ProtParam

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User-provided sequence:

```
10 20 30 40 50 60
MTKSNGEEPK MGGRMERFQQ GVRKRTLLAK KKVQNITKED VKSYLFRNAF VLLTVTAVIV

70 80 90 100
GTILGFTLRP YRMSYREVKY FSFPGELLMR MLQMLVLPLI I
```

References and documentation are available.

```
Number of amino acids: 101
Molecular weight: 11762.17
```

Theoretical pI: 10.48

```
Amino acid composition: CSV format
Ala (A)
         3
                  3.0%
Arg (R)
         9
                  8.9%
Asn (N)
         3
                  3.0%
                  1.0%
Asp (D)
         1
                  0.0%
         0
Cys (C)
Gln (Q)
         4
                  4.0%
Glu (E)
          6
                  5.9%
Gly (G)
         7
                  6.9%
His (H)
                  0.0%
         0
Ile (I)
         5
                 5.0%
Leu (L)
        13
                12.9%
         9
                 8.9%
Lys (K)
Met (M)
         7
                  6.9%
Phe (F)
         6
                  5.9%
Pro (P)
         4
                  4.0%
Ser (S)
         4
                  4.0%
Thr (T)
         7
                  6.9%
Trp (W)
         0
                  0.0%
Tyr (Y)
          4
                  4.0%
Val (V)
          9
                  8.9%
Pyl (0)
          0
                  0.0%
Sec (U)
                  0.0%
      0
                  0.0%
 (B)
       0
                  0.0%
 (Z)
 (X)
       0
                  0.0%
```

```
Total number of negatively charged residues (Asp + Glu): 7
Total number of positively charged residues (Arg + Lys): 18
```

Atomic composition:

Carbon	С	535
Hydrogen	Н	880
Nitrogen	N	144
0xygen	0	138
Sulfur	S	7

Formula: $C_{535}H_{880}N_{144}O_{138}S_7$ Total number of atoms: 1704

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<sup>-1</sup> cm<sup>-1</sup>, at 280 nm measured in water.

Ext. coefficient 5960
Abs 0.1% (=1 g/l) 0.507

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 37.08
This classifies the protein as stable.

Aliphatic index: 98.32

Grand average of hydropathicity (GRAVY): -0.019
```



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