

Bioinformatics project

Submitted to: Dr. Samina Shakeel

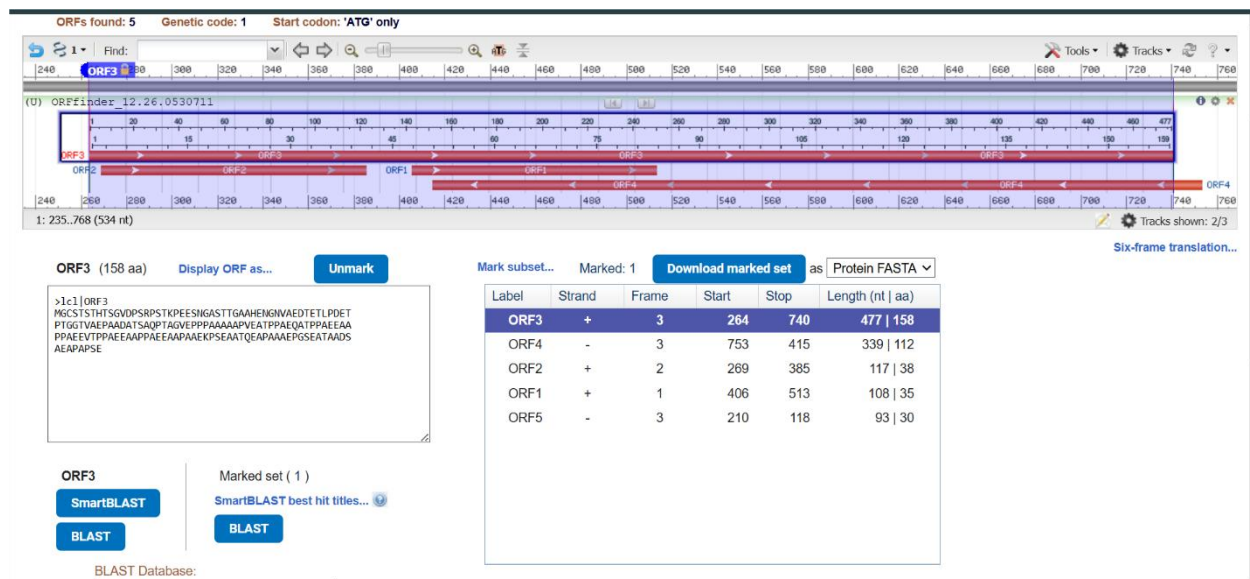
Submitted by: Sayeda Zahra Batool

Department: Biochemistry Bs 7th Morning

Task No: 3

Protein Analysis:

Conversion of mRNA into Protein:



Protein Sequence:

I took that from the above tool.

MGCSTSTHTSGVDPSRPSTKPEESNGASTTGAAHENGNAEDTETLPDET
PTGGTVAEPAADATSAQPTAGVEPPPPAAAAAPVEATPPAEQATPPAEEAA
PPAEVTPPAEEAAPPAAEEAAPAAEKPSEAATQEAPAAAEPGSEATAADS
AEAPAPSE

ProtParam:

Following shows the physical properties of protein.

[\[Documentation / Reference\]](#)

Number of amino acids: 158

Theoretical pI: 3.71

Molecular weight: 15162.91

Amino acid composition:

CSV format

Ala (A)	42	26.6%
Arg (R)	1	0.6%
Asn (N)	3	1.9%
Asp (D)	5	3.2%
Cys (C)	1	0.6%
Gln (Q)	3	1.9%
Glu (E)	25	15.8%
Gly (G)	9	5.7%
His (H)	2	1.3%
Ile (I)	0	0.0%
Leu (L)	1	0.6%
Lys (K)	2	1.3%
Met (M)	1	0.6%
Phe (F)	0	0.0%
Pro (P)	27	17.1%
Ser (S)	12	7.6%
Thr (T)	18	11.4%
Trp (W)	0	0.0%
Tyr (Y)	0	0.0%
Val (V)	6	3.8%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%

Extinction coefficients:

This protein does not contain any Trp residues. Experience shows that this could result in more than 10% error in the computed extinction coefficient. Extinction coefficients are in units of $M^{-1} cm^{-1}$, at 280 nm measured in water.

Ext. coefficient 0
Abs 0.1% (=1 g/l) 0.000, assuming all pairs of Cys residues form cystines

Ext. coefficient 0
Abs 0.1% (=1 g/l) 0.000, assuming all Cys residues are reduced

Estimated half-life:

The N-terminal of the sequence considered is M (Met).
The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).
>20 hours (yeast, in vivo).
>10 hours (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 65.42
This classifies the protein as unstable.

Aliphatic index: 40.06

Grand average of hydropathicity (GRAVY): -0.663

InterPro:

Shows the domain and family.



Function of that protein:

The primary function of this protein is to regulate muscle contraction. It works together with the Troponin complex on the actin filaments. When the muscle is at rest, Tropomyosin blocks the

binding sites, and when the muscle needs to contract, it moves to allow interaction between actin and myosin.