Certificate course

On

COMPUTATIONAL BIOLOGY

(2020-2021)

Conducted

by

Department of Biotechnology

Government College for Women (A)

Guntur- 522 001, AP

Contents

BROUCHURE OF THE CERTIFICATE COURSE

CERTIFICATE COURS IN COMPUTATIONAL BIOLOGY

GOVT COLLEGE FOR WOMEN (A), GUNTUR

Interested students can give their names in the department of Biotechnology

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CERTIFICATE COURSE

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- ✓ 30 SEATS
- ✓ HANDS ON TRAINING

Estd. 1942

GOVT. DEGREE COLLECGE FOR WOMEN (AUTONOMOUS), GUNTUR

Department of Biotechnology

Certificate course- Computational Biology

CC108AFM

2020-21

No. of Hrs. 30

Course Objectives:

- To introduce students to fundamental concepts in computational biology and bioinformatics.
- To develop skills in analyzing biological data using computational tools and databases.
- To enable students to perform basic sequence analysis, phylogenetic analysis, and structural prediction.

Course Outcomes:

- Students will proficiently utilize biological databases such as NCBI, Ensembl, and GenBank, retrieving and analyzing sequence information with tools like BLAST.
- Students will analyze protein sequences and structures, predict and model protein structures, and perform genome analysis, including sequence assembly and phylogenetic tree construction.
- Students will apply advanced techniques in systems biology.

Course Content: (Total Hours: 30)

UNIT I: Introduction to Computational Biology

Overview of Computational Biology: History and applications.

Introduction to biological databases and data sources (e.g., NCBI, Ensembl).

Understanding and using sequence information sources (e.g., GenBank, EMBL).

Basic techniques for data retrieval and analysis on web-based platforms. *(6 Hours)*

UNIT II: Protein Bioinformatics

Protein databases and resources (e.g., PDB, UniProt).

Analysis of protein sequences and structures.

Introduction to tools for protein sequence alignment and similarity searching (e.g., BLAST).

Protein structure prediction and modeling. *(8 Hours)*

UNIT III: Genome Analysis and Phylogenetics

Genome databases and annotation tools.

Basics of sequence assembly and gene prediction.

Phylogenetic analysis: constructing and interpreting phylogenetic trees.

Introduction to genetic variation and mutation analysis. *(8 Hours)*

UNIT IV: Advanced Topics in Computational Biology

Systems biology and network analysis.

Metagenomics and microbiome analysis.

Introduction to next-generation sequencing (NGS) data analysis.

Application of machine learning in computational biology. *(8 Hours)*

Practical Sessions:

1. Hands-on exercises with biological databases and sequence retrieval.
2. Using tools for sequence alignment (e.g., BLAST) and interpreting results.
3. Protein structure visualization and analysis using online resources (e.g., PDB, UniProt).
4. Genome annotation and basic phylogenetic analysis.
5. Application-based projects integrating course learnings.

Suggested Readings:

1. "Bioinformatics and Functional Genomics" by Jonathan Pevsner.
2. "Bioinformatics: Principles and Applications" by Zhumar Ghosh and Bibekanand Mallick.
3. "Introduction to Computational Biology" by Aurther M. Lesk.
4. Online tutorials and resources from NCBI (https://www.ncbi.nlm.nih.gov/).
5. PDB101 (https://pdb101.rcsb.org/), UniProt (http://www.uniprot.org/), and other relevant online platforms.

Department of Biotechnology

2020-21

Name of the Certificate course Conducted: Computational Biology

Name of the Course coordinator : Dr.S.Priyanka

No. of Students enrolled : 12

Date of commencement of classes : 30/03/2021

Date of ending of the course : 10/ 04 /2020

No. of classes conducted : 32

No. of students appeared for final exam : 12

No. of students passed final exam : 12

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- Computational Biology
2020-21
List of students Enrolled:

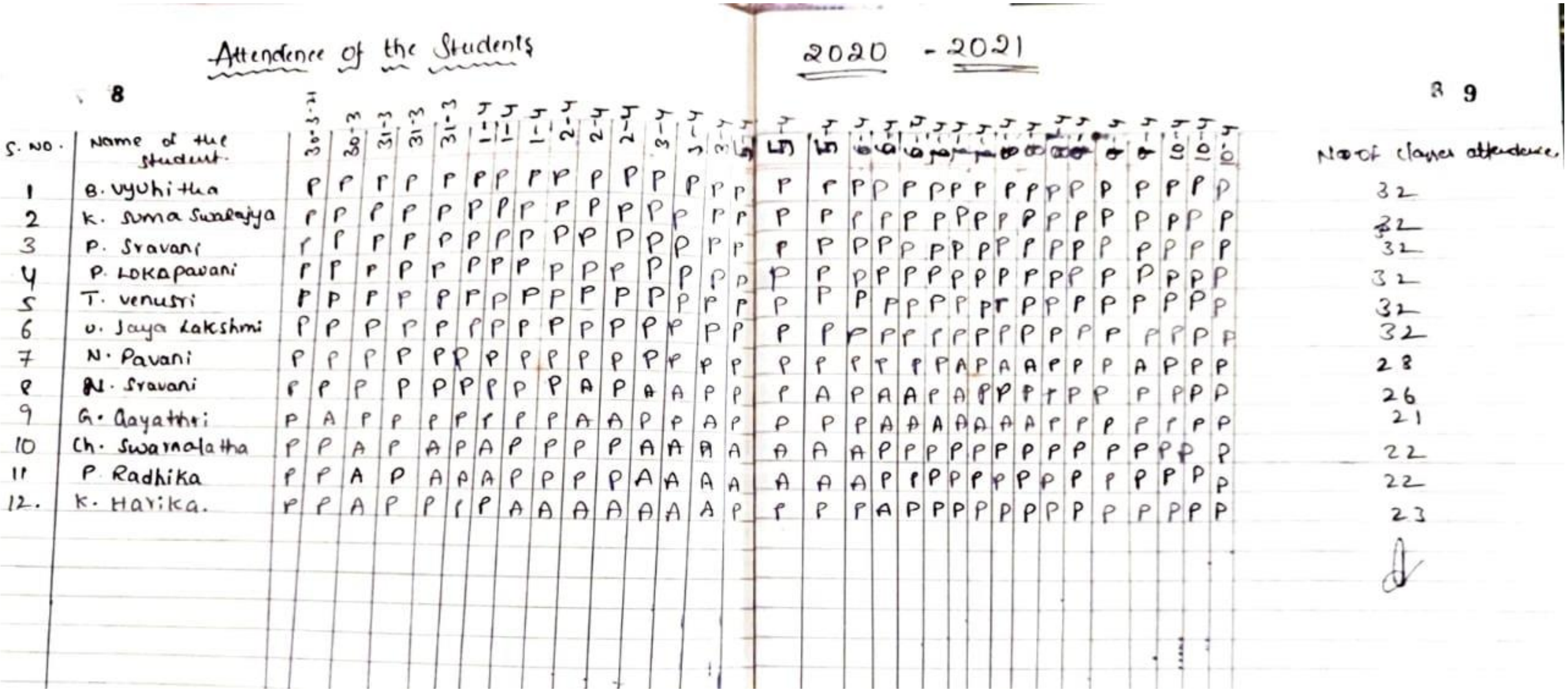
III B.SC BC.BT.C

S.No	Regd.No	Name Of The Student	No. of classes attended
1.	18407001	B.VYUHITHA	32
2.	18407003	K.SUMA SWARAJYA LAKSHMI	32
3.	18407005	P.SRAVANI	32
4.	18407006	P.LOKAPAVANI	32
5.	18407008	T.VENUSRI	32

III B.SC BC.Z.C

.S.No	Regd.No	Name Of The Student	No. of classes attended
1.	18405014	U.JAYA LAKSHMI	32
2.	18405011	N.PAVANI	28
3.	18405010	N.SRAVANI	26
4.	18405007	G.GAYATHRI	21
5.	18405004	CH.SWARNALATHA	22
6.	18405012	P.RADHIKA	22
7.	18408010	K.HARIKA	23

ATTENDANCE OF THE STUDENTS



Attendence of the Students 2020 - 2021

8

8 9

S. No.	Name of the student	30-3-21	30-3	31-3	31-3	31-3	1-4	1-4	1-4	2-4	2-4	2-4	3-4	3-4	3-4	5-4	5-4	5-4	6-4	6-4	6-4	7-4	7-4	7-4	8-4	8-4	8-4	8-4	9-4	9-4	10-4	10-4	10-4	No of classes attendence
1	B. Vyuhitha	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	P	32
2	K. Suma Swarajya	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	P	32
3	P. Sravani	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	P	32
4	P. Lokapavani	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	P	32
5	T. Venusri	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	P	32
6	V. Jaya Lakshmi	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	P	32
7	N. Pavani	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	P	A	P	A	A	P	P	P	A	P	P	P	28
8	N. Sravani	P	P	P	P	P	P	P	P	P	A	P	A	A	P	P	P	A	P	A	A	P	A	P	P	P	P	P	P	P	P	P	P	26
9	G. Gayathri	P	A	P	P	P	P	P	P	P	A	A	P	P	A	P	P	P	P	A	A	A	A	A	A	A	P	P	P	P	P	P	P	21
10	Ch. Swarnalatha	P	P	A	P	A	P	A	P	P	P	P	A	A	A	A	A	A	A	P	P	P	P	P	P	P	P	P	P	P	P	P	P	22
11	P. Radhika	P	P	A	P	A	P	A	P	P	P	P	A	A	A	A	A	A	A	P	P	P	P	P	P	P	P	P	P	P	P	P	P	22
12.	K. Harika.	P	P	A	P	P	P	P	A	A	A	A	A	A	A	P	P	P	P	A	P	P	P	P	P	P	P	P	P	P	P	P	P	23

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

Certificate course- Applied enzymology and basics of proteomics
2020-2021
Students Evaluation

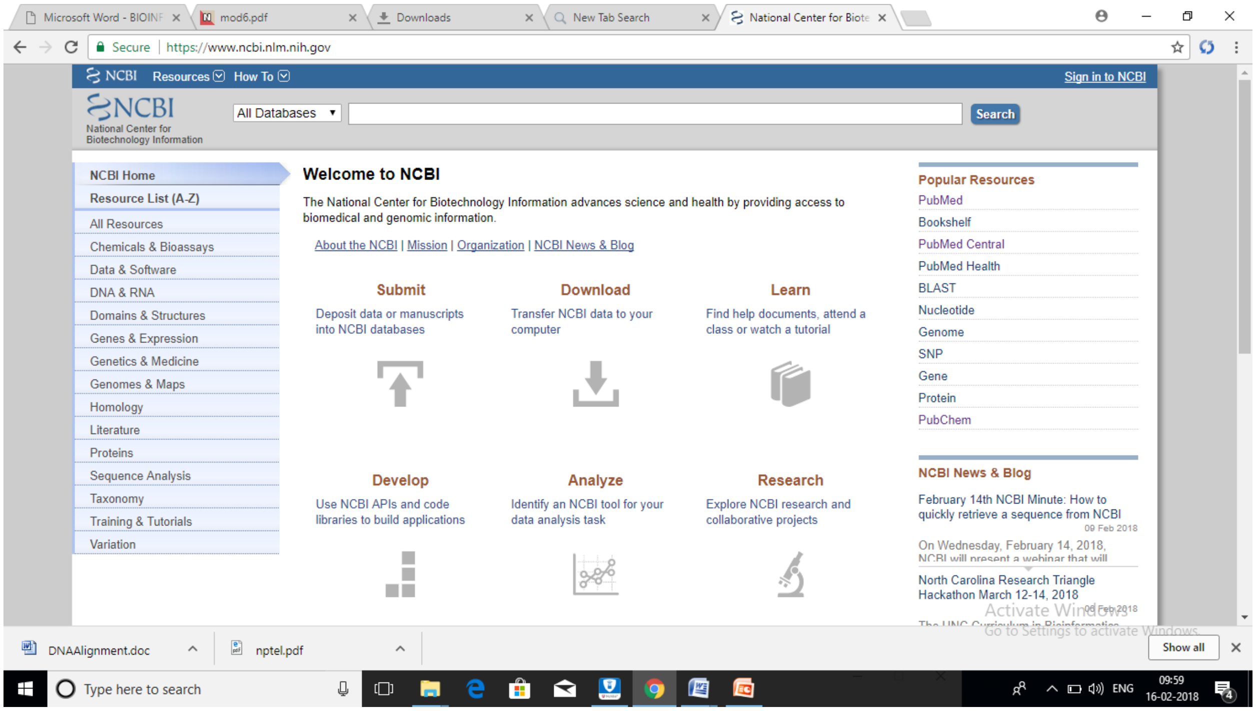
III B.SC BC.BT.C

S.No	Regd.No	Name Of The Student	No. of classes
1.	18407001	B.VYUHITHA	50
2.	18407003	K.SUMA SWARAJYA LAKSHMI	50
3.	18407005	P.SRAVANI	50
4.	18407006	P.LOKAPAVANI	50
5.	18407008	T.VENUSRI	50

III B.SC BT.B.C

.S.No	Regd.No	Name Of The Student	Marks
6	18405014	U.JAYA LAKSHMI	50
7	18405011	N.PAVANI	40
8.	18405010	N.SRAVANI	38
9.	18405007	G.GAYATHRI	40
10.	18405004	CH.SWARNALATHA	40
11.	18405012	P.RADHIKA	45
12.	18408010	K.HARIKA	40

Supporting Material
Soft wares/Platforms used



NCBI Home
Resource List (A-Z)
All Resources
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Genes & Expression
Genetics & Medicine
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Taxonomy
Training & Tutorials
Variation

Welcome to NCBI

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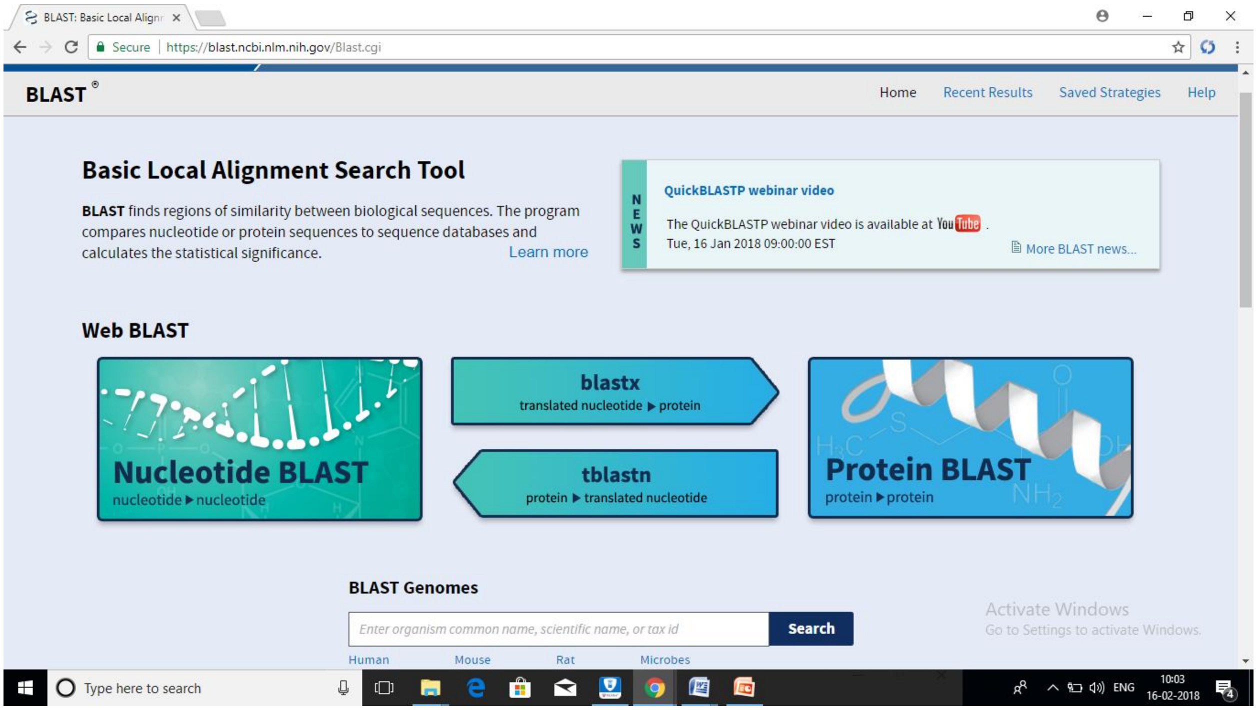
BLAST
Nucleotide
Genome
SNP
Gene
Protein
PubChem

NCBI News & Blog

February 14th NCBI Minute: How to quickly retrieve a sequence from NCBI
09 Feb 2018
On Wednesday, February 14, 2018, NCBI will present a webinar that will

North Carolina Research Triangle Hackathon March 12-14, 2018
08 Feb 2018
The UNC Curriculum in Bioinformatics

Activate Windows
Go to Settings to activate Windows.



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

Web BLAST

Nucleotide BLAST
nucleotide ▸ nucleotide

blastx
translated nucleotide ▸ protein

tblastn
protein ▸ translated nucleotide

Protein BLAST
protein ▸ protein

BLAST Genomes

Enter organism common name, scientific name, or tax id | Search

Human Mouse Rat Microbes

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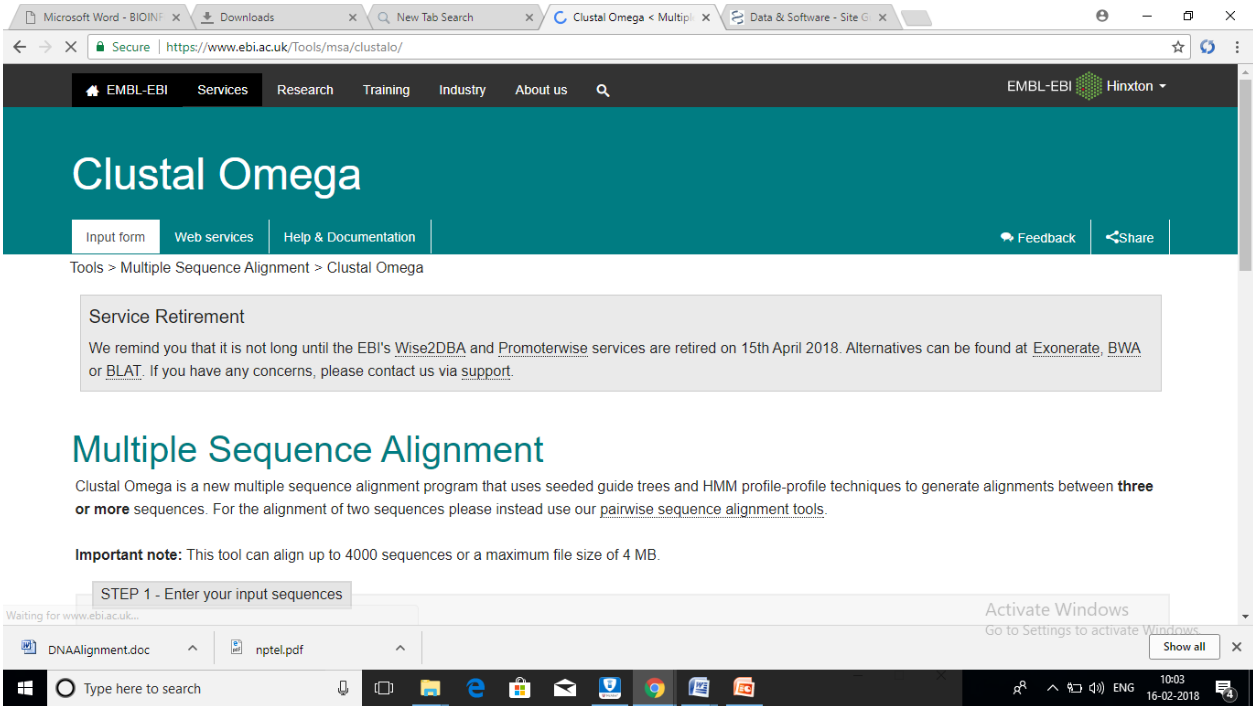


Clustal Omega

Tools > Multiple Sequence Alignment > Clustal Omega

Service Retirement

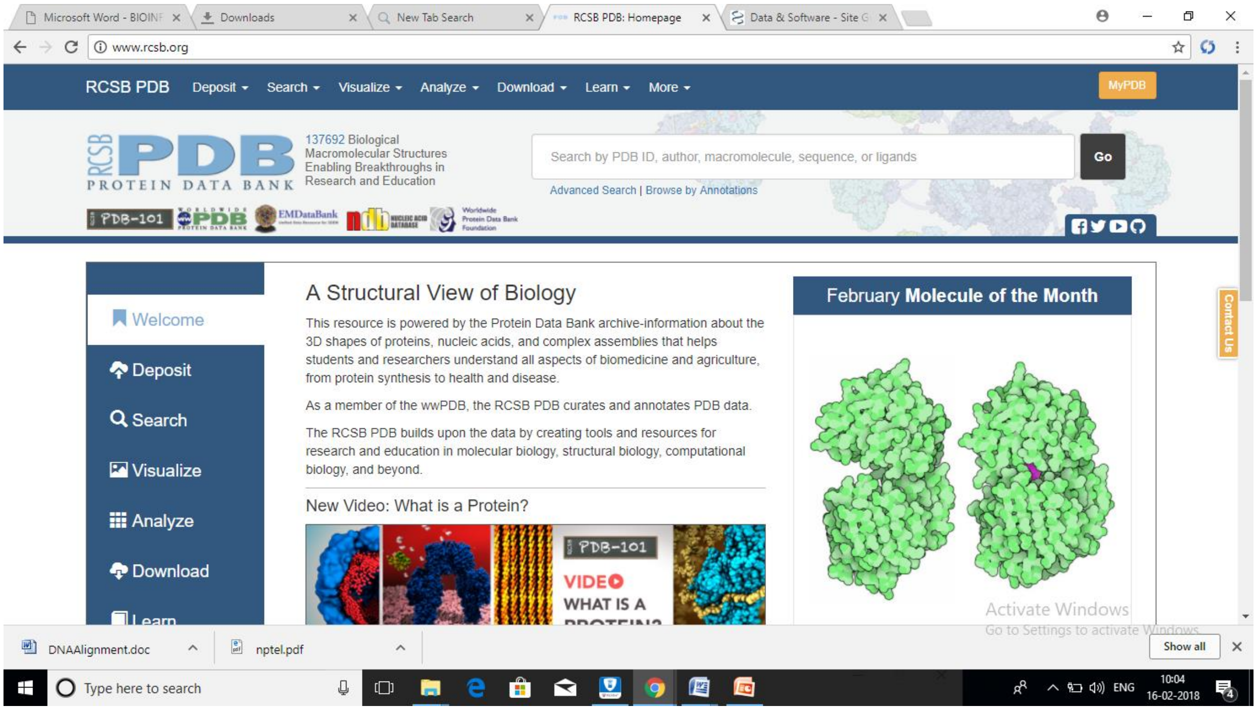
We remind you that it is not long until the EBI's Wise2DBA and Promoterwise services are retired on 15th April 2018. Alternatives can be found at Exonerate, BWA or BLAT. If you have any concerns, please contact us via support.

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

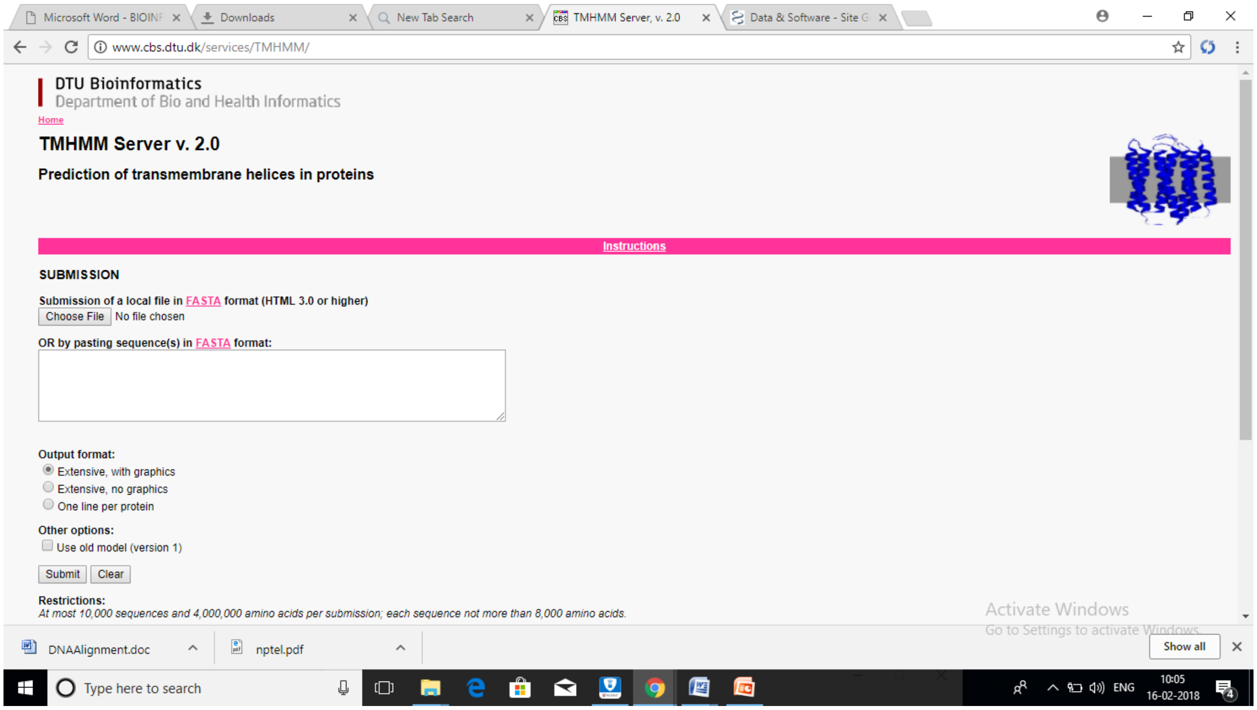
This resource is powered by the Protein Data Bank archive-information about the 3D shapes of proteins, nucleic acids, and complex assemblies that helps students and researchers understand all aspects of biomedicine and agriculture, from protein synthesis to health and disease.

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**



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

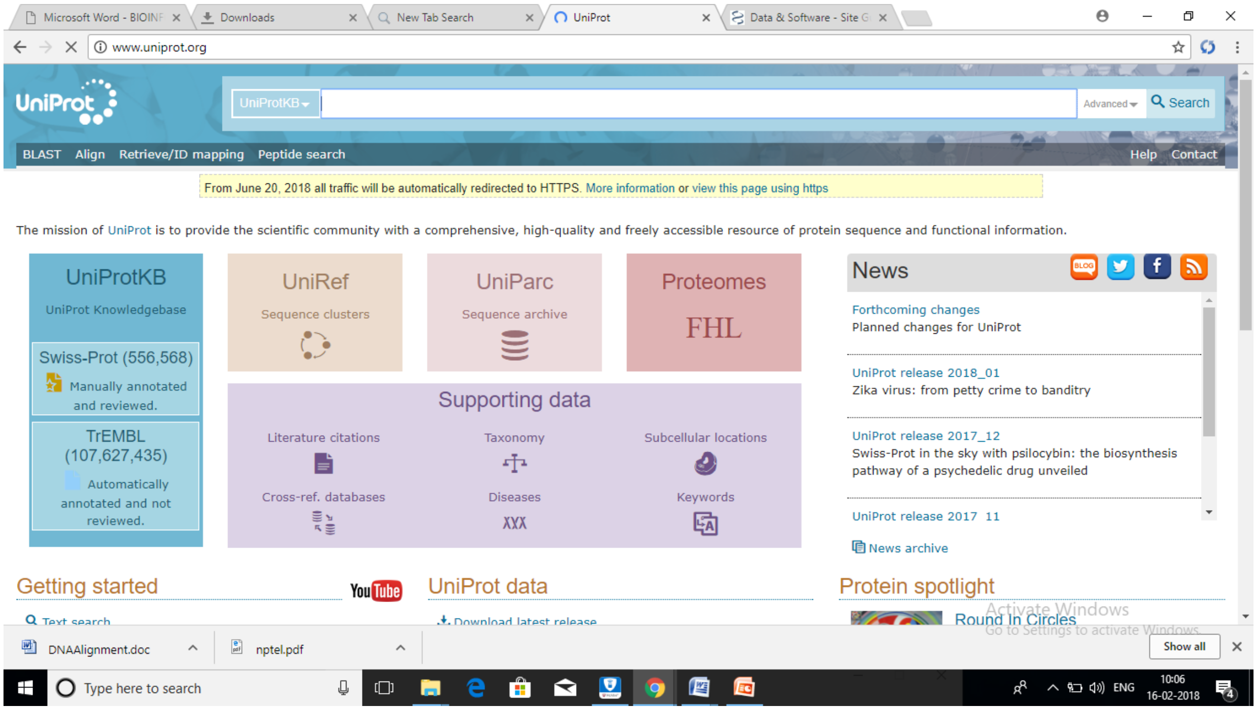
○ One line per protein

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.

Swiss-Prot (556,568)
Manually annotated and reviewed.

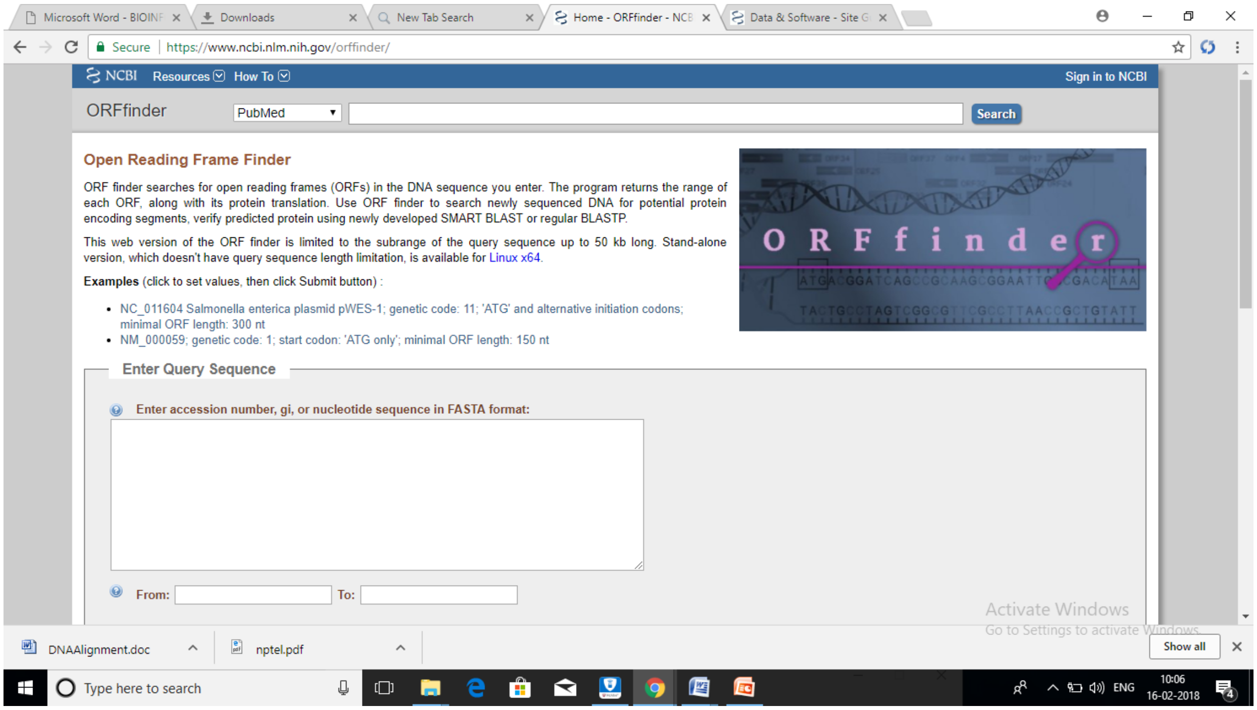
TrEMBL (107,627,435)
Automatically annotated and not reviewed.

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.

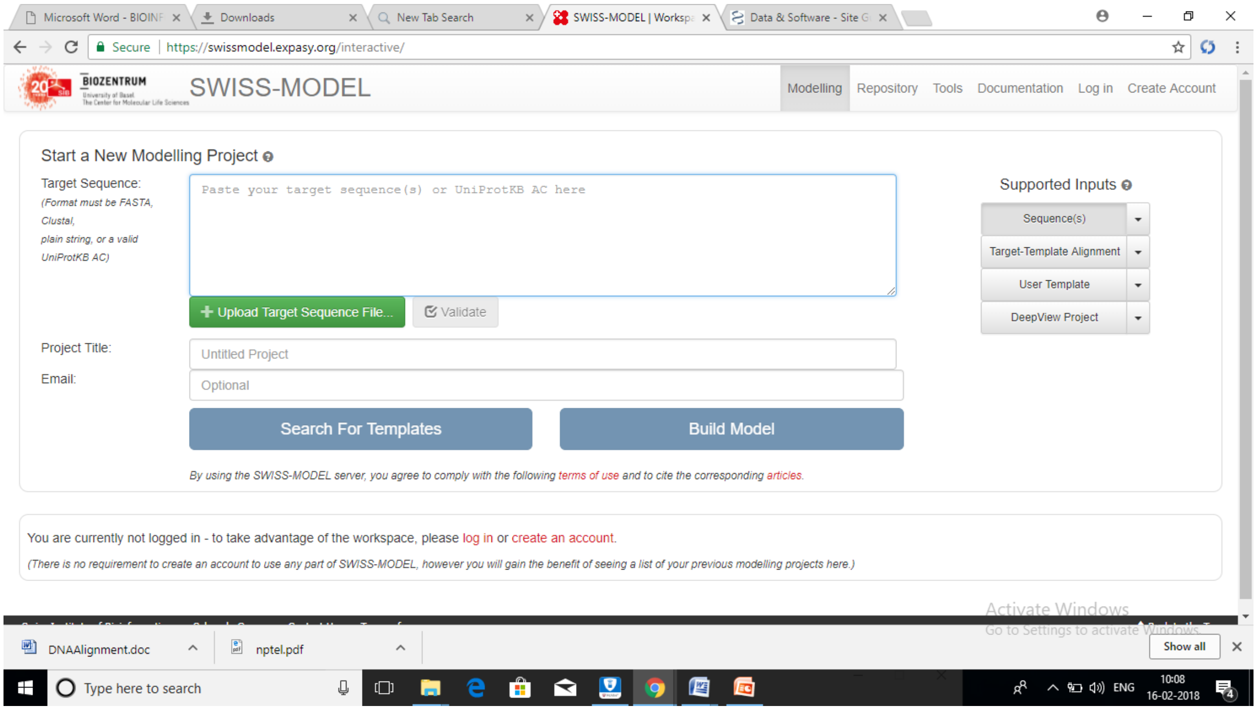
Examples (click to set values, then click Submit button) :

- 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

Enter Query Sequence

Enter accession number, gi, or nucleotide sequence in FASTA format:

From: **To:**



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`

Supported Inputs

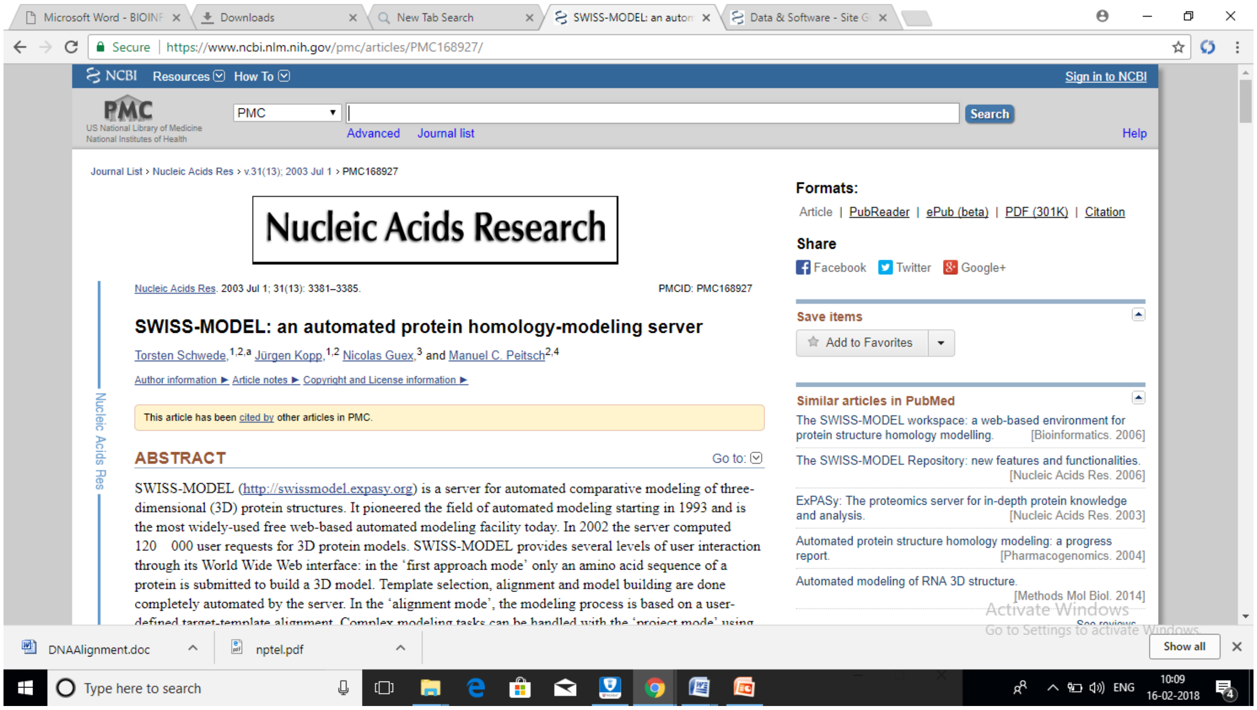
Project Title: Untitled Project

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.)



Journal List > Nucleic Acids Res > v.31(13); 2003 Jul 1 > PMC168927

Nucleic Acids Research

Nucleic Acids Res. 2003 Jul 1; 31(13): 3381–3385.   PMCID: PMC168927

SWISS-MODEL: an automated protein homology-modeling server

Torsten Schwede,[1,2,a] Jürgen Kopp,[1,2] Nicolas Guex,[3] and Manuel C. Peitsch[2,4]

Author information ► Article notes ► Copyright and License information ►

This article has been cited by other articles in PMC.

ABSTRACT   Go to:

SWISS-MODEL (http://swissmodel.expasy.org) is a server for automated comparative modeling of three-dimensional (3D) protein structures. It pioneered the field of automated modeling starting in 1993 and is the most widely-used free web-based automated modeling facility today. In 2002 the server computed 120 000 user requests for 3D protein models. SWISS-MODEL provides several levels of user interaction through its World Wide Web interface: in the 'first approach mode' only an amino acid sequence of a protein is submitted to build a 3D model. Template selection, alignment and model building are done completely automated by the server. In the 'alignment mode', the modeling process is based on a user-defined target-template alignment. Complex modeling tasks can be handled with the 'project mode' using

Formats:

Article | PubReader | ePub (beta) | PDF (301K) | Citation

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The SWISS-MODEL workspace: a web-based environment for protein structure homology modelling. [Bioinformatics. 2006]

The SWISS-MODEL Repository: new features and functionalities. [Nucleic Acids Res. 2006]

ExPASy: The proteomics server for in-depth protein knowledge and analysis. [Nucleic Acids Res. 2003]

Automated protein structure homology modeling: a progress report. [Pharmacogenomics. 2004]

Automated modeling of RNA 3D structure. [Methods Mol Biol. 2014]

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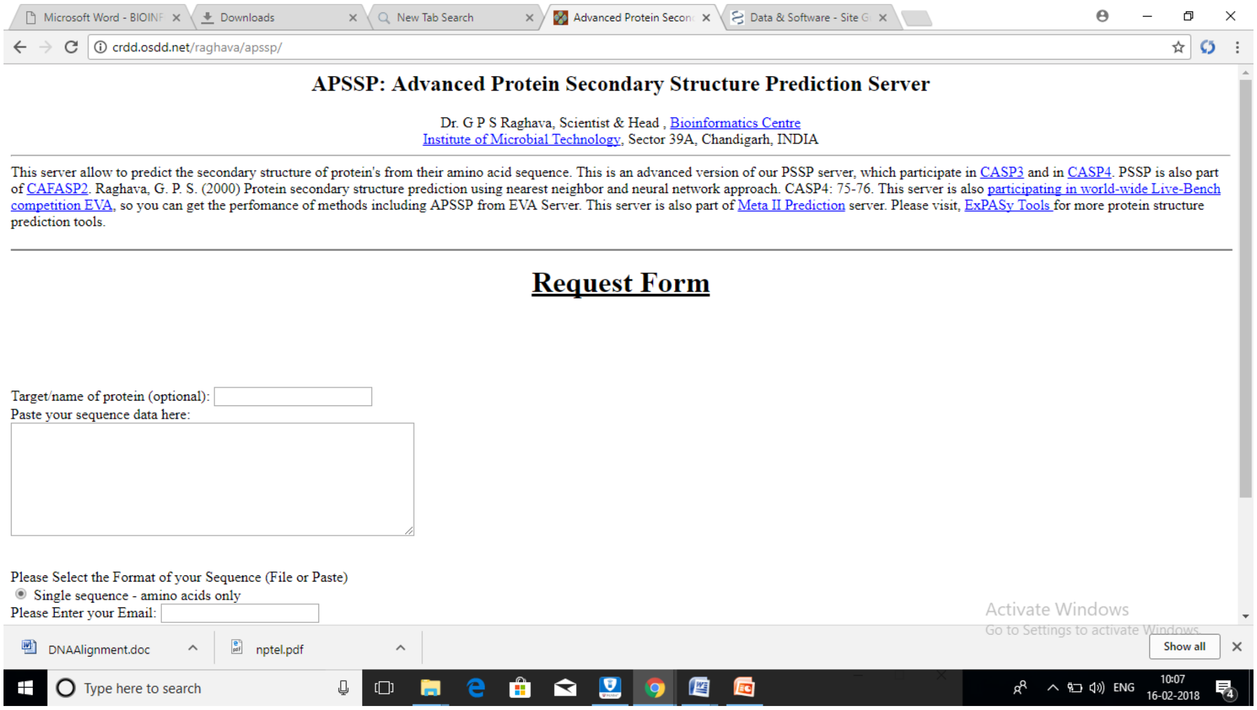

APSSP: Advanced Protein Secondary Structure Prediction Server

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:

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Go to Settings to activate Windows.

STUDENTS EVALUATION

Students were evaluated by Online Practical exam

- 10 Marks for each step
- Students were given Accession no. of various proteins
- Students were asked to paste the results in word document sequentially

List of Questions

1. Analyze the relationship between enzymes and their substrates to determine specificity and catalytic efficiency.
2. Utilize UNIPROT to identify and characterize proteins associated with provided accession numbers.
3. Conduct secondary structural analysis of specified proteins using SOPMA and PROTPARAM tools.
4. Locate the corresponding PDB entries for given accession numbers to access structural data.
5. Employ SWISS-MODEL, an online modeling tool, to generate protein models based on provided accession numbers.

CERTIFICATE OF THE CERTIFICATE COURSE

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 "COMPUTATIONAL BIOLOGY" conducted by the Department of Biotechnology from 30-03-2021 to 10-04-2021.

Course Coordinator
Dept. of Biotechnology

Estd. 1942

PRINCIPAL
Govt. College for
Women(A), Guntur