, MESRA, RANCHI**
**(END SEMESTER EXAMINATION)**

**CLASS: M. Sc./Pre-PHD** **SEMESTER : II/I**
**BRANCH: BIOTECHNOLOGY** **SESSION : SP/22**

**SUBJECT: BT421 PROTEOMICS**

**TIME: 2 HOURS** **FULL MARKS: 50**

INSTRUCTIONS:
1. The question paper contains 15 questions and total 50 marks.
2. Candidates need to attempt all questions maximum of 50 marks.
3. The missing data, if any, may be assumed suitably.
4. Before attempting the question paper, be sure that you have got the correct question paper.
5. Tables/Data hand book/Graph paper etc. to be supplied to the candidates in the examination hall.

----------NIL----------

## Q.1 to 5 Short answer type questions each of 2 marks

| | | |
|---|---|---|
| Q.1 | What are the characteristics of molten globule structure in protein folding? | [2] |
| Q.2 | Why staining and de-staining of the gel is performed? | [2] |
| Q.3 | How various tools and databases are useful in proteomics study? | [2] |
| Q.4 | How MALLS is useful in the determination of protein structure? | [2] |
| Q.5 | What you mean about engineering of a novel proteins? | [2] |

## Q.6 to 10 Short answer type questions each of 3 marks

| | | |
|---|---|---|
| Q.6 | Describe the forces that determine the protein structure | [3] |
| Q.7 | How SDS-PAGE may be useful in separating the proteins isolated from shoot and root sample? | [3] |
| Q.8 | How denaturation of a protein may affect the whole pathway or overall growth of a plant? | [3] |
| Q.9 | How circular dichroism is used in protein structure determination? | [3] |
| Q.10 | What concept needs to be considered while designing the new protein? | [3] |

## Q.11 to 15 Long answer type questions each of 5 marks

| | | |
|---|---|---|
| Q.11 | Using diagrammatic representation explain about key mechanism involved in the protein folding. | [5] |
| Q.12 | Give a diagrammatic sketch explaining the separation, staining, imaging and analysis of proteins isolated from leaf and shoot using 2D IEF SDS-PAGE. | [5] |
| Q.13 | Give a diagrammatic sketch describing the protein isolation, purification and mass spectrometry-based protein identification. | [5] |
| Q.14 | Draw a schematic diagram explaining protein crystallization and X-ray crystallography-based Rubisco protein structure determination from isolated crude protein solution. | [5] |
| Q.15 | Give a diagrammatic representation describing the strategies might be used to delete the AAG AAT AAC AGA sequences of hexokinase protein using site-directed mutagenesis. | [5] |

**:::::25/04/2022:::::**