Certificate course

On

Applied Enzymology and basics of proteomics

(2019-2020)

Conducted

by

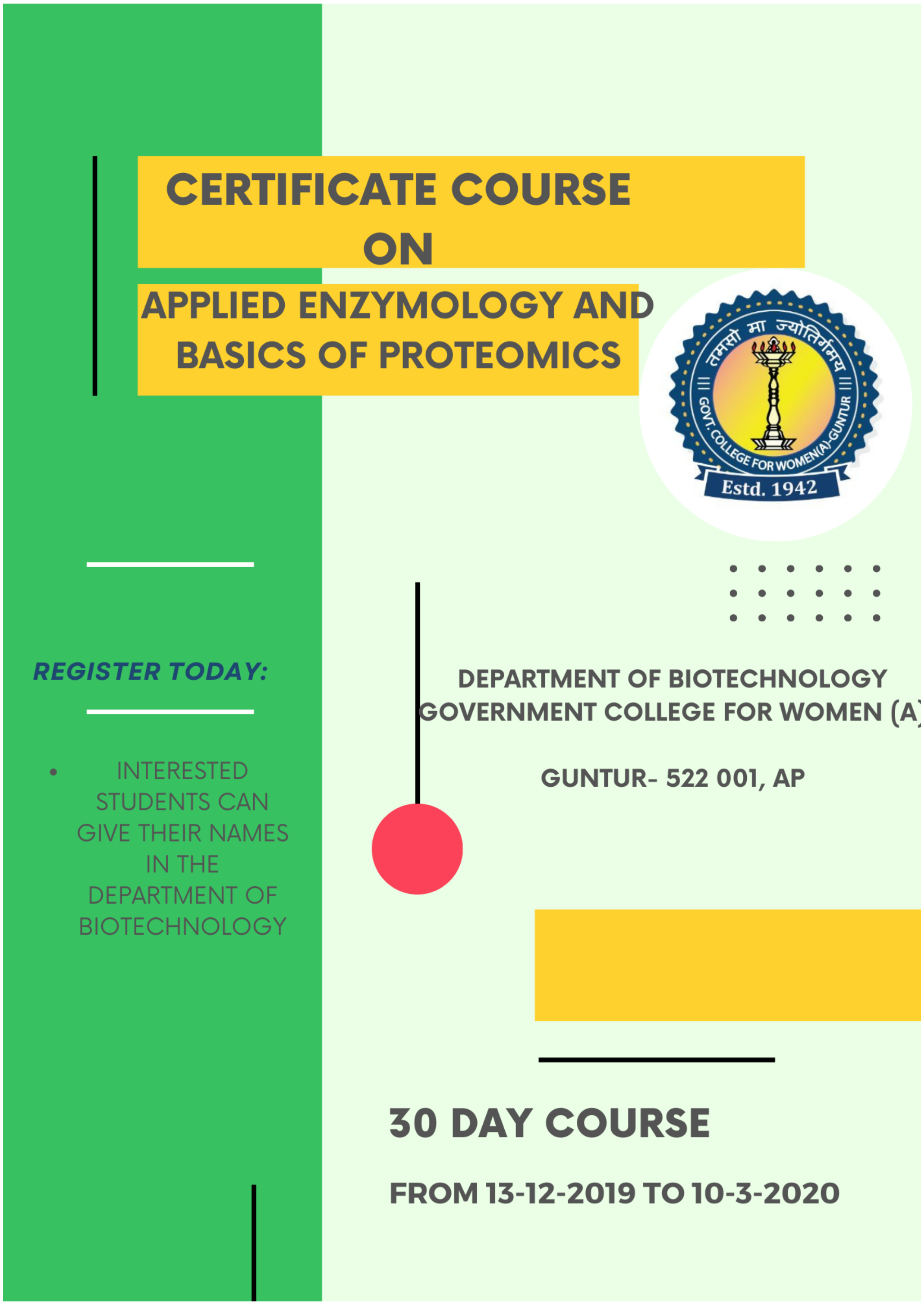
Department of Biotechnology

Government College for Women (A)

Guntur- 522 001, AP

Contents

BROUCHURE OF THE CERTIFICATE COURSE



CERTIFICATE COURSE ON APPLIED ENZYMOLOGY AND BASICS OF PROTEOMICS

REGISTER TODAY:

- INTERESTED STUDENTS CAN GIVE THEIR NAMES IN THE DEPARTMENT OF BIOTECHNOLOGY

DEPARTMENT OF BIOTECHNOLOGY
GOVERNMENT COLLEGE FOR WOMEN (A

GUNTUR- 522 001, AP

30 DAY COURSE

FROM 13-12-2019 TO 10-3-2020

GOVT. DEGREE COLLECGE FOR WOMEN (AUTONOMOUS), GUNTUR

Department of Biotechnology

Certificate course- Applied enzymology and basics of proteomics

CC108AFM

2019-20

No. of Hrs. 30

Course Description: This course provides an introduction to the principles and applications of enzymology and proteomics in biotechnology and related fields. Students will learn about the structure, function, and regulation of enzymes, as well as the fundamentals of proteomics techniques for studying protein expression, structure, and function.

Course Objectives:

1. To understand the principles of enzymology and their applications in biotechnology.
2. To introduce students to the basics of proteomics and its relevance in biological research.
3. To develop practical skills in enzyme assays and proteomics techniques.

Course Outcomes:

- Students will understand enzyme classification, kinetics, regulation, and their practical applications in biotechnology.
- Students will learn protein separation, identification, and characterization techniques essential for proteomics studies.
- Students will gain hands-on experience with enzyme assays and proteomics workflows, applying these techniques to real-world scenarios in drug discovery and diagnostics.

Unit 1: Enzymology

- Introduction to enzymes: Classification, nomenclature, and properties.
- Enzyme kinetics: Michaelis-Menten kinetics, Lineweaver-Burk plot, and enzyme inhibition.
- Regulation of enzyme activity: Allosteric regulation, enzyme induction, and enzyme repression.
- Practical applications of enzymes in biotechnology: Enzyme immobilization, industrial applications, and biocatalysis.

Unit 2: Basics of Proteomics

- Introduction to proteomics: Definition, scope, and importance.
- Protein separation techniques: Gel electrophoresis, chromatography, and mass spectrometry.
- Protein identification and characterization: Database searching, peptide sequencing, and bioinformatics tools.
- Functional proteomics: Protein-protein interactions, post-translational modifications, and protein localization studies.

Unit 3: Applied Techniques in Enzymology and Proteomics

- Enzyme assays: Spectrophotometric assays, colorimetric assays, and fluorometric assays.
- Proteomics workflows: Sample preparation, protein separation, identification, and data analysis.
- Case studies and applications: Use of enzymology and proteomics techniques in drug discovery, diagnostics, and personalized medicine.
- Hands-on laboratory sessions: Practical demonstrations and experiments related to enzyme assays and proteomics techniques.

SUGGESTED READING

1. Ghosh Z. and Bibekanand M. (2008) Bioinformatics: Principles and Applications. Oxford University Press.

2. Pevsner J. (2009) Bioinformatics and Functional Genomics. II Edition. Wiley-Blackwell.

3. Campbell A. M., Heyer L. J. (2006) Discovering Genomics, Proteomics and Bioinformatics. II Edition. Benjamin Cummings.

GOVT. DEGREE COLLEGE FOR WOMEN (AUTONOMOUS), GUNTUR
Department of Biotechnology

2019-20

Name of the Certificate course Conducted: Applied enzymology and basics of proteomics

Name of the Course coordinator : Dr.S.Priyanka

No. of Students enrolled : 14

Date of commencement of classes : 13/12/2019

Date of ending of the course : 10/ 03 /2020

No. of classes conducted : 32

No. of students appeared for final exam : 14

No. of students passed final exam : 14

Over all participation of the students : Satisfactory

Over all feed back of the students : Excellent

GOVT. DEGREE COLLEGE FOR WOMEN (AUTONOMOUS), GUNTUR
Department of Biotechnology

Certificate course- Applied enzymology and basics of proteomics
2019-20
List of students Enrolled:

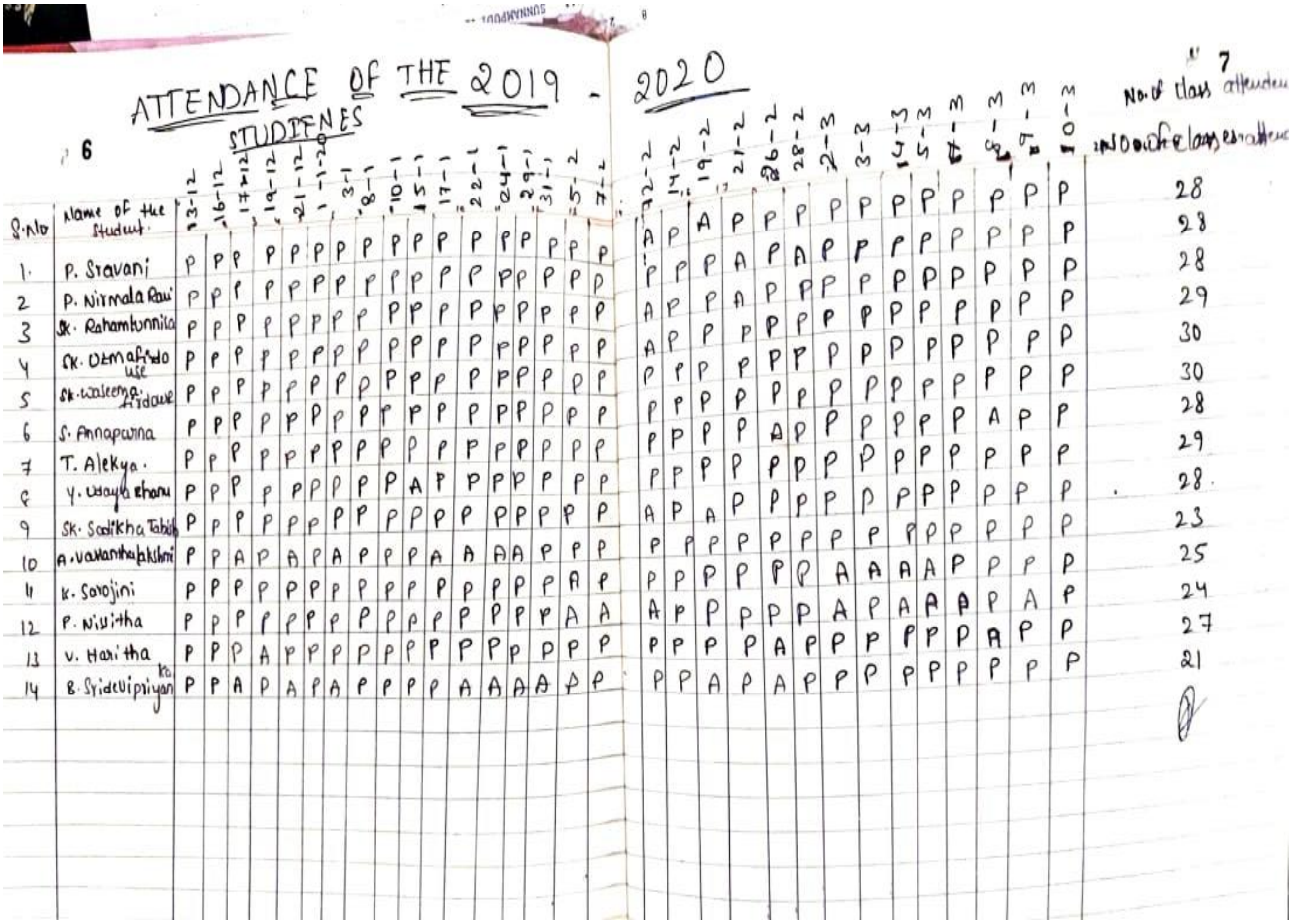
III B.SC BT.B.C

.S.No	Regd.No	Name Of The Student	No. of classes attended
1.	17406002	P.Sravani	28
2.	17406003	P.Nirmala Rani	28
3.	17406005	Sk.Rahamtunnisa	28
4.	17406006	Sk. Uzma firdouse	29
5.	17406007	skWaseema firdouse	30
6.	17406008	S.Annapurna	30
7.	17406009	T.Alekya	28
8.	17406011	Y.Udaya Bhanu	29
9.	17406012	Sk.Sadikha Tabish	28

III B.SC BC.BT.C

S.No	Regd.No	Name Of The Student	No. of classes
1.	17407001	A.Vasantha lakshmi	23
2.	17407002	K.Sarojini	25
3.	17407003	P.Nissitha	24
4.	17407005	V.Haritha	27
5.	17407006	B.Sridevi priyanka	21

ATTENDANCE OF THE STUDENTS



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ATTENDANCE OF THE 2019 - 2020 STUDIENES

7

S.No	Name of the Student.	13-12	16-12	17-12	19-12	21-12	1-1-20	3-1	8-1	10-1	15-1	17-1	22-1	24-1	29-1	31-1	5-2	7-2	12-2	14-2	19-2	21-2	26-2	28-2	2-3	3-3	4-3	5-3	6-3	7-3	9-3	10-3	No. of class attendance
1.	P. Sravani	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	A	P	A	P	P	P	P	P	P	P	P	P	P	P	28
2	P. Nirmala Rani	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	A	P	A	P	P	P	P	P	P	P	P	28
3	Sk. Rahamtunnisa	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	A	P	P	A	P	P	P	P	P	P	P	P	P	P	28
4	Sk. Uzmafirdouse	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	A	P	P	P	P	P	P	P	P	P	P	P	P	P	29
5	Sk. waseema firdaus	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	30
6	S. Annapurna	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	30
7	T. Alekya.	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	A	P	P	P	P	P	P	A	P	P	28
8	Y. Udaya Bhanu	P	P	P	P	P	P	P	P	P	A	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	29
9	Sk. Sadikha Tabish	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	A	P	A	P	P	P	P	P	P	P	P	P	P	P	28.
10	A. Vasantha lakshmi	P	P	A	P	A	P	A	P	P	P	A	A	A	A	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	23
11	K. Sarojini	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	A	P	P	P	P	P	P	P	A	A	A	A	P	P	P	P	25
12	P. Nisitha	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	A	A	A	P	P	P	P	P	A	P	A	A	A	P	A	P	24
13	V. Haritha	P	P	P	A	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	A	P	P	P	P	P	P	A	P	P	27
14	B. Sridevi priyanka	P	P	A	P	A	P	A	P	P	P	P	A	A	A	A	P	P	P	P	A	P	A	P	P	P	P	P	P	P	P	P	21

GOVT. DEGREE COLLEGE FOR WOMEN (AUTONOMOUS), GUNTUR

Department of Biotechnology

Certificate course- Applied enzymology and basics of proteomics

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Students Evaluation

III B.SC BT.B.C

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11.	17406003	P.Nirmala Rani	48
12.	17406005	Sk.Rahamtunnisa	48
13.	17406006	Sk. Uzma firdouse	49
14.	17406007	skWaseema firdouse	50
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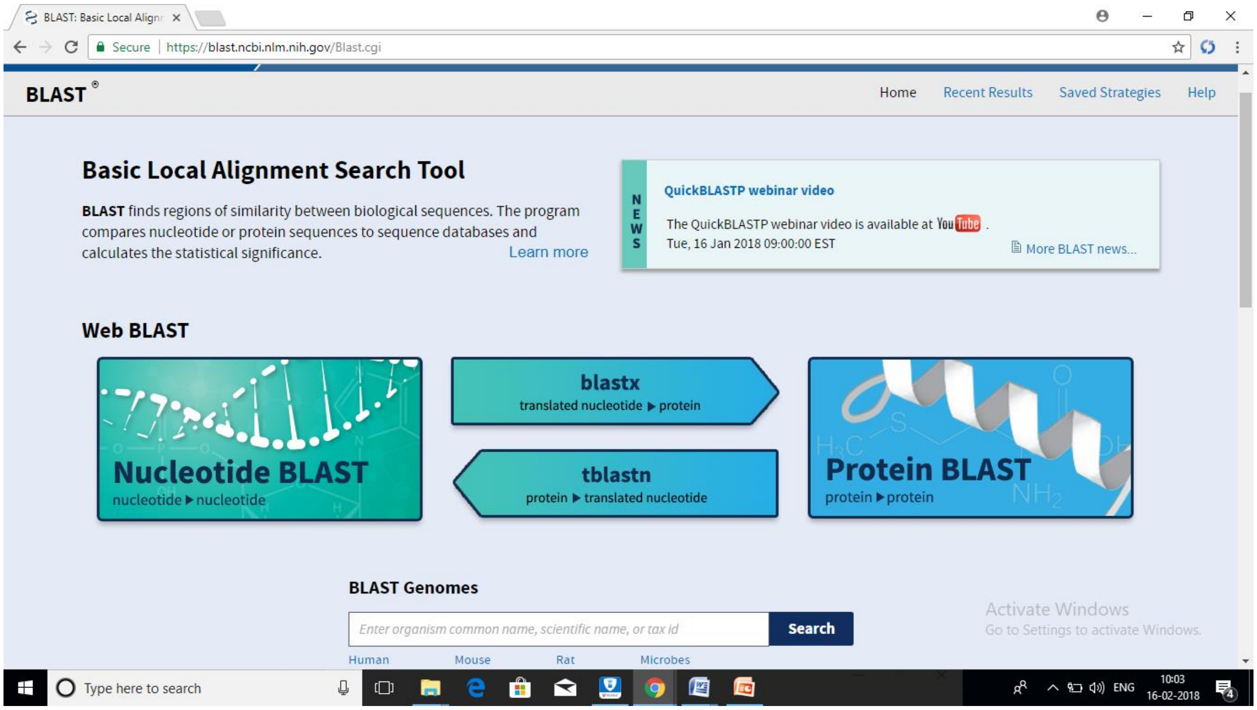
3.	17407003	P.Nissitha	44
4.	17407005	V.Haritha	47
5.	17407006	B.Sridevi priyanka	47

Supporting Material
Soft wares/Platforms used



Basic Local Alignment Search Tool

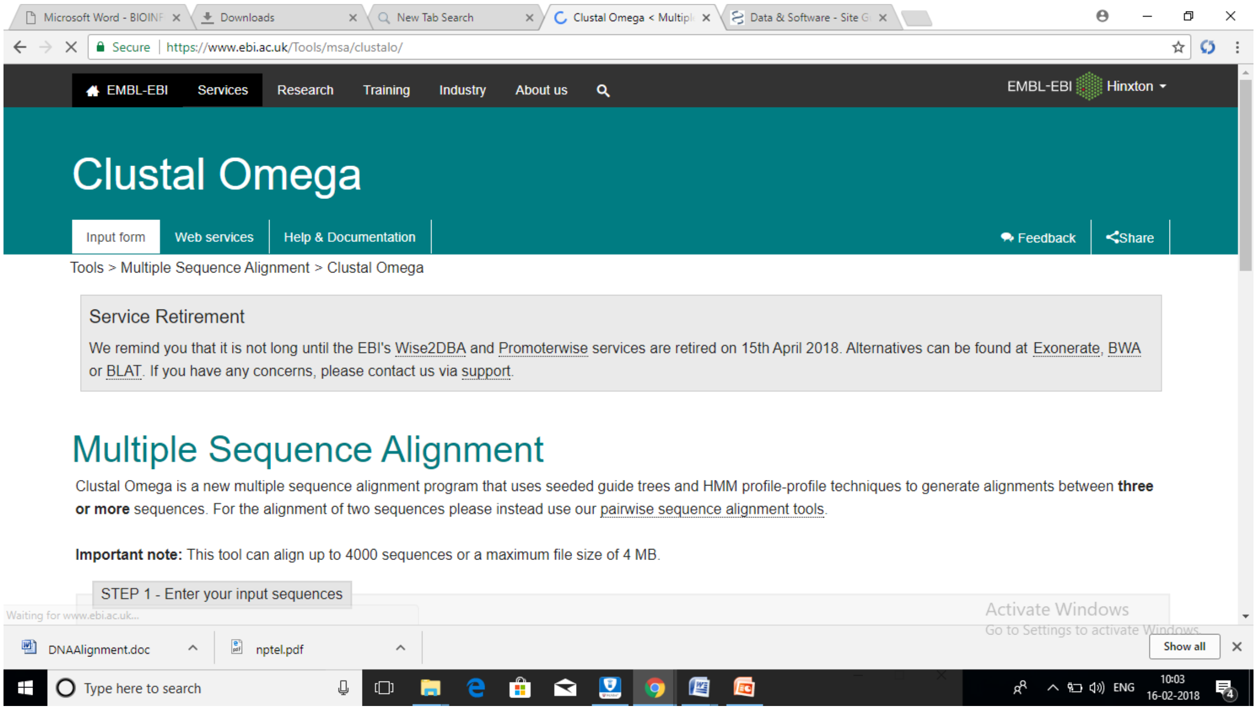
BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. Learn more

QuickBLASTP webinar video

The QuickBLASTP webinar video is available at YouTube.

Tue, 16 Jan 2018 09:00:00 EST

More BLAST news...



Clustal Omega

Tools > Multiple Sequence Alignment > Clustal Omega

Service Retirement

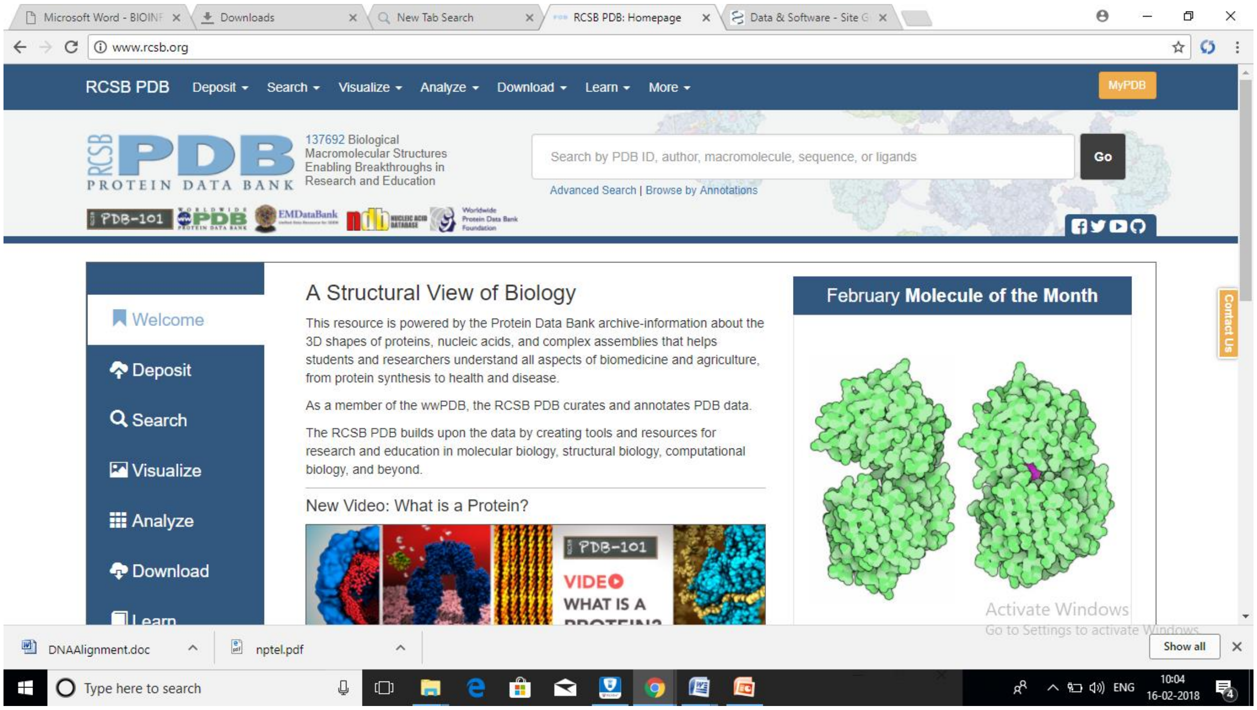
We remind you that it is not long until the EBI's Wise2DBA and Promoterwise services are retired on 15th April 2018. Alternatives can be found at Exonerate, BWA or BLAT. If you have any concerns, please contact us via support.

Multiple Sequence Alignment

Clustal Omega is a new multiple sequence alignment program that uses seeded guide trees and HMM profile-profile techniques to generate alignments between **three or more** sequences. For the alignment of two sequences please instead use our pairwise sequence alignment tools.

Important note: This tool can align up to 4000 sequences or a maximum file size of 4 MB.

STEP 1 - Enter your input sequences



137692 Biological Macromolecular Structures Enabling Breakthroughs in Research and Education

A Structural View of Biology

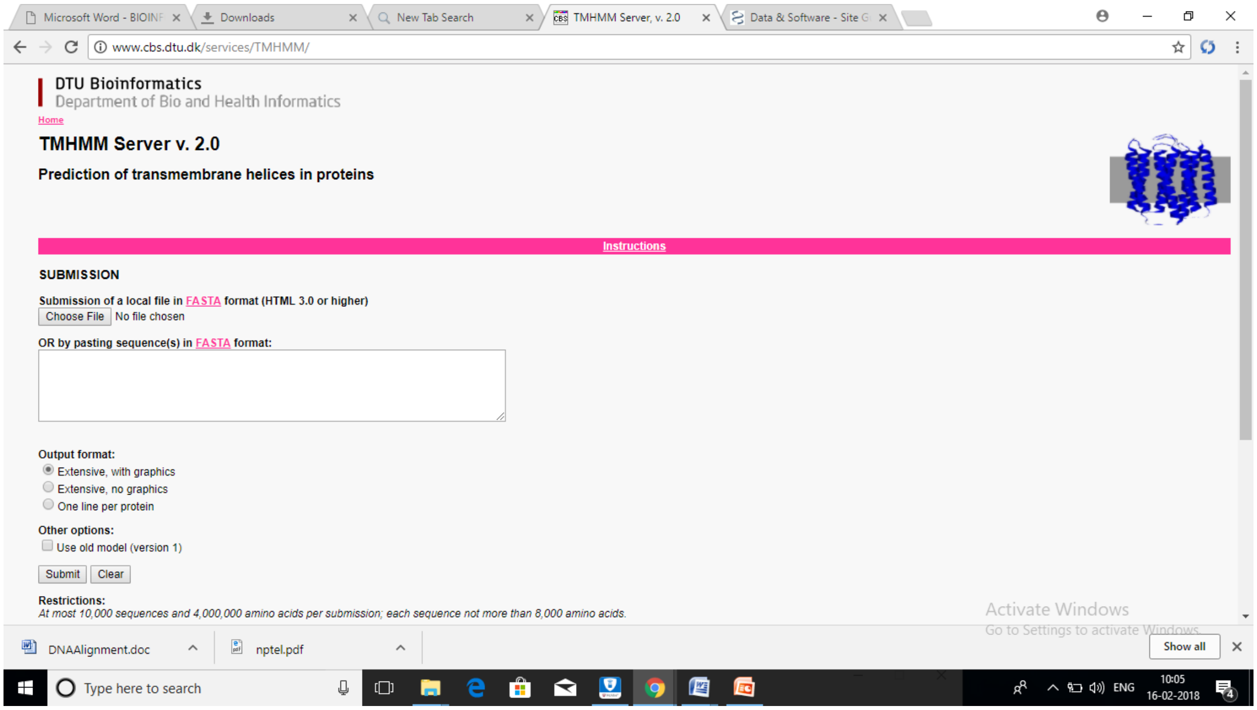
This resource is powered by the Protein Data Bank archive-information about the 3D shapes of proteins, nucleic acids, and complex assemblies that helps students and researchers understand all aspects of biomedicine and agriculture, from protein synthesis to health and disease.

As a member of the wwPDB, the RCSB PDB curates and annotates PDB data.

The RCSB PDB builds upon the data by creating tools and resources for research and education in molecular biology, structural biology, computational biology, and beyond.

New Video: What is a Protein?

February Molecule of the Month



DTU Bioinformatics
Department of Bio and Health Informatics

TMHMM Server v. 2.0

Prediction of transmembrane helices in proteins

SUBMISSION

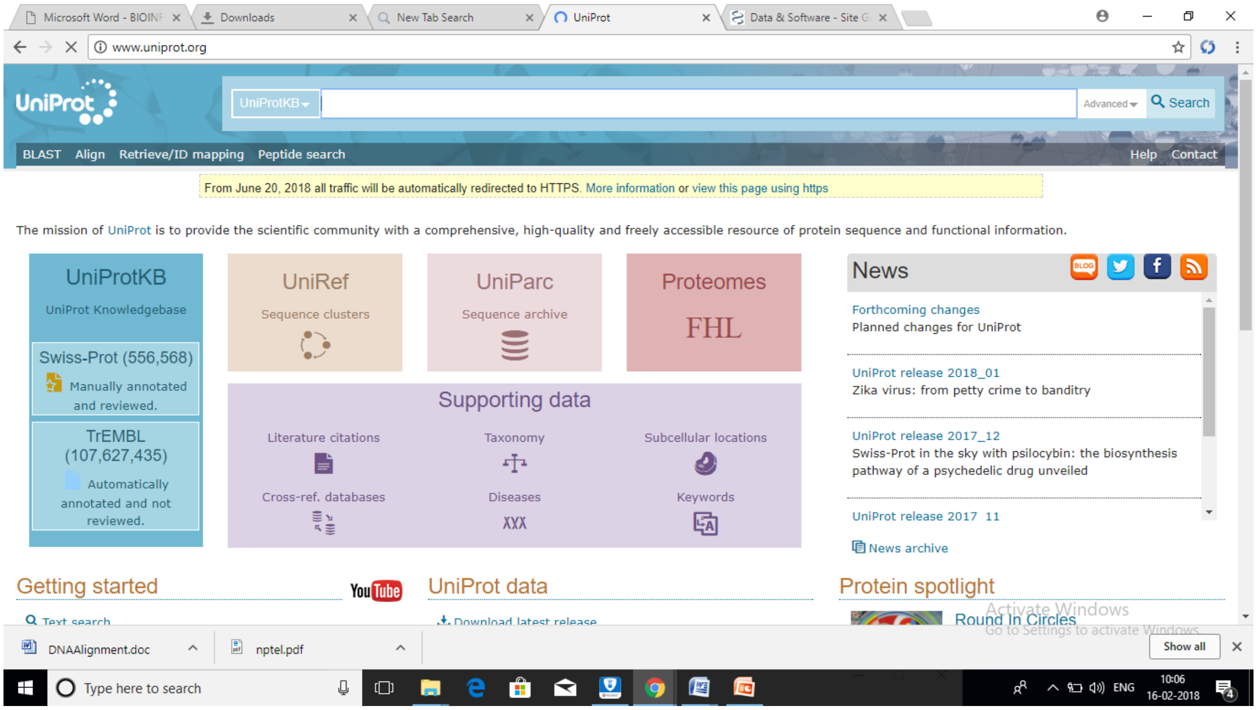
Submission of a local file in FASTA format (HTML 3.0 or higher)
No file chosen

OR by pasting sequence(s) in FASTA format:

Output format:
● Extensive, with graphics
○ Extensive, no graphics
○ One line per protein

Other options:
☐ Use old model (version 1)

Restrictions:
At most 10,000 sequences and 4,000,000 amino acids per submission; each sequence not more than 8,000 amino acids.



From June 20, 2018 all traffic will be automatically redirected to HTTPS. More information or view this page using https

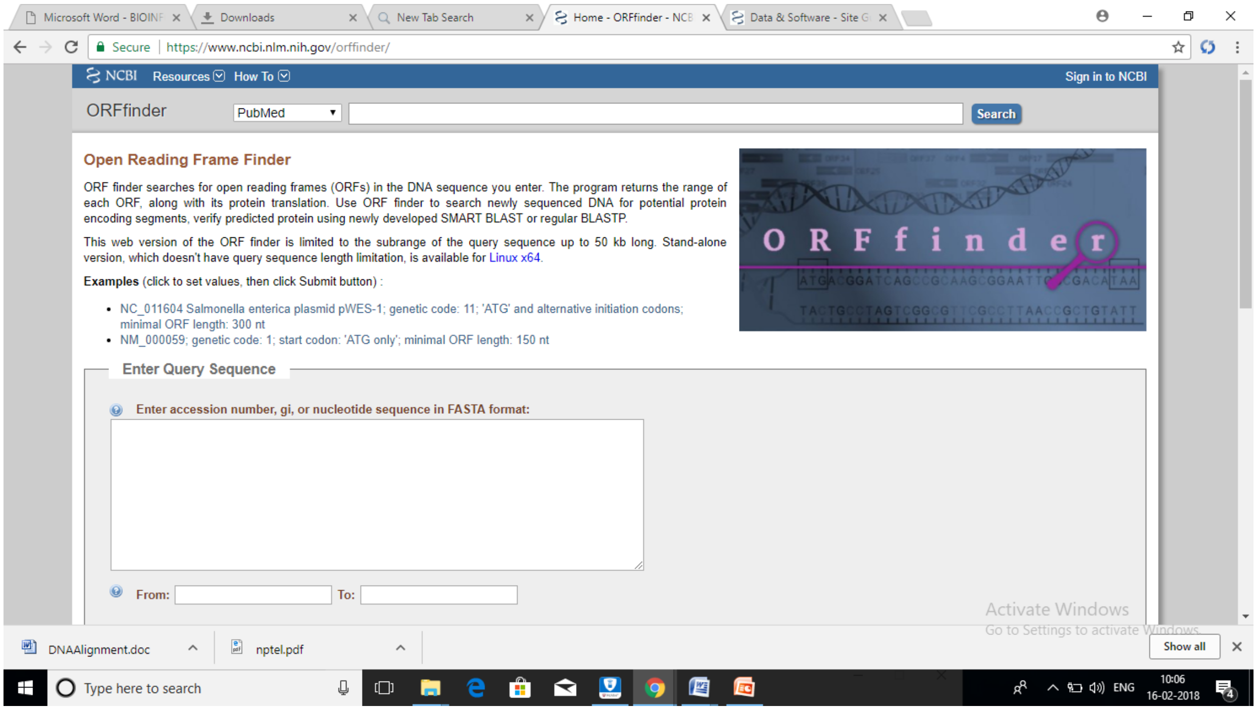
The mission of UniProt is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.

Forthcoming changes
Planned changes for UniProt

UniProt release 2018_01
Zika virus: from petty crime to banditry

UniProt release 2017_12
Swiss-Prot in the sky with psilocybin: the biosynthesis pathway of a psychedelic drug unveiled

UniProt release 2017_11



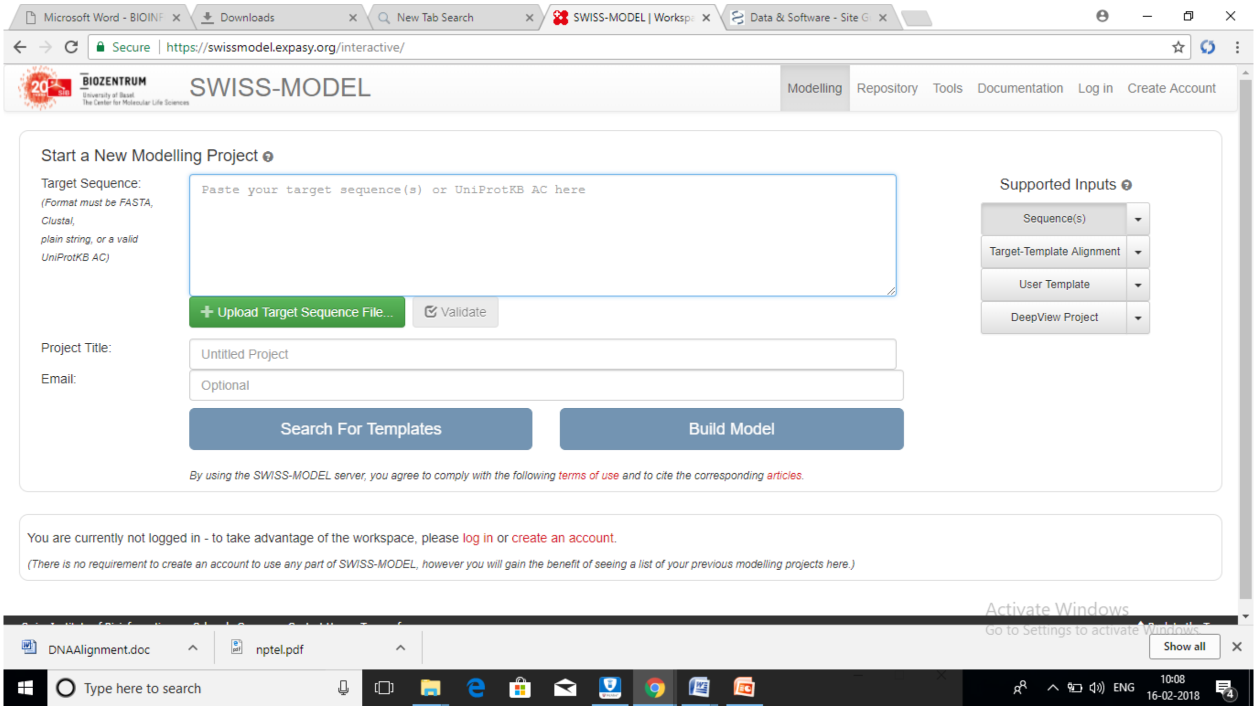
Open Reading Frame Finder

ORF finder searches for open reading frames (ORFs) in the DNA sequence you enter. The program returns the range of each ORF, along with its protein translation. Use ORF finder to search newly sequenced DNA for potential protein encoding segments, verify predicted protein using newly developed SMART BLAST or regular BLASTP.

This web version of the ORF finder is limited to the subrange of the query sequence up to 50 kb long. Stand-alone version, which doesn't have query sequence length limitation, is available for Linux x64.

Examples (click to set values, then click Submit button) :

- NC_011604 Salmonella enterica plasmid pWES-1; genetic code: 11; 'ATG' and alternative initiation codons; minimal ORF length: 300 nt
- NM_000059; genetic code: 1; start codon: 'ATG only'; minimal ORF length: 150 nt



Start a New Modelling Project

Target Sequence: (Format must be FASTA, Clustal, plain string, or a valid UniProtKB AC)

Paste your target sequence(s) or UniProtKB AC here

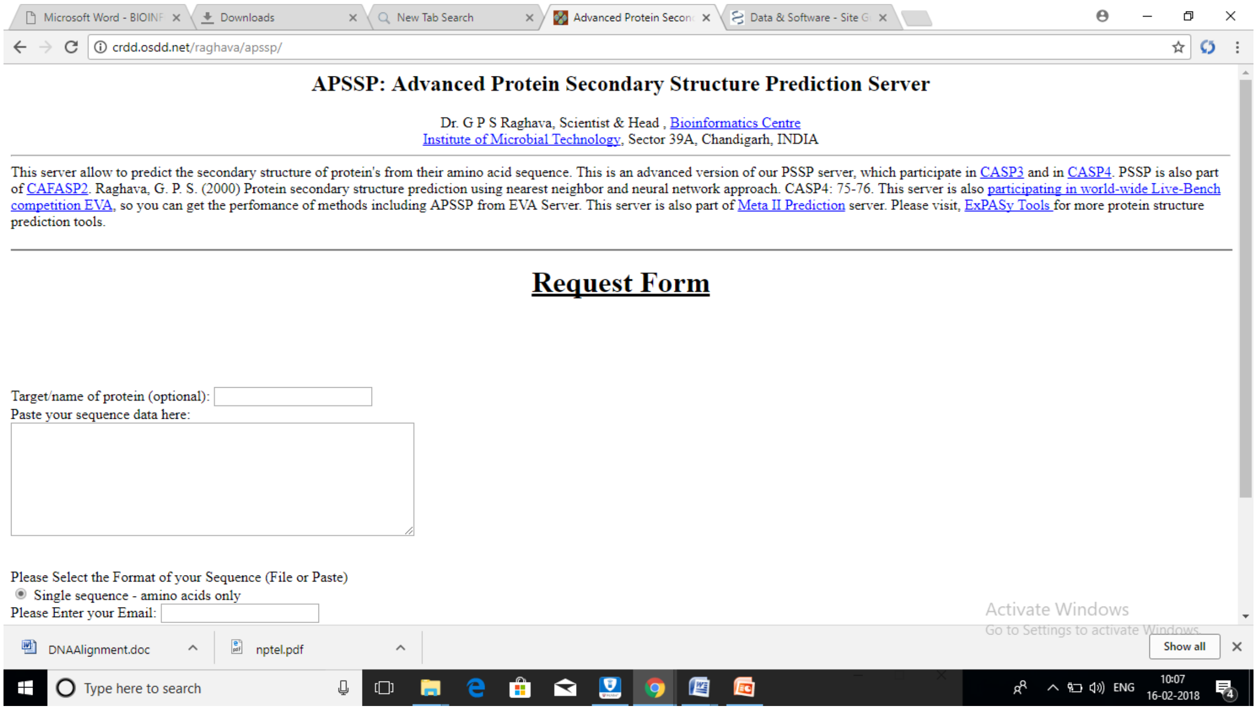
Project Title: Untitled Project

Email: Optional

By using the SWISS-MODEL server, you agree to comply with the following terms of use and to cite the corresponding articles.

You are currently not logged in - to take advantage of the workspace, please log in or create an account.

(There is no requirement to create an account to use any part of SWISS-MODEL, however you will gain the benefit of seeing a list of your previous modelling projects here.)



APSSP: Advanced Protein Secondary Structure Prediction Server

Dr. G P S Raghava, Scientist & Head , Bioinformatics Centre
Institute of Microbial Technology, Sector 39A, Chandigarh, INDIA

This server allow to predict the secondary structure of protein's from their amino acid sequence. This is an advanced version of our PSSP server, which participate in CASP3 and in CASP4. PSSP is also part of CAFASP2. Raghava, G. P. S. (2000) Protein secondary structure prediction using nearest neighbor and neural network approach. CASP4: 75-76. This server is also participating in world-wide Live-Bench competition EVA, so you can get the perfomance of methods including APSSP from EVA Server. This server is also part of Meta II Prediction server. Please visit, ExPASy Tools for more protein structure prediction tools.

Request Form

Target/name of protein (optional):

Paste your sequence data here:

Please Select the Format of your Sequence (File or Paste)

● Single sequence - amino acids only

Please Enter your Email:

Protein Structure Prediction

Protein structures are stable conformations of a polypeptide chain. They are critically important in maintaining a protein three-dimensional structure. The highly regular and repeated structural elements include α-helices and β-sheets. It has been estimated that nearly 50% of residues of a protein fold into either α-helices and β-strands. As a review, an α-helix is a spiral-like structure with 3.6 amino acid residues per turn. The structure is stabilized by hydrogen bonds between residues i and $i + 4$. Prolines normally do not occur in the middle of helical segments, but can be found at the end positions of α-helices.

A β-sheet consists of two or more β-strands having an extended zigzag conformation. The structure is stabilized by hydrogen bonding between residues of adjacent strands, which actually may be long-range interactions at the primary structure level. β-Strands at the protein surface show an alternating pattern of hydrophobic and hydrophilic residues; buried strands tend to contain mainly hydrophobic residues.

Protein secondary structure prediction refers to the prediction of the conformational state of each amino acid residue of a protein sequence as one of the three possible states, namely, helices, strands, or coils, denoted as H, E, and C, respectively.

The prediction is based on the fact that secondary structures have a regular arrangement of amino acids, stabilized by hydrogen bonding patterns. The structural regularity serves the foundation for prediction algorithms.

STUDENTS EVALUATION

Students were evaluated by an exam with 50 marks.

Total of 15 questions are given out of which student has to write 10 questions.

Each question carries 5 marks.

Question paper for certificate course

Title: Applied Enzymology and Basics of Proteomics
Total Marks: 50 Time: 2hrs

Answer any 10 questions. Each question carries 5 marks.

1. Define the term "enzyme" and describe its role in biological systems. Provide an example of an enzyme and its specific function.
2. How do enzymes catalyze biochemical reactions? Explain with the help of an example.
3. Compare and contrast competitive and non-competitive enzyme inhibition. Give examples of each type of inhibition.
4. Discuss the importance of enzyme immobilization in biotechnological applications. Provide two examples of enzyme immobilization techniques.
5. Describe the principles of gel electrophoresis in protein separation. How is gel electrophoresis used in proteomics research?
6. Explain the process of peptide sequencing using mass spectrometry. How does mass spectrometry contribute to protein identification in proteomics?
7. What are post-translational modifications (PTMs) in proteins? Give examples of two common PTMs and their functional significance.
8. How are enzymes used in the food industry? Provide two examples of food products that are manufactured using enzyme technology.
9. Define proteomics and its significance in modern biology. Discuss two major techniques used in proteomics research.
10. Describe the role of proteomics in personalized medicine. Give an example of how proteomics can be applied in disease diagnosis or treatment.
11. Explain the concept of enzyme kinetics. Discuss the Michaelis-Menten equation and its parameters.
12. How can enzyme activity be measured using spectrophotometry? Provide a brief protocol for conducting a spectrophotometric enzyme assay.
13. Discuss the advantages and disadvantages of using recombinant enzymes in industrial processes. Give two examples of industrially important recombinant enzymes.
14. What is protein-protein interaction (PPI) analysis in proteomics? Describe one experimental technique used for studying PPIs.
15. Explain the significance of enzyme-substrate specificity in biocatalysis. Give an example of an enzyme-substrate pair and their specificity.

DISTRIBUTION OF CERTIFICATES BY THE PRINCIPAL TO THE STUDENTS

GOVT COLLEGE FOR WOMEN, GUNTUR

(AN AUTONOMOUS INSTITUTION WITH CPE STATUS)

CERTIFICATE OF ACHIEVEMENT

This is to certify Ms. ___________________________________ of ___________________________ successfully completed the Certificate Course in "APPLIED ENZYMOLOGY & BASICS OF PROTEOMICS" conducted by the Department of Biotechnology from 13-12-2019 to 10-03-2020.

Course Coordinator
Dept. of Biotechnology

Estd. 1942

PRINCIPAL
Govt. College for
Women(A), Guntur