Proforma for submitting a proposal to PGPEC for introducing a new subject

1. Department proposing the subject:	Dept. of Biotechnology
2. Subject No.:	
3. Subject title:	**Computational Structural Biology**
4. Subject structure and credits:	L-T-P: 3-0-0 Credits: 3
5. Status of the subject:	Elective (for M.Tech/Ph.D.)
6. Pre-requisites for the subject:	None
7. Overview, Objectives and Content:	

Overview:

Functional units of a cell can be described as complex assemblies of several macromolecules. The fundamental building blocks for these complex assemblies are proteins and nucleic acids. Recent advantages in the field of structural genomics provide us the 3-dimensional repertoire of the cellular assemblies exemplified by nuclear pore complex, GroEl and so on, and help us to understand the molecular mechanism behind different cellular functions of these assemblies. However, the experimental methods to determine the structures of macromolecules and their assemblies have some limitations, and to overcome this, several computational methods have been developed. These methods have been widely used in the prediction of the structure of macromolecules such as protein, DNA and RNA, as well as they have been very successful in the prediction of the complexes involving them. They are also being used for *de novo* design of proteins with specific function. Computational Structural Biology not only help us to elucidate the structure of the large assemblies such as the ribosome complexes, chaperonin, and multi-enzyme complexes etc.; but also help us to understand the structural mechanism of their folding, function and assembly. Their stability, mode of assembly, biological function and target properties depend on the interactions between the component subunits. Study of these complex assemblies is not only important for their functional role in the cellular system but also they serve as major therapeutic targets in human healthcare.

Objectives: To impart fundamental knowledge on the principles and strategies of the understanding of macromolecular assemblies and their interactions. The course is intended for the postgraduate students to develop understanding and learn techniques and skills involved in Computational Structural Biology and to build up concept about their uses in the prediction of folding, assembly and function of the macromolecules. After completion of the course, the student will be competent to design the strategies for computational prediction of macromolecules and their complexes as well as understanding the structural mechanism of the function of these assemblies.

Contents:

i) Fundamentals of biomolecular structure: Key concepts for the protein, DNA and RNA structures. Molecular interactions in tertiary structure, Fold space and evolution of the proteins. The quaternary structure of proteins and their association. Base-pair geometry in nucleic acids, conformation of the sugar phosphate backbone. DNA quadruplexes, RNA duplexes. Mismatched in bulged RNA. Structure and function of Ribosome.
[5hr]

ii) Computational aspects of macromolecular structure and assemblies: The structure of macromolecules and their file format. Introduction to computer programs to handle these files. Methodology for all atom contact analysis. Methods for structural comparison. Mapping protein fold space. The impact of structural genomics. [7hr]

iii) Structure and function assignment of macromolecules: Computational methods for structural assignment of proteins and nucleic acids. Identification of structural domains. Folding of protein and nucleic acids. Flexibility in macromolecules. Surface cleft and binding pockets. High throughput function prediction. Structure prediction and overview on CASP. [7hr]

iv) Structural annotation of Genomes: Availability of completed genomes. Methodologies available for identifying structural protein domains in genomes. Structural genome annotation resources.
[3hr]

v) Macromolecular interactions: Bonded and non-bonded interactions involved in folding and assembly of macromolecules. Analysis of intra and intermolecular interactions in the stability of macromolecules and their assembly. Prediction of protein-protein and protein-nucleic acids interactions. Overview on docking methods HADDOCK, ATTRACT, HEX, ligand design, and validating data sets. Search algorithms in docking and scoring function. Binding site prediction and annotation. Overview on CAPRI.
[8hr]

vi) Cellular machines: Overview on the structure of Ribosome, Proteasome, Nucleosome, Viral capsids. Computational tools for the structural analysis of the macromolecular interactions in these assemblies to understand their assembly pathways. [4hr]

vii) Computational Structural Biology and Drug Discovery: Historical development. Modern drug discovery. Drug targets identification and assessment (ex. Kinases and other ATPases; Proteases). Protein flexibility and drug design. Protein-protein interaction *hot spots*. Towards personalized medicine.
[3hr]

viii) Future challenges: Folding process for membrane proteins. Computational methods for the identification of membrane proteins and the prediction of their structures. The significance and impacts of protein disordered and conformational variants.
[3hr]

8. Name of the faculty member(s) of the department who have the necessary expertise and will be willing to teach the subject currently:

Dr.Ranjit Prasad Bahadur

Prof. Amit K. Das

9. Will the subject require appointment of adjunct faculty? If yes, the number of such adjunct faculty:

No

10. Do the content of the subject have an overlap with any other subject offered in the Institute? If yes, give details:

No

11. Suggested reading/text books/reference books:

(i) Proteins structures and molecular properties by T. E. Creighton.

(ii) Structural Bioinformatics by Jenny Gu and Philip E. Bourne

(iii) Bioinformatics and Functional Genomics by J. Pevsner

(iv) Protein-protein complexes; analysis, modeling and drug design. Edited by Martin Zacharias.

(v) Computational Structural Biology: Methods and Applications by Torsten Schwede and Manuel C. Peitsch.

(vi) Molecular conformation and Biological interactions by P. Balaram and S. Ramaseshan.

12. Name of the departments/centers/schools/programs whose students are expected to take up the course:

The students of M.Tech, and Ph.D. scholars of the following departments/centers/schools are expected to take up the course:

(i) Biotechnology

(ii) Agriculture & Food Engineering

(iii) Chemistry

(iv) Medical Science & Technology

(v) Computer Science

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Date:_____ Signature of the head of the Dept./Center/School