Bioinformatics Tools Assignment

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Program: BS 7th (M)
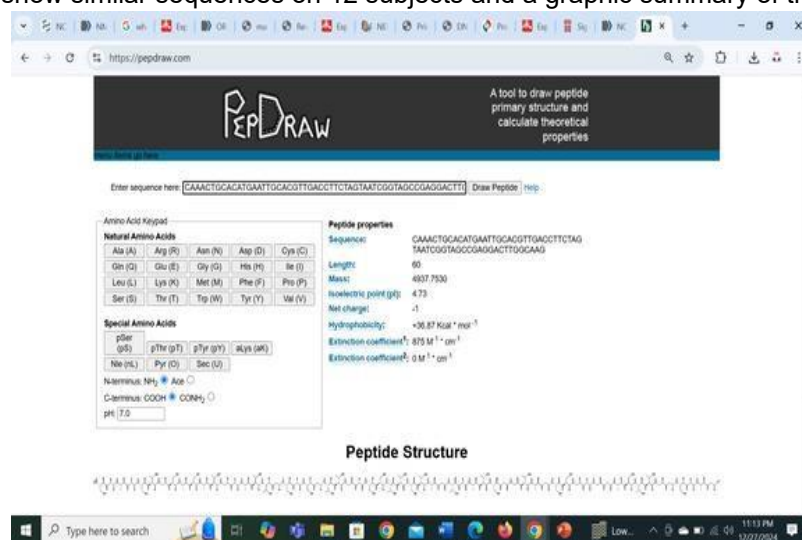
Reg: 04032213027

DNA Sequence Used

CAAACTGCACATGAATTGCACGTTGACCTTCTAGTAATCGGTAGCCGAGGACTTGGC
AAGATTAAAAGGGCTTTCTTGGGTAGTGTGAGCGACTATTGTGCTCATCATGTGCAA
TGTCCTATTCTCATTGTGAAGCCACCCAAGGAAAACCCCAAAAGCAGCTAATTAAC
AAGGATATATCATGTGCCAGTCTATGAACAATGTCATTTACTTGATGATGAATAAAC
ACAAGTTCATTGAGGATTATAAAACTTATGTATATATTAATTATATTATCAATAAAT
GGAGGTTGTATCTGTTGTCTCAATAGCTAGCCCAGTCCACAGGCAATAGGTTTTTGG
GTAAAAGCCAGTCGTCACAACTAGTGCAATCTGAATATTTGACCCTCATTCCTCTGG
TAACGCAAGTTGCTGCAGCTTATGTGGCTCTGTATTTGGTTTTAATAAATATAACAA
TTCAAATTAGAGATATCTAGCACTTCAACCTCGATGGAACAAA
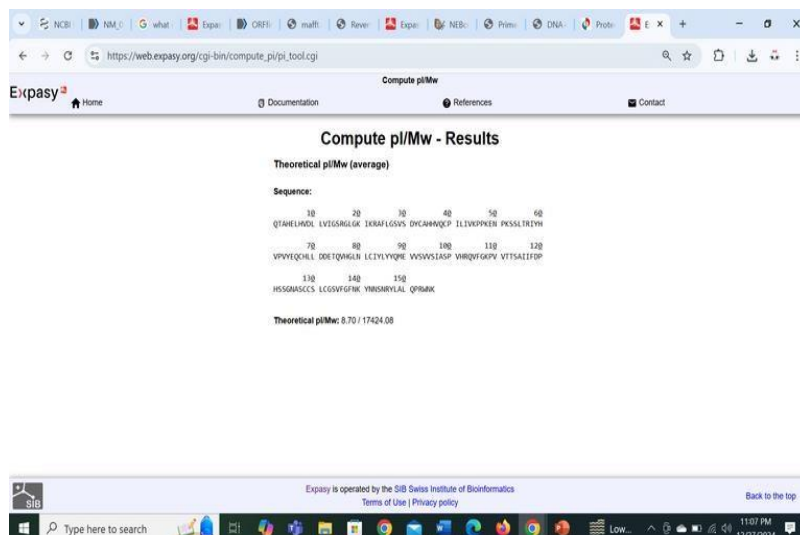
BLAST

BLAST results show similar sequences on 12 subjects and a graphic summary of the top hits.
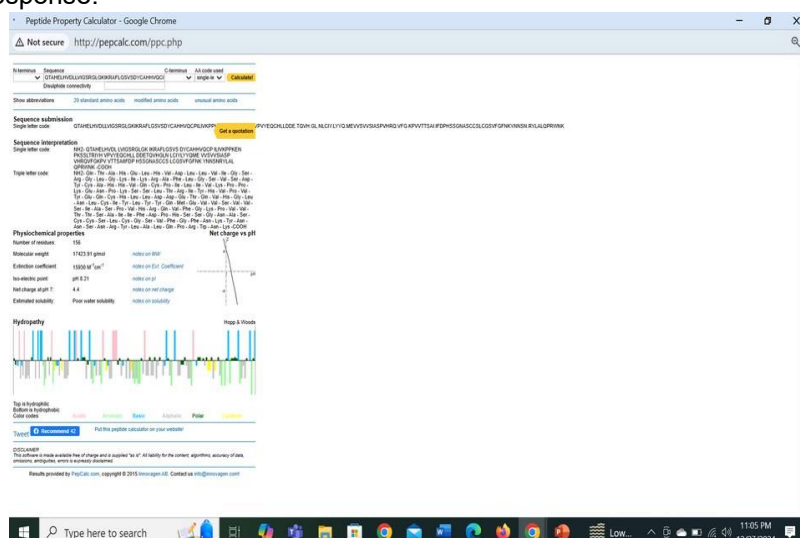

Hydropathy Plot

The hydropathy plot, which shows the hydrophobicity of amino acids on protein sequence.

PEP DRAW & Reverse Complement

This is structure of peptide from my sequence and I found reverse compliment of my sequence.

ORF Finder & Signal P 4.1

The analysis shows four potential open reading frames, with the largest spanning 182-391 nucleotides, and predicts a signal peptide with a cleavage site between positions 16 and 17.

Compute pI/Mw - Results

Theoretical pI/Mw (average)

Sequence:
```
        10         20         30         40         50         60
QTAHELHVDL LVIGSRGLGK IKRAFLGSVS DYCAHHVQCP ILIVKPPKEN PKSSLTRIYH

        70         80         90        100        110        120
VPVYEQCHLL DDETQVHGLN LCIYLYVQME VVSVVSIASP VHRQVFGKPV VTTSAIIFDP

       130        140        150
HSSGNASCCS LCGSVFGFNK YNNSNRYLAL QPR&NK
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Theoretical pI/Mw: 8.70 / 17424.08

Conserved Domain (CDD)

The analysis identified a conserved domain, HUP A, in the input sequence, suggesting a potential role in stress response.

DNA Stats

The analysis shows that the 498 bp linear sequence has 38% GC content and 62% AT content and can be cut by 19 different restriction enzymes, including both frequent and rare cutters.

Expasy Translate Tool

The Expasy Translate tool translated the nucleotide sequence into six possible protein sequences based on different reading frames.

Primer 3 & Transcription/Translation

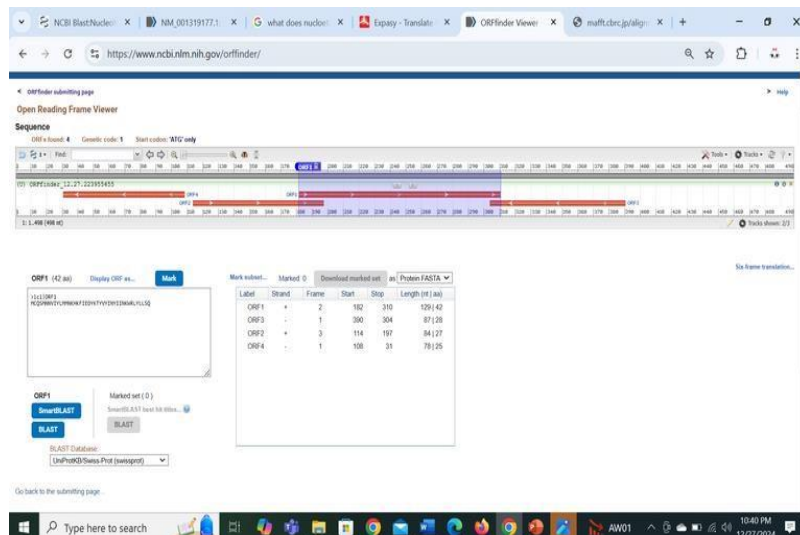It shows primer pairs, pair 1 is good pair and below I use Transcription and translation tool to analyze Amino Acid sequence from DNA Sequence.

Expasy Compute pI/Mw (ProtParam)

The Expasy Compute pI/Mw tool calculated the (pI) of the protein : 8.70 and (Mw) to be 17424.08 Da.

Additional Bioinformatics Tools

STRING Tool

The STRING tool is used to predict protein–protein interaction networks, helping to understand functional associations between proteins derived from the analyzed sequence.

CELLO Tool

The CELLO tool predicts the subcellular localization of proteins based on their amino acid composition, providing insight into where the translated protein may function inside the cell.

RNAfold Tool

The RNAfold tool predicts the secondary structure of RNA sequences using minimum free energy models, helping to understand RNA stability and folding patterns derived from the DNA sequence.